

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
3 January 2003 (03.01.2003)

PCT

(10) International Publication Number
WO 03/000898 A1

(51) International Patent Classification⁷: **C12N 15/29**,
15/82, C12Q 1/68, A01H 5/00, G06F 17/00, C07K 14/415

(21) International Application Number: PCT/IB01/01105

(22) International Filing Date: 22 June 2001 (22.06.2001)

(25) Filing Language: English

(26) Publication Language: English

(71) Applicant (for all designated States except US): **SYNGENTA PARTICIPATIONS AG** [CH/CH]; Schwarzwaldallee 215, CH-4058 Basel (CH).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **CHANG, Hur-Song** [CN/US]; Torrey Mesa Research Institute, 3115 Merryfield Row, San Diego, CA 92121 (US). **CHEN, Wenqiong** [CN/US]; Torrey Mesa Research Institute, 3115 Merryfield Row, San Diego, CA 92121 (US). **COOPER, Bret** [US/US]; Torrey Mesa Research Institute, 3115 Merryfield Row, San Diego, CA 92121 (US). **GLAZEBROOK, Jane** [US/US]; Torrey Mesa Research Institute, 3115 Merryfield Row, San Diego, CA 92121 (US). **GOFF, Stephen, Arthur** [US/US]; Torrey Mesa Research Institute, 3115 Merryfield Row, San Diego, CA 92121 (US). **HOU, Yu-Ming** [CN/US]; Torrey Mesa Research Institute, 3115 Merryfield Row, San Diego, CA 92121 (US). **KATAGIRI, Fumiaki** [JP/US]; Torrey Mesa Research Institute, 3115 Merryfield Row, San Diego, CA 92121 (US). **QUAN, Sheng** [CN/US]; Torrey Mesa Research Institute, 3115 Merryfield Row, San Diego, CA 92121 (US). **TAO, Yi** [CN/US]; Torrey Mesa Research Institute, 3115 Merryfield Row, San Diego, CA 92121 (US). **WHITHAM, Steve**

[US/US]; 4025 Berkshire Avenue, Ames, IA 50010 (US). **XIE, Zhiyi** [CN/US]; Apartment 225, 8933 Lombard Place, San Diego, CA 92122 (US). **ZHU, Tong** [CN/US]; Torrey Mesa Research Institute, 3115 Merryfield Row, San Diego, CA 92121 (US). **ZOU, Guangzhou** [CN/US]; Torrey Mesa Research Institute, 3115 Merryfield Row, San Diego, CA 92121 (US).

(74) Agent: **BASTIAN, Werner**; c/o Syngenta Participations AG, Intellectual Property, P.O. Box, CH-4002 Basel (CH).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

- with international search report
- with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: PLANT GENES INVOLVED IN DEFENSE AGAINST PATHOGENS

(57) Abstract: Methods to identify genes, the expression of which are altered in response to pathogen infection, are provided, as well as the genes identified thereby and their corresponding promoters.

WO 03/000898 A1

PLANT GENES INVOLVED IN DEFENSE AGAINST PATHOGENS

Cross-Reference to Related Applications

This application claims the benefit of the filing date of U.S. application Serial No. 60/213,634, filed on June 23, 2000, U.S. application Serial No. 60/214,926, filed on June 23, 2000, U.S. application Serial No. 60/261,320, filed on January 12, 2001, U.S. application Serial No. 60/264,353, filed on January 26, 2001, and U.S. application Serial No. 60/273,879, filed on March 7, 2001 under 35 U.S.C. § 119(e).

Field of the Invention

The present invention generally relates to the field of plant molecular biology, and more specifically to the regulation of gene expression in plants in response to pathogen exposure.

Background of the Invention

Plants are capable of activating a large array of defense mechanisms in response to pathogen attack, some of which are preexisting and others are inducible. Pathogens must specialize to circumvent the defense mechanisms of the host, especially those biotrophic pathogens that derive their nutrition from an intimate association with living plant cells. If the pathogen can cause disease, the interaction is said to be compatible, but if the plant is resistant, the interaction is said to be incompatible. A crucial factor determining the success of these mechanisms is the speed of their activation. Consequently, there is considerable interest in understanding how plants recognize pathogen attack and control expression of defense mechanisms.

Some potential pathogens trigger a very rapid resistance response called gene-for-gene resistance. This occurs when the pathogen carries an avirulence (*avr*) gene that triggers specific recognition by a corresponding host resistance (*R*) gene. *R* gene specificity is generally quite narrow, in most cases only pathogens carrying a particular *avr* gene are recognized. Recognition is thought to be mediated by ligand-receptor binding. *R* genes have been studied extensively in recent years. For a review of *R* genes, see Ellis et al. (1998); Jones et al. (1997); and Ronald (1998).

One of the defense mechanisms triggered by gene-for-gene resistance is programmed cell death at the infection site. This is called the hypersensitive response, or HR. Pathogens that induce the HR, or cause cell death by other means, activate a systemic resistance response

called systemic acquired resistance (SAR). During SAR, levels of salicylic acid (SA) rise throughout the plant, defense genes such as pathogenesis related (PR) genes are expressed, and the plant becomes more resistant to pathogen attack. SA is a crucial component of this response. Plants that cannot accumulate SA due to the presence of a transgene that encodes an SA-degrading enzyme (*nahG*), develop a HR in response to challenge by avirulent pathogens, but do not exhibit systemic expression of defense genes and do not develop resistance to subsequent pathogen attack (Ryals et al., 1996). The nature of the systemic signal that triggers SAR is a subject of debate (Shulaev et al., 1995; Vernooji et al., 1994). SA clearly moves from the site of the HR to other parts of the plant, but if this is the signal, it must be effective at extremely low concentration (Willitset et al., 1998).

SAR is quite similar to some reactions that occur locally in response to attack by virulent (those that cause disease) or avirulent (those that trigger gene-for-gene resistance) pathogens. In general, activation of defense gene expression occurs more slowly in response to virulent pathogens than in response to avirulent pathogens. Some pathogens trigger expression of defense genes through a different signaling pathway that requires components of the jasmonic acid (JA) and ethylene signaling pathways (Creelman et al., 1997).

One approach to understanding the signal transduction networks that control defense mechanisms is to use genetic methods to identify signaling components and determine their roles within the network. Considerable progress has been made using this approach in *Arabidopsis*-pathogen model systems.

R gene signal transduction

Genes such as *NDR1* and *EDS1*, as well as *DND1* and the lesion-mimic genes, likely act in signal transduction pathways downstream from *R-avr* recognition. *NDR1* and *EDS1* are required for gene-for-gene mediated resistance to avirulent strains of the bacterial pathogen *Pseudomonas syringae* and the oomycete pathogen *Peronospora parasitica*. Curiously, *ndr1* mutants are susceptible to one set of avirulent pathogens, whereas *eds1* mutants are susceptible to a non-overlapping set (Aarts et al., 1998). The five cloned *R* genes that require *EDS1* all belong to the subset of the nucleotide binding site-leucine rich repeat (NBS-LRR) class of *R* genes that contain sequences similar to the cytoplasmic domains of *Drosophila* Toll and mammalian interleukin 1 transmembrane receptors (TIR-NBS-LRR). The two genes that require *NDR1* belong to the leucine-zipper (LZ-NBS-LRR) subclass of NBS-LRR genes. There is another LZ-NBS-LRR gene, *RPP8*, that does not require *EDS1* or *NDR1*, so the correlation between *R* gene structure and requirement for *EDS1* or *NDR1* is not perfect.

Nevertheless, these results show that *R* genes differ in their requirements for downstream factors and that these differences are correlated with *R* gene structural type.

NDR1 encodes a protein with two predicted transmembrane domains (Century et al. 1997). *RPM1*, which requires *NDR1* to mediate resistance, is membrane-associated, despite the fact that its primary sequence does not include any likely membrane-integral stretches (Boyes et al., 1998). It is possible that part of the function of *NDR1* is to hold *R* proteins close to the membrane. *EDS1* encodes a protein with blocks of homology to triacyl glycerol lipases (Falk et al., 1999). The significance of this homology is not known, but it is tempting to speculate that *EDS1* is involved in synthesis or degradation of a signal molecule. *EDS1* expression is inducible by SA and pathogen infection, suggesting that *EDS1* may be involved in signal amplification (Falk et al., 1999).

It has been extremely difficult to isolate mutations in genes other than the *R* genes that are required for gene-for-gene resistance. A selection procedure was devised (McNellis et al., 1998) on the basis of precisely controlled inducible expression of the *avr* gene *avrRpt2* in plants carrying the corresponding resistance gene *RPS2*. Expression of *avrRpt2* in this background is lethal, as it triggers a systemic HR. It is now possible to select for mutants with subtle defects in gene-for-gene signaling by requiring growth on a concentration of inducer slightly higher than the lethal dose.

Putative plant receptor proteins encoded by *RPP* genes (recognition of *P. parasitica*) mediate specific recognition of *Peronospora* isolates and trigger defense reactions. Recently, McDowell et al. (2000) reported that two members of this class, *RPP7* and *RPP8* (the latter of which encodes a LZ-NBS-LRR type R protein) were not significantly suppressed by mutations in either *EDS1* or *NDR1*, and that *RPP7* resistance was also not compromised by mutations in *EIN2*, *JAR1* or *COI1*, which affect ethylene or jasmonic acid signaling, or in *coil/npr1* or *coil/NahG* backgrounds. The authors suggested that *RPP7* initiates resistance through a novel signaling pathway that is independent of salicylic acid accumulation or jasmonic acid response components.

SA-dependent signaling

SA levels increase locally in response to pathogen attack, and systemically in response to the SAR-inducing signal. SA is necessary and sufficient for activation of PR gene expression and enhanced disease resistance. Physiological analyses and characterization of certain lesion-mimic mutants strongly suggest that there is a positive autoregulatory loop affecting SA concentrations (Shirasu et al., 1997; Hunt et al., 1997; Weymann et al., 1995).

Several mutants with defects in SA signaling have been characterized. These include *npr1*, in which expression of *PR* genes in response to SA is blocked; *cpr1*, *cpr5*, and *cpr6*, which constitutively express *PR* genes; the *npr1* suppressor *ssil*; *pad4*, which has a defect in SA accumulation; and *eds5*, which has a defect in *PR1* expression.

5 Expression of the defense genes *PR1*, *BG2*, and *PR5* in response to SA treatment requires a gene called *NPR1* or *NIM1*. Mutations in *npr1* abolish SAR, and cause enhanced susceptibility to infection by various pathogens (Cao et al., 1994; Delaney et al., 1995; Glazebrook et al., 1996; Shah et al., 1997). *NPR1* appears to be a positive regulator of *PR* gene expression that acts downstream from SA. *NPR1* encodes a novel protein that contains
10 ankyrin repeats (which are often involved in protein-protein interactions (Cao et al., 1997; Ryals et al., 1997), and that is localized to the nucleus in the presence of SA (Dong et al., 1998). Consequently, it is unlikely that *NPR1* acts as a transcription factor to directly control *PR* gene expression, but its nuclear localization suggests that it may interact with such transcription factors.

15 *PAD4* appears to act upstream from SA. In *pad4* plants infected with a virulent *P. syringae* strain, SA levels, synthesis of the antimicrobial compound camalexin, and *PR1* expression are all reduced (Zhou et al., 1998). SA is necessary, but not sufficient, for activation of camalexin synthesis (Zhou et al., 1998; Zhao et al., 1996). The camalexin defect in *pad4* plants is reversible by exogenous SA (Zhou et al., 1998). Mutations in *pad4* do not
20 affect SA levels, camalexin synthesis, or *PR1* when plants are infected with an avirulent *P. syringae* strain (Zhou et al., 1998). Taken together, these results suggest that *PAD4* is required for signal amplification to activate the SA pathway in response to pathogens that do not elicit a strong defense response (Zhou et al., 1998).

JA-dependent signaling

25 JA signaling affects diverse processes including fruit ripening, pollen development, root growth, and response to wounding (Creelman et al., 1997). The *jar1* and *coi1* mutants fail to respond to JA (Feys et al., 1994; Staswick et al., 1992). *COI1* has been cloned, and found to encode protein containing leucine-rich repeats and a degenerate F-box motif (Xie et al., 1998). These features are characteristic of proteins that function in complexes that ubiquitinate
30 protein targeted for degradation.

 In the past few years it has become apparent that JA plays an important role in regulation of pathogen defenses. For example, the induction of the defensin gene *PDF1.2* after

inoculation of *Arabidopsis* with the avirulent pathogen *Alternaria brassicicola* does not require SA or NPR1, but does require ethylene and JA signaling (Penninck et al., 1996).

SA signaling and JA signaling pathways are interconnected in complicated ways. Studies in other systems have shown that SA signaling and JA signaling are mutually inhibitory (Creelman et al., 1997; Harms et al., 1998). However, synthesis of camalexin in response to *P. syringae* infection is blocked in *nahG* (Zhou et al., 1998; Zhao et al., 1996) and *coil* (Glazebrook, 1999) plants, strongly suggesting that camalexin synthesis requires both SA and JA signaling.

Induced systemic resistance (ISR)

Some rhizosphere-associated bacteria promote disease resistance (van Loon et al., 1998). This phenomenon, called ISR, has been studied using *Pseudomonas fluorescens* strain WCS417r to colonize *Arabidopsis* roots (Pieterse et al., 1996). Colonized plants are more resistant to infection by the fungal pathogen *Fusarium oxysporum* f sp *raphani* and *P. syringae* (Pieterse et al., 1996). ISR occurs in *nahG* plants, indicating that it is not a SA-dependent phenomenon (Pieterse et al., 1996). Rather, ISR appears to be JA- and ethylene-dependent. The observation that ethylene can induce ISR in *jarl* mutants led to the hypothesis that ISR requires a JA signal followed by an ethylene signal (Pieterse et al., 1998). No changes in gene expression associated with ISR have been detected (Pieterse et al., 1998), suggesting that it is different from activation of *PDF1.2* expression by *A. brassicicola*.

Curiously, ISR requires *NPR1* (Pieterse et al., 1996). This was unexpected in light of the fact that NPR1 was previously known to be involved only in SA-dependent processes and ISR is SA-independent. If the SA-dependent signal is received, NPR1 mediates a resistance response characterized by *PR1* expression, whereas if the ISR signal is received, NPR1 mediates a different resistance response. It is difficult to imagine how this could occur, unless NPR1 is interacting with different 'adapter' molecules to mediate the different signals. The ankyrin repeats found in NPR1 could function in protein-protein interactions between NPR1 and adapter proteins. Identification of proteins that interact with NPR1, and characterization of plants with loss-of-function mutations affecting those proteins, would be very helpful for understanding how NPR1 acts in each pathway. It would also be worthwhile to determine if the *ssi1* or *cpr6* mutations suppress the ISR defect of *npr1* mutants.

Relevance to disease resistance

Characterization of the effects of various mutations on resistance to different pathogens has revealed that there is considerable variation in the extent to which pathogens are affected

by defense mechanisms. SAR is known to confer resistance to a wide array of pathogens, including bacteria, fungi, oomycetes, and viruses. JA signaling is important for limiting the growth of certain fungal pathogens. In *Arabidopsis*, the SA pathway mutants *npr1* and *pad4* show enhanced susceptibility to *P. syringae* and *P. parasitica* (Cao et al., 1994; Delaney et al., 1995; Shah et al., 1997; Zhou et al., 1998; Glazebrook et al., 1997).

Overexpression of rate-limiting defense response regulators may cause the signaling network to respond faster or more strongly to pathogen attack, thereby improving resistance. For example, overexpression of *NPR1* caused increased resistance to *P. syringae* and *P. parasitica* in a dosage dependent manner (Cao et al., 1998). Moreover, *NPR1*-overexpression had no obvious deleterious effects on plant growth, in contrast to mutations that lead to constitutive overexpression of defense responses, which generally cause dwarfism.

Promoters for gene expression of plant pathogen defense genes

Promoters (and other regulatory components) from bacteria, viruses, fungi and plants have been used to control gene expression in plant cells. Numerous plant transformation experiments using DNA constructs comprising various promoter sequences fused to various foreign genes (for example, bacterial marker genes) have led to the identification of useful promoter sequences. It has been demonstrated that sequences up to 500-1,000 bases in most instances are sufficient to allow for the regulated expression of foreign genes. However, it has also been shown that sequences much longer than 1 kb may have useful features which permit high levels of gene expression in transgenic plants. The expression of genes encoding proteins that are useful for protecting plants from pathogen attack may have deleterious effects on plant growth if expressed constitutively. Consequently, it is desirable to have promoter sequences that control expression of these gene(s) in such a way that expression is absent or very low in the absence of pathogens, and high in the presence of pathogens.

Thus, what is needed is the identification of plant genes useful to confer resistance to a pathogen(s) and plant promoters, the expression of which is altered in response to pathogen attack.

Summary of the Invention

The invention generally provides an isolated nucleic acid molecule (polynucleotide) comprising a plant nucleotide sequence obtained or isolatable from a gene, the expression of which is altered, either increased or decreased, in response to pathogen infection. In one embodiment, the plant nucleotide sequence comprises an open reading frame, while in another

embodiment, the plant nucleotide sequence comprises a promoter. A promoter sequence of the invention directs transcription of a linked nucleic acid segment, e.g., a linked plant DNA comprising an open reading frame for a structural or regulatory gene, in a host cell, such as a plant cell, in response to pathogen infection of that cell. As used herein, a "pathogen" includes
5 bacteria, fungi, oomycetes, viruses, nematodes and insects, e.g., aphids (see Hammond-Kosack and Jones, 1997). Moreover, the expression of a plant nucleotide sequence of the invention comprising a promoter may be altered in response to one or more species of bacteria, nematode, fungi, oomycete, virus, or insect. Likewise, the expression of a plant nucleotide sequence of the invention comprising an open reading frame may be useful to confer tolerance
10 or resistance of a plant to one or more species of bacteria, nematode, fungi, oomycete, virus or insect.

The nucleotide sequence preferably is obtained or isolatable from plant DNA. In particular, the nucleotide sequence is obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%,
15 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-953 and 2137-2661 or a fragment (portion) thereof which encodes a partial length polypeptide having substantially the same activity of the full-length
20 polypeptide, a rice gene comprising one of SEQ ID NOs:2000-2129 or SEQ ID NOs:2662-6813, or a *Chenopodium* gene comprising one of SEQ ID NOs:1954-1966.

The present invention also provides an isolated nucleic acid molecule comprising a plant nucleotide sequence that directs transcription of a linked nucleic acid segment in a host cell, e.g., a plant cell. The nucleotide sequence preferably is obtained or isolatable from plant
25 genomic DNA. In particular the plant DNA is obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising
30 any one of SEQ ID NOs:1-953, a rice gene comprising one of SEQ ID NOs:2000-2129 or SEQ ID NOs:2662-4737, or a *Chenopodium* gene having any one of SEQ ID NOs:1954-1966, the expression of which is increased or decreased in response to pathogen infection. Preferred promoters comprise DNA obtained or isolatable from a gene encoding a polypeptide which is

substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising a promoter according to
5 SEQ ID NOs:2137-2661, a rice gene comprising a promoter according to SEQ ID NOs:4738-6813 or a fragment thereof (i.e., promoters isolatable from any one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813) which increases or decreases transcription of a linked nucleic acid segment in response to pathogen infection.

The invention also provides uses for an isolated nucleic acid molecule, e.g., DNA or
10 RNA, comprising a plant nucleotide sequence comprising an open reading frame encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis*, *Chenopodium* or
15 rice gene comprising an open reading frame comprising any one of SEQ ID NOs:1-953, 1954-1966, 2000-2129, 2662-4737, or the complement thereof. For example, these open reading frames may be useful to prepare plants that over- or under-express the encoded product or to prepare knockout plants.

The promoters and open reading frames of the invention can be identified by any
20 method. For example, they can be identified by employing an array of nucleic acid samples, e.g., each sample having a plurality of oligonucleotides, and each plurality corresponding to a different plant gene, on a solid substrate, e.g., a DNA chip, and probes corresponding to nucleic acid which is up- or down-regulated in response to pathogen infection in one or more ecotypes or species of plant relative to a control (e.g., a water control, nucleic acid from an
25 uninfected plant or nucleic acid from a mutant plant). Thus, genes that are upregulated or downregulated in response to pathogen infection can be systematically identified.

As described herein, GeneChip® technology was utilized to discover a plurality of genes, the expression of which is altered after pathogen infection. The *Arabidopsis* oligonucleotide probe array consists of probes from about 8,100 unique *Arabidopsis* genes,
30 which covers approximately one third of the genome. This genome array permits a broader, more complete and less biased analysis of gene expression. Using labeled cRNA probes, expression levels were determined by laser scanning and genes generally selected for expression levels that were > 2 fold over the control.

For example, using this approach, 953 genes were identified, the expression of which was altered after infection of wild-type *Arabidopsis* plants with a pathogen (SEQ ID NOs: 1-953). In addition, 745 genes were identified, the expression which was increased after infection of wild-type *Arabidopsis* with *Pseudomonas syringae* (SEQ ID NOs: 2-6, 8-13, 16, 18, 22-23, 25, 28-29, 31-32, 35-37, 39-43, 45-47, 49-50, 52, 54-55, 57-58, 60-66, 70-72, 74, 76-77, 79, 81, 83, 85, 87-90, 92, 94, 97, 100-107, 111-115, 117-125, 127-135, 138-140, 142-153, 156-158, 160, 162-165, 168-170, 173-181, 183-184, 186-188, 190-198, 200-201, 203-211, 214-215, 218-224, 227-232, 234-249, 251-262, 264, 266-268, 270, 272-275, 277-281, 283, 286-294, 297-298, 302, 304-306, 308-326, 328-339, 341, 344-345, 347, 350-351, 353-358, 361-371, 373-377, 379-386, 388-390, 392, 394-400, 402-406, 408-410, 412-417, 419-427, 429-433, 435-443, 445-452, 454-457, 459-460, 462-464, 466-470, 473-475, 478-479, 481-482, 484-187, 489-494, 496-498, 500-501, 503-506, 508, 510, 512-515, 517-523, 526, 528-529, 531-538, 540, 544-548, 550-558, 560, 563-568, 570, 572-577, 579-580, 582-585, 588-594, 596, 598-600, 602-603, 605-606, 608-612, 614-617, 619-624, 626-630, 632-639, 642, 644, 646-651, 653-657, 659-665, 667-671, 673-678, 681-689, 691-693, 695-713, 715-717, 719, 721-727, 729-733, 736-738, 740, 742, 744, 746, 748-752, 755-756, 758-760, 762-769, 771, 774, 776-781, 783-788, 790-796, 798-799, 802, 804-808, 810-815, 817-831, 833-848, 850-855, 857-869, 871-880, 882-900, 903-907, 909, 911-915, 918-920, 922-925, 927, 929, 931-938, 940, 943-945, 947, and 950-953). Of the 745 genes, the expression of 530 of those genes was altered in at least one mutant *Arabidopsis* after infection with *Pseudomonas syringae* (SEQ ID NOs: 2, 4-6, 11-13, 18, 22-23, 28, 31, 36, 39-43, 45, 47, 49-50, 52, 54-55, 57-58, 60-61, 63-66, 71-72, 74, 77, 81, 83, 85, 87-89, 92, 97, 100-107, 111-112, 114-115, 117-120, 122, 125, 127-128, 134, 128-140, 143-144, 148-151, 153, 156-157, 160, 165, 168-170, 173-174, 176-180, 183, 187-188, 191, 193-194, 197-198, 200, 203-210, 214, 219-224, 227, 230-232, 235-237, 239-240, 243-246, 248-249, 251-254, 256-258, 261, 264, 266-268, 270, 272-275, 277-278, 280, 283, 286-287, 290-293, 297, 302, 305-306, 308-310, 312-316, 321-326, 328-331, 333, 336-339, 341, 345, 351, 353, 355-358, 361-363, 365-366, 368-371, 373, 375, 377, 379-381, 384-385, 388-390, 392, 394-400, 402-406, 410, 412, 415-416, 419-420, 422-425, 429-433, 435-439, 441-443, 445-452, 454, 459-460, 463, 466, 468-470, 473, 481-482, 485-486, 489, 491-494, 497-498, 500-501, 503, 505-506, 508, 510, 513-515, 517, 520-521, 523, 528-529, 531, 533-538, 540, 545-548, 550-551, 553-554, 556-558, 560, 566-567, 575, 580, 582-584, 588-593, 596, 598-600, 602-603, 605-606, 608-610, 612, 614, 616, 620-622, 627-629, 633-634, 636-639, 644, 646, 648-651, 654-657, 659, 661-663, 667, 669, 673-

674, 677, 682, 684-687, 689, 691-693, 697, 699, 701, 703-708, 713, 717, 719, 721-727, 730-733, 736, 740, 744, 746, 749-752, 755-756, 758-760, 762-764, 766-769, 774, 776-778, 780-781, 786, 788, 791-796, 799, 802, 804-808, 810-812, 815, 818-821, 823-825, 827-829, 831, 833-836, 838-843, 845, 847-848, 852-853, 855, 858, 860-869, 871-874, 876, 878-880, 884-887, 889, 892-894, 896-900, 904-907, 911-915, 918-920, 922-924, 931, 933, 938, 943-945, 947, and 950-952). Of the 530, 81 encode regulatory factors (SEQ ID NOs: 39, 52, 60, 63, 81, 83, 106, 107, 115, 117, 118, 168, 174, 176, 179, 204, 207, 208, 220, 221, 248, 258, 268, 275, 280, 309, 323, 326, 329, 351, 419, 422, 429, 430, 432, 459, 460, 468, 469, 473, 500, 505, 506, 508, 529, 531, 533, 535, 538, 545, 553, 602, 606, 608, 610, 614, 616, 634, 654, 655, 684, 686, 687, 691, 717, 751, 752, 766, 777, 815, 831, 834, 835, 839, 841, 847, 876, 884, 906, 920, and 924).

As also described herein, 333 genes were identified that are useful to confer improved resistance to plants to bacterial infection (SEQ ID NOs: 12-13, 18, 23, 36, 39-40, 43, 45, 50, 52, 57-58, 60-61, 64, 71-72, 81, 87-89, 97, 100, 102-105, 107, 111-112, 115, 119-120, 122, 125, 127-128, 140, 144, 148-150, 153, 165, 168-169, 176-177, 179, 183, 188, 191, 193-194, 197-198, 203-206, 208-209, 214, 219-222, 227, 230, 232, 237, 244-246, 248-249, 251-253, 258, 261, 264, 266, 268, 273-275, 283, 287, 290, 293, 297, 302, 305-306, 308, 312-315, 321-322, 324, 326, 330, 333, 338, 341, 345, 353, 356-358, 362-363, 366, 369, 371, 375, 377, 380, 384-385, 389, 392, 394-395, 398-399, 402-404, 406, 410, 415, 419, 422, 425, 429-430, 433, 435-439, 443, 445-452, 454, 463, 466, 468-470, 473, 486, 489, 491-492, 4894, 498, 500-501, 503, 508, 513-514, 517, 529, 533-538, 548, 550, 553-554, 4556-558, 566, 575, 580, 582-583, 590-591, 593, 600, 602, 609-610, 612, 614, 620-622, 627-629, 637-638, 644, 649, 654-657, 659, 663, 667, 669, 673-674, 677, 684-685, 689, 691-693, 699, 703-705, 708, 719, 721, 724-726, 730-732, 744, 746, 749-750, 752, 755-756, 758, 760, 762-764, 767, 769, 774, 780-781, 786, 788, 791-792, 794-796, 799, 804-808, 810-812, 815, 818-819, 823, 828-829, 833, 840841, 843, 847, 852-853, 858, 860, 862-865, 867-868, 872-874, 876, 885-887, 889, 892-894, 896-900, 904-905, 907, 911-914, 918-920, 922-924, 931, 933, 938, 947, 950, and 952).

Further, 296 genes were identified that are useful to confer improved resistance to plants to fungal infection (SEQ ID NOs: 2, 4, 6, 11-13, 18, 22-23, 31, 41-43, 49-50, 54, 57-58, 61, 64-66, 71-72, 74, 77, 85, 87, 89, 92, 97, 101, 103, 106-107, 112, 114, 117-119, 125, 128, 134, 138, 143, 149, 151, 156-157, 165, 169-170, 174, 176-180, 187-188, 191, 193, 206, 208, 219-220, 222, 224, 231, 236, 239, 243-245, 251-254, 256-257, 267, 272, 287, 290, 292, 297, 302, 312-313, 315-316, 321-322, 324-325, 328, 330, 345, 351, 353, 355-357, 362-363, 366,

368-371, 373, 375, 379, 381, 384, 388-390, 392, 395-400, 405, 410, 415-416, 419, 422, 424, 431-432, 435-436, 438-439, 447, 459-460, 470, 473, 481-482, 489, 491, 493-494, 500-501, 505-506, 513-514, 517, 520-521, 523, 528-529, 531, 535, 537-538, 540, 545-548, 551, 553-554, 557-558, 566, 575, 580, 582, 584, 589, 591, 593, 596, 598-599, 603, 605, 608-609, 612, 628, 633-634, 636-637, 639, 646, 648, 650-651, 656, 661, 663, 667, 674, 685-687, 689, 691, 693, 697, 699, 701, 705, 707, 713, 723-724, 726, 736, 740, 749, 751-752, 756, 758-759, 764, 766-768, 774, 776, 778, 780, 792-796, 799, 802, 806, 810-812, 818, 820-821, 825, 827-829, 833-836, 838-839, 841-843, 848, 855, 860-861, 866, 868-869, 871, 873-874, 876, 878-880, 889, 892, 898-900, 904-905, 907, 915, 918, 922, 924, 933, 943-945, 947, and 951).

In addition, 288 genes were identified that are useful to confer improved resistance to plants to infection with more than one pathogen, e.g., pathogens that include bacteria, oomycetes and viruses (SEQ ID NOs: 12-13, 18, 23, 36, 39-40, 43, 45, 50, 52, 57-58, 60-61, 64, 71-72, 81, 87-88, 100, 102-105, 107, 111-112, 115, 119-120, 122, 125, 127-128, 140, 148-150, 153, 168-169, 176-177, 188, 191, 193-194, 197-198, 203-206, 209, 219-222, 227, 232, 237, 244-246, 248-249, 251-253, 258, 261, 264, 266, 268, 273-275, 283, 287, 290, 293, 297, 302, 305-306, 308, 312-315, 324, 326, 330, 333, 341, 345, 353, 356, 358, 366, 371, 375, 377, 380, 385, 389, 392, 394, 398, 402-404, 406, 410, 415, 419, 425, 429-430, 433, 435-438, 443, 445-447, 449-452, 454, 463, 466, 468-470, 473, 486, 489, 492, 494, 498, 500-501, 503, 508, 513-514, 517, 533-538, 548, 550, 553-554, 57-558, 566, 575, 582-583, 590-591, 593, 600, 602, 609-610, 612, 620-622, 627-629, 637-638, 644, 649, 654-657, 659, 667, 669, 673, 677, 684, 689, 692-693, 703-705, 719, 721, 724-726, 730-732, 744, 746, 749-750, 752, 755-756, 760, 762-764, 767, 769, 774, 780-781, 786, 788, 791-792, 795-796, 805-808, 810-812, 815, 818-819, 823, 828, 833, 840-841, 843, 852-853, 858, 860, 862-865, 867-868, 872-874, 876, 887, 889, 893-894, 896-898, 900, 905, 907, 911-914, 918-920, 922-923, 931, 933, 938, 947, 950, and 952).

Using the same approach described above, 25 genes were identified (SEQ ID NOs: 1, 15, 19, 20, 24, 26, 27, 34, 38, 51, 56, 59, 67-69, 99, 116, 155, 159, 182, 212, 284, 372, 444, and 789), the expression of which was decreased at 6 hours in an *avr2* plant. Also identified were 33 genes (SEQ ID NOs: 17, 70, 76, 81, 84, 109, 123, 144, 160, 230, 265, 268, 269, 271, 323, 333, 385, 427, 428, 430, 457, 505, 569, 597, 602, 606, 616, 708, 730, 741, 812, 862, and 942), the expression of which was elevated in an incompatible or a compatible interaction in four *Arabidopsis* ecotypes infected with bacteria. Eight of the genes were upregulated by 3 hours in an incompatible interaction, 18 of the genes were upregulated by 6 hours, but not at 3

hours, in an incompatible interaction, and 6 of the genes were upregulated in a compatible interaction.

Further identified were 33 genes, the expression of which was induced early after infection (SEQ ID NOs:17, 21, 80, 81, 156, 174, 176, 221, 227, 296, 302, 303, 306, 333, 340, 360, 500, 505, 524, 575, 601, 602, 614, 628, 687, 733, 782, 811, 835, 862, 900, 905, and 912), 10 genes, the expression of which was decreased early after infection (SEQ ID NOs:30, 73, 282, 541, 640, 679, 761, 870, 917, and 930), and 135 genes, 107 of which were induced at 3 and/or 6 hours after infection, and 28 of which were decreased after infection (SEQ ID NOs:7, 21, 33, 44, 46, 60, 82, 86, 91, 93, 106, 110, 119, 122, 130, 131, 136, 141, 154, 161, 166-168, 171, 176, 185, 189, 199, 200, 202, 203, 213, 225, 227, 248, 261, 262, 266, 274, 285, 300, 301, 302, 320, 326, 341, 345, 348, 349, 360, 366, 378, 406, 409, 422, 425, 434, 441, 443, 446, 449, 454, 461, 471, 475, 476, 483, 485, 499, 500, 511, 512, 516, 527, 530, 533, 543, 545, 549, 550, 552, 567, 575, 578, 586, 590, 608, 611, 615, 618, 625, 631, 643, 656, 658, 659, 666, 668, 671, 680, 690, 694, 704, 706, 711, 714, 718, 721, 728, 734, 738, 757, 770, 772, 791, 807, 811, 813, 816, 827, 857, 864, 868, 875, 881, 893, 901, 905, 908, 912, 916, 939, 941, 951, and 952).

In a similar approach, 48 genes that were upregulated in response to infection, e.g., bacterial or fungal infection, as well as 46 of the corresponding promoter containing regions, were identified. Thirty-six of the genes were upregulated in response to bacterial, e.g., *Pseudomonas*, infection (the promoters for genes corresponding to SEQ ID NOs: 104-106, 119, 123, 129, 131, 151-152, 183, 191, 198, 200, 227, 249, 274, 302, 358, 415, 481, 547, 566, 582, 628, 633, 639, 656, 673, 793, 818, 827, 864, 874, 880, and 904-905), while 23 of the genes were upregulated in response to fungal, e.g., *Botrytis*, infection (SEQ ID NOs: 18, 71, 119, 123, 129, 151, 191, 244, 245, 302, 545, 547, 562, 566, 637, 653, 747, 756, 774, 793, 842, 864, and 905). Twenty-five of the genes were upregulated only in response to bacterial, e.g., *Pseudomonas*, infection (the promoters for genes corresponding to SEQ ID NOs: 104-106, 131, 152, 183, 198, 200, 227, 249, 274, 358, 415, 481, 582, 628, 633, 639, 656, 673, 818, 827, 874, 880, and 904 are provided in SEQ ID NOs:1001-1025), 10 of the genes were upregulated only in response to fungal, e.g., *Botrytis*, infection (the promoters for genes corresponding to SEQ ID NOs:18, 71, 244, 245, 545, 562, 637, 653, 747, 756, 774, and 842 are provided in SEQ ID NOs:1026-1035), and 11 genes were upregulated in response to both bacterial and fungal infection (the promoters for genes corresponding to SEQ ID NOs:119, 123, 129, 151, 191, 302, 547, 566, 793, 864, and 905 are provided in SEQ ID NOs:1036-1046).

As also described hereinbelow, 129 *Arabidopsis* genes (SEQ ID NOs: 3, 51, 54, 60, 61, 66, 75, 76, 78, 88, 95, 96, 101, 106, 108, 123, 126, 128, 129, 131, 137, 145-147, 150, 158, 169, 170, 172, 173, 197, 200, 216, 219, 224, 230, 233, 237, 249, 250, 263, 274, 275, 276, 299, 307, 323, 333, 342, 346, 359, 382, 383, 387, 391, 393, 401, 411, 415, 427, 442, 455, 459, 466, 477, 481, 485, 487, 502, 511, 515, 525, 534, 539, 542, 560, 571, 577, 579, 584, 587, 595, 600, 627, 638, 645, 654, 659, 668, 681, 688, 695, 696, 706, 708, 730, 742, 753, 775, 785, 786, 791, 797, 800, 801, 809, 817, 819, 820, 823, 827, 847, 856, 875, 885, 896, 902, 910, 921, 922, 923, 925, 926, 928, 946, and 952) were identified that were upregulated in response to viral infection, and 46 *Arabidopsis* genes were identified that were downregulated in response to viral infection (SEQ ID NOs: 14, 48, 53, 98, 217, 226, 295, 327, 343, 352, 369, 404, 407, 418, 453, 458, 465, 472, 480, 488, 495, 507, 509, 513, 514, 559, 561, 581, 604, 607, 613, 641, 652, 672, 720, 735, 739, 743, 745, 754, 773, 803, 832, 849, 948, and 949).

Also provided are nucleic acid molecules comprising a nucleotide sequence comprising an open reading frame expressed in response to pathogen infection comprising SEQ ID NOs: 209, 216, 262, 267, 317, 386, 425, 440 and 800. These sequences are useful to over- or under-express the encoded product, or prepare knock-out plants which have an altered response to pathogen infection.

The invention therefore provides a method in which the open reading frame of a plant pathogen resistance gene, e.g., a gene that is associated with a response to pathogen infection, which is altered in a plant in response to infection is identified and isolated. A transgene comprising the isolated open reading frame may be introduced to and expressed in a transgenic plant, e.g., prior to infection, e.g., constitutively, or early and/or rapidly after infection, or in regulatable (inducible) fashion, e.g., after exposure to a chemical or using a promoter that is upregulated after infection, so as to confer resistance to that transgenic plant to the pathogen relative to a corresponding plant which does not have the transgene. The expression of the transgene is preferably at higher than normal levels, and under the regulation of a promoter that allows very fast and high induction in response to the presence of a pathogen or under cycling promoters (e.g., circadian clock regulated promoters), such that the encoded gene product(s) is maintained at sufficiently high levels to provide enhanced resistance or tolerance. The invention further provides a method in which a gene in a plant which is downregulated in response to infection, is disrupted or the expression of that gene is further downregulated, e.g., using antisense expression, so as to result in a plant that has enhanced resistance to infection,

and which disruption or downregulation preferably has little or no detrimental effect(s) on the host plant.

As also described herein, it was found that the early incompatible response was similar to the late compatible response, suggesting that early expression of plant pathogen-resistance genes is important for resistance. Also, various plant strains were found to respond differently to the same pathogen, but there was also an identifiable global pattern of response. Thus, the comparison of the expression patterns in incompatible and compatible interactions in one or more ecotypes can lead to identifying subsets of key responding genes and clusters of genes that are key (early) responders. In addition, the observed global expression pattern indicated that the least resistant strain tested (Ws) had a low basal level of pathogen-upregulated genes and a high level of pathogen-downregulated genes compared to the most resistant strain (Ler). Thus, plant strains that are more resistant to pathogens have a gene expression phenotype in which genes that are upregulated in response to infection are already expressed at a higher than normal basal level, and those genes that are downregulated are expressed at a lower than normal basal level.

The genes and promoters described hereinabove can be used to identify orthologous genes and their promoters which are also likely useful to enhance resistance of plants to pathogens. Moreover, the orthologous promoters are useful to express linked open reading frames. In addition by aligning the promoters of these orthologs, novel *cis* elements can be identified that are useful to generate synthetic promoters.

Hence, the isolated nucleic acid molecules of the invention include the orthologs of the *Arabidopsis*, *Chenopodium* and rice sequences disclosed herein, i.e., the corresponding nucleic acid molecules in organisms other than *Arabidopsis*, *Chenopodium* and rice, including, but not limited to, plants other than *Arabidopsis*, *Chenopodium* and rice, preferably cereal plants, e.g., corn, wheat, rye, turfgrass, sorghum, millet, sugarcane, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, tobacco, sugarbeet, or rice. An ortholog is a gene from a different species that encodes a product having the same function as the product encoded by a gene from a reference organism. Databases such GenBank or one found at <http://bioserver.myongjiac.kr/rjce.html> (for rice) may be employed to identify sequences related to the *Arabidopsis* or *Chenopodium* sequences, e.g., orthologs in cereal crops such as rice. Alternatively, recombinant DNA techniques such as hybridization or PCR may be employed to identify sequences related to the *Arabidopsis* sequences. The encoded ortholog products likely have at least 70% sequence identity to each other. Hence, the invention

includes an isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide having at least 70% identity to a polypeptide encoded by one or more of the *Arabidopsis*, *Chenopodium* or rice sequences disclosed herein. For example, promoter sequences within the scope of the invention are those which direct expression of an open reading frame which encodes a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising SEQ ID NOs:1-953.

The genes and promoters described hereinabove can be used to identify orthologous genes and their promoters which are also likely expressed in a particular tissue and/or development manner. Moreover, the orthologous promoters are useful to express linked open reading frames. In addition, by aligning the promoters of these orthologs, novel *cis* elements can be identified that are useful to generate synthetic promoters. Hence, the isolated nucleic acid molecules of the invention include the orthologs of the *Arabidopsis* sequences disclosed herein, i.e., the corresponding nucleotide sequences in organisms other than *Arabidopsis*, including, but not limited to, plants other than *Arabidopsis*, preferably cereal plants, e.g., corn, wheat, rye, turfgrass, sorghum, millet, sugarcane, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, tobacco, sugarbeet, or rice. An orthologous gene is a gene from a different species that encodes a product having the same or similar function, e.g., catalyzing the same reaction as a product encoded by a gene from a reference organism. Thus, an ortholog includes polypeptides having less than, e.g., 65% amino acid sequence identity, but which ortholog encodes a polypeptide having the same or similar function. Databases such as GenBank or one found at <http://bioserver.myongji.ac.kr/rjce.html> (for rice) may be employed to identify sequences related to the *Arabidopsis* sequences, e.g., orthologs in cereal crops such as rice, wheat, sunflower or alfalfa. SEQ ID NOs: 6286 and 4210, for example, are the rice promoter and open reading frame for rice peroxidase, the ortholog of the *Arabidopsis* gene comprising SEQ ID NO: 50. SEQ ID NOs: 3311, 5387, 3791 and 5867 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO:609; SEQ ID NOs: 2699, 4775, 3463, 5539, 3584, 5660, 4451, 6527, 4595 and 6671 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO: 139.

Preferably, the promoters of the invention include a consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, of any one of SEQ ID NOs:2137-2661, SEQ ID NOs:4738-6813 or the promoter orthologs thereof, which include the minimal promoter region. Preferably, the nucleotide

sequence that includes the promoter region includes at least one copy of a TATA box. Thus, the invention provides plant promoters, including orthologs of *Arabidopsis* promoters corresponding to genes comprising any one of SEQ ID NOs: 1-953. The present invention further provides a composition, an expression cassette or a recombinant vector containing the
5 nucleic acid molecule of the invention, and host cells comprising the expression cassette or vector, e.g., comprising a plasmid. In particular, the present invention provides an expression cassette or a recombinant vector comprising a promoter of the invention linked to a nucleic acid segment which, when present in a plant, plant cell or plant tissue, results in transcription of the linked nucleic acid segment.

10 In its broadest sense, the term "substantially similar" when used herein with respect to a nucleotide sequence means that the nucleotide sequence is part of a gene which encodes a polypeptide having substantially the same structure and function as a polypeptide encoded by a gene for the reference nucleotide sequence, e.g., the nucleotide sequence comprises a promoter from a gene that is the ortholog of the gene corresponding to the reference nucleotide
15 sequence, as well as promoter sequences that are structurally related the promoter sequences particularly exemplified herein, i.e., the substantially similar promoter sequences hybridize to the complement of the promoter sequences exemplified herein under high or very high stringency conditions. The term "substantially similar" thus includes nucleotide sequences wherein the sequence has been modified, for example, to optimize expression in particular
20 cells, as well as nucleotide sequences encoding a variant polypeptide comprising one or more amino acid substitutions relative to the (unmodified) polypeptide encoded by the reference sequence, which substitution(s) does not alter the activity of the variant polypeptide relative to the unmodified polypeptide. In its broadest sense, the term "substantially similar" when used herein with respect to polypeptide means that the polypeptide has substantially the same
25 structure and function as the reference polypeptide. The percentage of amino acid sequence identity between the substantially similar and the reference polypeptide is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, up to at least 99%, wherein the reference polypeptide is a
30 polypeptide encoded by an *Arabidopsis* gene comprising any one of SEQ ID NOs:1-953, a *Chenopodium* gene comprising any one of SEQ ID NOs:1954-1966, or a rice gene comprising any one of SEQ ID NOs:2000-2129 or 2662-4737. One indication that two polypeptides are substantially similar to each other, besides having substantially the same function, is that an

agent, e.g., an antibody, which specifically binds to one of the polypeptides, specifically binds to the other.

Sequence comparisons maybe carried out using a Smith-Waterman sequence alignment algorithm (see e.g., Waterman (1995) or <http://www.hsc.usc.edu/software/seqaln/index.html>).

- 5 The localS program, version 1.16, is preferably used with following parameters: match: 1, mismatch penalty: 0.33, open-gap penalty: 2, extended-gap penalty: 2. Further, a nucleotide sequence that is "substantially similar" to a reference nucleotide sequence hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

- Hence, the present invention further provides an expression cassette or a vector containing the nucleic acid molecule comprising an open reading frame of the invention operably linked to a promoter, or comprising a promoter of the invention operably linked to an open reading frame or portion thereof, and the vector may be a plasmid. Such cassettes or vectors, when present in a plant, plant cell or plant tissue result in transcription of the linked nucleic acid fragment in the plant. The expression cassettes or vectors of the invention may optionally include other regulatory sequences, e.g., transcription terminator sequences, operator, repressor binding site, transcription factor binding site, and/or an enhancer and may be contained in a host cell. The expression cassette or vector may augment the genome of a transformed plant or may be maintained extrachromosomally. The expression cassette or vector may further have a Ti plasmid and be contained in an *Agrobacterium tumefaciens* cell; it may be carried on a microparticle, wherein the microparticle is suitable for ballistic transformation of a plant cell; or it may be contained in a plant cell or protoplast. Further, the expression cassette can be contained in a transformed plant or cells thereof and the plant may be a dicot or a monocot. In particular, the plant may be a cereal plant.

The invention also provides sense and anti-sense nucleic acid molecules corresponding to the open reading frames identified herein as well as their orthologs. Also provided are expression cassettes, e.g., recombinant vectors, and host cells, comprising the nucleic acid

molecule of the invention, e.g., one which comprises a nucleotide sequence which encodes a polypeptide the expression of which is altered in response to pathogen infection.

The present invention further provides a method of augmenting a plant genome by contacting plant cells with a nucleic acid molecule of the invention, e.g., one isolatable or obtained from a plant gene encoding a polypeptide that is substantially similar to a polypeptide encoded by an *Arabidopsis*, *Chenopodium* or rice gene comprising a sequence comprising any one of SEQ ID NOs: 1-953, 1954-1966, 2000-2129 or 2662-4737 so as to yield transformed plant cells; and regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the nucleic acid molecule in the cells of the plant. The nucleic acid molecule may be present in the nucleus, chloroplast, mitochondria and/or plastid of the cells of the plant. The present invention also provides a transgenic plant prepared by this method, a seed from such a plant and progeny plants from such a plant including hybrids and inbreds. Preferred transgenic plants are transgenic maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice, wheat, rye, turfgrass, millet, sugarcane, tomato, or potato.

The invention also provides a method of plant breeding, e.g., to prepare a crossed fertile transgenic plant. The method comprises crossing a fertile transgenic plant comprising a particular nucleic acid molecule of the invention with itself or with a second plant, e.g., one lacking the particular nucleic acid molecule, to prepare the seed of a crossed fertile transgenic plant comprising the particular nucleic acid molecule. The seed is then planted to obtain a crossed fertile transgenic plant. The plant may be a monocot or a dicot. In a particular embodiment, the plant is a cereal plant.

The crossed fertile transgenic plant may have the particular nucleic acid molecule inherited through a female parent or through a male parent. The second plant may be an inbred plant. The crossed fertile transgenic may be a hybrid. Also included within the present invention are seeds of any of these crossed fertile transgenic plants.

The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate progeny plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means.

Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic plants according to the invention can be used for the breeding of improved plant lines that for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can be obtained that, due to their optimized genetic "equipment", yield harvested product of better quality than products that were not able to tolerate comparable adverse developmental conditions.

The nucleic acid molecules of the invention, their encoded polypeptides and compositions thereof, are: for open reading frames, useful to provide resistance to pathogens to alter expression of a particular gene corresponding to the open reading frame by decreasing or eliminating expression of that plant gene or by overexpressing a particular gene product, and as a diagnostic for the presence or absence of the pathogen by correlating the expression level or pattern of expression of one or more of the nucleic acid molecules or polypeptides of the invention; and for promoters, useful to alter the expression of a linked open reading frame in response to pathogen infection. As one embodiment of the invention includes isolated nucleic acid molecules that have increased expression in response to pathogen infection, the invention further provides compositions and methods for enhancing resistance to pathogen infection. The compositions of the invention include plant nucleic acid sequences and the amino acid sequences for the polypeptides or partial-length polypeptides encoded thereby which are described herein, or other plant nucleic acid sequences and the amino acid sequences for the polypeptides or partial-length polypeptides encoded thereby which are operably linked to a promoters are useful to provide tolerance or resistance to a plant to a pathogen, preferably by preventing or inhibiting pathogen infection. Methods of the invention involve stably transforming a plant with one or more of at least a portion of these nucleotide sequences which confer tolerance or resistance operably linked to a promoter capable of driving expression of that nucleotide sequence in a plant cell. By "portion" or "fragment", as it relates to a nucleic acid molecule, sequence or segment of the invention, when it is linked to other sequences for expression, is meant a sequence comprising at least 80 nucleotides, more preferably at least 150 nucleotides, and still more preferably at least 400 nucleotides. If not employed for expressing, a "portion" or "fragment" means at least 9, preferably 12, more preferably 15, even more preferably at least 20, consecutive nucleotides, e.g., probes and primers

(oligonucleotides), corresponding to the nucleotide sequence of the nucleic acid molecules of the invention. By "resistant" is meant a plant which exhibits substantially no phenotypic changes as a consequence of infection with the pathogen. By "tolerant" is meant a plant which, although it may exhibit some phenotypic changes as a consequence of infection, does not have a substantially decreased reproductive capacity or substantially altered metabolism.

A method of combating a pathogen in an agricultural crop is also provided. The method comprises introducing to a plant, plant cell, or plant tissue an expression cassette comprising a nucleic acid molecule of the invention comprising an open reading frame so as to yield a transformed differentiated plant, transformed cell or transformed tissue. Transformed cells or tissue can be regenerated to provide a transformed differentiated plant. The transformed differentiated plant preferably expresses the nucleic acid molecule in an amount that confers resistance to the transformed plant to pathogen infection relative to a corresponding nontransformed plant. The present invention also provides a transformed plant prepared by the method, progeny and seed thereof. Examples of plant viruses which may be combated by the present invention include single stranded RNA viruses (with and without envelope), double stranded RNA viruses, and single and double stranded DNA viruses such as (but not limited to) tobacco mosaic virus, cucumber mosaic virus, turnip mosaic virus, turnip vein clearing virus, oilseed rape mosaic virus, tobacco rattle virus, pea enation mosaic virus, barley stripe mosaic virus, potato viruses X and Y, carnation latent virus, beet yellows virus, maize chlorotic virus, tobacco necrosis virus, turnip yellow mosaic virus, tomato bushy stunt virus, southern bean mosaic virus, barley yellow dwarf virus, tomato spotted wilt virus, lettuce necrotic yellows virus, wound tumor virus, maize streak virus, and cauliflower mosaic virus. Other pathogens within the scope of the invention include, but are not limited to, fungi such as *Cochliobolus carbonum*, *Phytophthora infestans*, *Phytophthora sojae*, *Colletotrichum*, *Melampsora lini*, *cladosporium fulvum*, *Heminthosporium maydia*, *Peronospora parasitica*, *Puccinia sorghi*, and *Puccinia polysora*; bacteria such as *Phytophthora secalis*, *Pseudomonas glycinea*, *Xanthomonas oryzae* and, *Fusarium oxysporum*; and nematodes such as *Globodera rostochiensis*.

For example, the invention provides a nucleic acid molecule comprising a plant nucleotide sequence comprising at least a portion of a key effector gene(s) responsible for host resistance to particular pathogens. To provide resistance or tolerance to a pathogen in a plant, this sequence may be overexpressed individually, in the sense or antisense orientation, or in combination with other sequences to confer improved disease resistance or tolerance to a plant

relative to a plant that does not comprise and/or express the sequence. The overexpression may be constitutive, or it may be preferable to express the effector gene(s) in a tissue-specific manner or from an inducible promoter including a promoter which is responsive to external stimuli, such as chemical application, or to pathogen infection, e.g., so as to avoid possible deleterious effects on plant growth if the effector gene(s) was constitutively expressed. In one embodiment of the invention, the promoter employed may be one that is rapidly and transiently and/or highly transcribed after pathogen infection.

A transformed (transgenic) plant of the invention includes plants, the genome of which is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields, e.g., under conditions of pathogen infection, and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and probes.

For example, the invention includes a pathogen, e.g., virus, tolerant or resistant plant and seed thereof having stably integrated and expressed within its genome, a nucleic acid molecule of the invention. The normal fertile transformed (transgenic) plant may be selfed to yield a substantially homogenous line with respect to viral resistance or tolerance. Individuals of the line, or the progeny thereof, may be crossed with plants which optionally exhibit the trait. In a particular embodiment of the method, the selfing and selection steps are repeated at least five times in order to obtain the homogenous (isogenic) line. Thus, the invention also provides transgenic plants and the products of the transgenic plants.

The invention further includes a nucleotide sequence which is complementary to one (hereinafter "test" sequence) which hybridizes under low, moderate or stringent conditions with the nucleic acid molecules of the invention as well as RNA which is encoded by the nucleic acid molecule. When the hybridization is performed under stringent conditions, either the test or nucleic acid molecule of invention is preferably supported, e.g., on a membrane or DNA chip. Thus, either a denatured test or nucleic acid molecule of the invention is preferably first bound to a support and hybridization is effected for a specified period of time at a temperature of, e.g., between 55 and 70°C, in double strength citrate buffered saline (SC) containing 0.1% SDS followed by rinsing of the support at the same temperature but with a buffer having a reduced SC concentration. Depending upon the degree of stringency required

such reduced concentration buffers are typically single strength SC containing 0.1% SDS, half strength SC containing 0.1% SDS and one-tenth strength SC containing 0.1% SDS.

The invention further provides a method to identify an open reading frame in the genome of a plant cell, the expression of which is altered by pathogen infection of that cell.

5 The method comprises contacting a solid substrate comprising a plurality of samples comprising isolated plant nucleic acid of a probe comprising plant nucleic acid, e.g., cRNA, isolated from a pathogen infected plant so as to form a complex. Each individual sample comprises one or more nucleic acid sequences (e.g., oligonucleotides) corresponding to at least a portion of a plant gene. The method may be employed with nucleic acid samples and probes
10 from any organism, e.g., any prokaryotic or eukaryotic organism. Preferably, the nucleic acid sample and probes are from a plant, such as a dicot or monocot. More preferably the nucleic acid samples and probes are from a cereal plant. Even more preferably the nucleic acids and probes are from a crop plant. A second plurality of samples on a solid substrate, i.e., a DNA chip, each comprising a plurality of samples comprising isolated plant nucleic acid is contacted
15 with a probe comprising plant nucleic acid isolated from an uninfected or infected control (mutant) plant so as to form a complex. Then complex formation between the samples and probes comprising nucleic acid from infected or control cells compared. For example, potato virus X, tobacco mosaic virus, tobnavirus, cucumber mosaic virus and geminivirus are known to infect *Arabidopsis*. Thus, *Arabidopsis* genes, the expression of which is altered in response
20 to infection by any of these viruses, can be identified. Regions that are 5N to the start codon for the gene can then be identified and/or isolated.

The invention further provides a method for identifying a plant cell infected with a pathogen. The method comprises contacting nucleic acid obtained from a plant cell suspected of being infected with a pathogen with oligonucleotides corresponding to a portion of a
25 plurality of sequences selected from SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737 under conditions effective to amplify those sequences. Then the presence of the amplified product is detected or determined. The presence of two or more amplified products, e.g., in an amount that is different than the amount of the corresponding amplified products from an uninfected plant, each corresponding to two or more SEQ ID NOs: 1-953, 1954-1966, 2000-
30 2129, or 2662-4737 is indicative of pathogen infection.

The invention further provides a method for identifying a plant cell infected with a pathogen. The method comprises contacting a protein sample obtained from a plant cell suspected of being infected with a pathogen with an agent that specifically binds a polypeptide

encoded by an open reading frame comprising SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737 so as to form a complex. Then the presence or amount of complex formation is detected or determined.

The invention provides an additional method for identifying a plant cell infected with a pathogen. The method comprises hybridizing a probe selected from SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737 to nucleic acid obtained from a plant cell suspected of being infected with a pathogen. The amount of the probe hybridized to nucleic acid obtained from a cell suspected of being infected with a virus is compared to hybridization of the probe to nucleic acid isolated from an uninfected cell. A change in the amount of at least two probes that hybridize to nucleic acid isolated from a cell suspected of being infected by a virus relative to hybridization of at least two probes to nucleic acid isolated from an uninfected cell is indicative of viral infection.

A method to shuffle the nucleic acids of the invention is provided. This method involves fragmentation of a nucleic acid corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-953, 1954-1966, 2000-2129 or 2662-4737, the orthologs thereof, and the corresponding genes, followed by religation. This method allows for the production of polypeptides having altered activity relative to the native form of the polypeptide. Accordingly, the invention provides cells and transgenic plants containing nucleic acid segments produced through shuffling that encode polypeptides having altered activity relative to the corresponding native polypeptide.

A computer readable medium containing the nucleic acid sequences of the invention as well as methods of use for the computer readable medium are provided. This medium allows a nucleic acid segment corresponding to a nucleic acid sequence listed in SEQ ID NOs:1-953, 2137-2661, 1954-1966, 2000-2129, 2662-4737 or 4738-6813 to be used as a reference sequence to search against databases. This medium also allows for computer-based manipulation of a nucleic acid sequence corresponding to a nucleic acid sequence listed in SEQ ID NOs :1-953, 2137-2661, 1954-1966, 2000-2129, 2662-4737 or 4738-6813, and the corresponding gene and polypeptide encoded by the nucleic acid sequence.

Therefore, another embodiment of the present invention provides a method of using known inducers or inhibitors of genes identified as being important in plant-pathogen interactions to induce genes that are important in resistance, or to inhibit genes that are downregulated in resistance.

Thus, some of the isolated nucleic acid molecules of the invention are useful in a method of combating a pathogen in an agricultural crop. The method comprises introducing to a plant an expression cassette comprising a nucleic acid molecule of the invention so as to yield a transformed differentiated plant. The transformed differentiated plant expresses the nucleic acid molecule in an amount that confers resistance to the transformed plant to infection relative to a corresponding nontransformed plant.

Detailed Description of the Invention

I. Definitions

10

The term "gene" is used broadly to refer to any segment of nucleic acid associated with a biological function. Thus, genes include coding sequences and/or the regulatory sequences required for their expression. For example, gene refers to a nucleic acid fragment that expresses mRNA or functional RNA, or encodes a specific protein, and which includes regulatory sequences. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

The term "native" or "wild type" gene refers to a gene that is present in the genome of an untransformed cell, i.e., a cell not having a known mutation.

A "marker gene" encodes a selectable or screenable trait.

The term "chimeric gene" refers to any gene that contains 1) DNA sequences, including regulatory and coding sequences, that are not found together in nature, or 2) sequences encoding parts of proteins not naturally adjoined, or 3) parts of promoters that are not naturally adjoined. Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences that are derived from different sources, or comprise regulatory sequences and coding sequences derived from the same source, but arranged in a manner different from that found in nature.

A "transgene" refers to a gene that has been introduced into the genome by transformation and is stably maintained. Transgenes may include, for example, genes that are either heterologous or homologous to the genes of a particular plant to be transformed. Additionally, transgenes may comprise native genes inserted into a non-native organism, or chimeric genes. The term "endogenous gene" refers to a native gene in its natural location in

the genome of an organism. A "foreign" gene refers to a gene not normally found in the host organism but that is introduced by gene transfer.

An "oligonucleotide" corresponding to a nucleotide sequence of the invention, e.g., for use in probing or amplification reactions, may be about 30 or fewer nucleotides in length (e.g., 9, 12, 15, 18, 20, 21 or 24, or any number between 9 and 30). Generally specific primers are upwards of 14 nucleotides in length. For optimum specificity and cost effectiveness, primers of 16 to 24 nucleotides in length may be preferred. Those skilled in the art are well versed in the design of primers for use processes such as PCR. If required, probing can be done with entire restriction fragments of the gene disclosed herein which may be 100's or even 1000's of nucleotides in length.

The terms "protein," "peptide" and "polypeptide" are used interchangeably herein.

The nucleotide sequences of the invention can be introduced into any plant. The genes to be introduced can be conveniently used in expression cassettes for introduction and expression in any plant of interest. Such expression cassettes will comprise the transcriptional initiation region of the invention linked to a nucleotide sequence of interest. Preferred promoters include constitutive, tissue-specific, developmental-specific, inducible and/or viral promoters. Such an expression cassette is provided with a plurality of restriction sites for insertion of the gene of interest to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes. The cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of interest, and a transcriptional and translational termination region functional in plants. The termination region may be native with the transcriptional initiation region, may be native with the DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also, Guerineau et al., 1991; Proudfoot, 1991; Sanfacon et al., 1991; Mogen et al., 1990; Munroe et al., 1990; Ballas et al., 1989; Joshi et al., 1987.

"Coding sequence" refers to a DNA or RNA sequence that codes for a specific amino acid sequence and excludes the non-coding sequences. It may constitute an "uninterrupted coding sequence", i.e., lacking an intron, such as in a cDNA or it may include one or more introns bounded by appropriate splice junctions. An "intron" is a sequence of RNA which is contained in the primary transcript but which is removed through cleavage and re-ligation of the RNA within the cell to create the mature mRNA that can be translated into a protein.

The terms "open reading frame" and "ORF" refer to the amino acid sequence encoded between translation initiation and termination codons of a coding sequence. The terms "initiation codon" and "termination codon" refer to a unit of three adjacent nucleotides ('codon') in a coding sequence that specifies initiation and chain termination, respectively, of protein synthesis (mRNA translation).

A "functional RNA" refers to an antisense RNA, ribozyme, or other RNA that is not translated.

The term "RNA transcript" refers to the product resulting from RNA polymerase catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complementary copy of the DNA sequence, it is referred to as the primary transcript or it may be a RNA sequence derived from posttranscriptional processing of the primary transcript and is referred to as the mature RNA. "Messenger RNA" (mRNA) refers to the RNA that is without introns and that can be translated into protein by the cell. "cDNA" refers to a single- or a double-stranded DNA that is complementary to and derived from mRNA.

"Regulatory sequences" and "suitable regulatory sequences" each refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences include enhancers, promoters, translation leader sequences, introns, and polyadenylation signal sequences. They include natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. As is noted above, the term "suitable regulatory sequences" is not limited to promoters.

"5' non-coding sequence" refers to a nucleotide sequence located 5' (upstream) to the coding sequence. It is present in the fully processed mRNA upstream of the initiation codon and may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency (Turner et al., 1995).

"3' non-coding sequence" refers to nucleotide sequences located 3' (downstream) to a coding sequence and include polyadenylation signal sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The use of different 3' non-coding sequences is exemplified by Ingelbrecht et al., 1989.

The term "translation leader sequence" refers to that DNA sequence portion of a gene

between the promoter and coding sequence that is transcribed into RNA and is present in the fully processed mRNA upstream (5') of the translation start codon. The translation leader sequence may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency.

5 The term "mature" protein refers to a post-translationally processed polypeptide without its signal peptide. "Precursor" protein refers to the primary product of translation of an mRNA. "Signal peptide" refers to the amino terminal extension of a polypeptide, which is translated in conjunction with the polypeptide forming a precursor peptide and which is required for its entrance into the secretory pathway. The term "signal sequence" refers to a
10 nucleotide sequence that encodes the signal peptide.

 The term "intracellular localization sequence" refers to a nucleotide sequence that encodes an intracellular targeting signal. An "intracellular targeting signal" is an amino acid sequence that is translated in conjunction with a protein and directs it to a particular sub-cellular compartment. "Endoplasmic reticulum (ER) stop transit signal" refers to a carboxy-
15 terminal extension of a polypeptide, which is translated in conjunction with the polypeptide and causes a protein that enters the secretory pathway to be retained in the ER. "ER stop transit sequence" refers to a nucleotide sequence that encodes the ER targeting signal. Other intracellular targeting sequences encode targeting signals active in seeds and/or leaves and vacuolar targeting signals.

20 "Pathogen" as used herein includes but is not limited to bacteria, fungi, yeast, oomycetes and virus, e.g., American wheat striate mosaic virus mosaic (AWSMV), barley stripe mosaic virus (BSMV), barley yellow dwarf virus (BYDV), Brome mosaic virus (BMV), cereal chlorotic mottle virus (CCMV), corn chlorotic vein banding virus (CCVBV), maize chlorotic mottle virus (MCMV), maize dwarf mosaic virus (MDMV), A or B, wheat streak
25 mosaic virus (WSMV), cucumber mosaic virus (CMV), cynodon chlorotic streak virus (CCSV), Johnsongrass mosaic virus (JGMV), maize bushy stunt or mycoplasma-like organism (NJILO), maize chlorotic dwarf virus (MCDV), maize chlorotic mottle virus (MCMV), maize dwarf mosaic virus (MDMV) strains A, D, E and F, maize leaf fleck virus (MLFV), maize line virus (NELV), maize mosaic virus (MMV), maize mottle and chlorotic stunt virus, maize
30 pellucid ringspot virus (MPRV), maize raya gruesa virus (MRGV), maize rayado fino virus (MRFV), maize red leaf and red stripe virus (MRSV), maize ring mottle virus (MRMV), maize rio cuarto virus (MRCV), maize rough dwarf virus (MRDV), maize sterile stunt virus (strains of barley yellow striate virus), maize streak virus (MSV), maize chlorotic stripe, maize

hoja Maize stripe virus blanca, maize stunting virus, maize tassel abortion virus (MTAV), maize vein enation virus (MVEV), maize wallaby ear virus (MAVEV), maize white leaf virus, maize white line mosaic virus (NTVVLMV), millet red leaf virus (NMV), Northern cereal mosaic virus (NCMV), oat pseudorosette virus, oat sterile dwarf virus (OSDV), rice black-streaked dwarf virus (RBSDV), rice stripe virus (RSV), sorghum mosaic virus (SrMV),
 5 formerly sugarcane mosaic virus (SCMV) strains H, I and M, sugarcane Fiji disease virus (FDV), sugarcane mosaic virus (SCMV) strains A, B, D, E, SC, BC, Sabi and NM vein enation virus, and wheat spot mosaic virus (WSMV).

Bacterial pathogens include but are not limited to *Pseudomonas avenae* subsp. *avenae*,
 10 *Xanthomonas campestris* pv. *holcicola*, *Enterobacter dissolvens*, *Erwinia dissolvens*, *Erwinia carotovora* subsp. *carotovora*, *Erwinia chrysanthemi* pv. *zeae*, *Pseudomonas andropogonis*, *Pseudomonas syringae* pv. *coronafaciens*, *Clavibacter michiganensis* subsp., *Corynebacterium michiganense* pv. *nebraskense*, *Pseudomonas syringae* pv. *syringae*, *Herniparasitic bacteria* (see under fungi), *Bacillus subtilis*, *Erwinia stewartii*, and *Spiroplasma kunkelii*.

Fungal pathogens include but are not limited to *Collelotrichum graminicola*,
 15 *Glomerella graminicola* Politis, *Glomerella lucumanensis*, *Aspergillus flavus*, *Rhizoctonia solani* Kuhn, *Thanatephorus cucumeris*, *Acremonium strictum* W. Gams, *Cephalosporium acremonium* Auct. non Corda Black *Lasiodiplodia theobromae* = *BoIr odiplodia y theobromae* Borde blanco *Marasmiellus* sp., *Physoderma maydis*, *Cephalosporium Corticium sasakii*,
 20 *Curvularia clavata*, *C. maculans*, *Cochhobolus eragrostidis*, *Curvularia inaequahs*, *C. intermedia* (teleomorph *Cochhobolus intermedius*), *Curvularia lunata* (teleomorph: *Cochliobolus lunatus*), *Curvularia pallescens* (teleomorph - *Cochliobolus pallescens*), *Curvularia senegalensis*, *C. luberculata* (teleomorph: *Cochliobolus tuberculatus*), *Didymella exitalis* *Diplodiaftumenti* (teleomorph - *Botryosphaeriafestucae*), *Diplodia maydis* =
 25 *Stenocarpella maydis*, *Stenocarpella macrospora* = *Diplodia macrospora*, *Sclerophthora rayssiae* var. *zeae*, *Sclerophthora macrospora* = *Sclerospora macrospora*, *Sclerospora graminicola*, *Peronosclerospora maydis* = *Sclerospora maydis*, *Peronosclerospora philippinensis*, *Sclerospora philippinensis*, *Peronosclerospora sorghi* = *Sclerospora sorghi*, *Peronosclerospora spontanea* = *Sclerospora spontanea*, *Peronosclerospora sacchari* =
 30 *Sclerospora sacchari*, *Nigrospora oryzae* (teleomorph: *Khuskia oryzae*) A. *Iternaria alternala* = *A. tenuis*, *Aspergillus glaucus*, *A. niger*, *Aspergillus spp.*, *Botrytis cinerea*, *Cunninghamella* sp., *Curvulariapallescens*, *Doratomyces slemonitis* = *Cephalotrichum slemonitis*, *Fusarium culmorum*, *Gonatobotrys simplex*, *Pithomyces maydicus*, *Rhizopus microsporus* Tiegh., *R.*

- stolonifer* = *R. nigricans*, *Scopulariopsis brumptii*, *Claviceps gigantea* (anamorph: *Sphacelia* sp.) *Aureobasidium zeae* = *Kabatiella zeae*, *Fusarium subglutinans* = *F. moniliforme* var. *subglutinans*, *Fusarium moniliforme*, *Fusarium avenaceum* (teleomorph - *Gibberella avenacea*), *Botryosphaeria zeae* = *Physalospora zeae* (anamorph: *Allacrophoma zeae*),
- 5 *Cercospora sorghi* = *C. sorghi* var. *maydis*, *Helminthosporium pedicellatum* (teleomorph: *Setosphaeriapedicellata*), *Cladosporium cladosporioides* = *Hormodendrum cladosporioides*, *C. herbarum* (teleomorph - *Mycosphaerella tassiana*), *Cephalosporium maydis*, *A. Iternaria alternata*, *A. scochyta maydis*, *A. tritici*, *A. zeicola*, *Bipolaris victoriae*, *Helminthosporium victoriae* (teleomorph *Cochhoholus victoriae*), *C sativus* (anamorph: *Bipolaris sorokiniana* =
- 10 *H. sorokinianum* = *H. sativum*), *Epicoccum nigrum*, *Exserohilum prolatum* = *Drechslera prolata* (teleomorph: *Setosphaeriaprolata*), *Graphium penicillioides*, *Leptosphaeria maydis*, *Leptothyrium zeae*, *Ophiosphaerella herpotricha* (anamorph - *Scolecosporiella* sp.), *Pataphaeosphaeria michotii*, *Phoma* sp., *Septoria zeae*, *S. zeicola*, *S. zeina* *Setosphaeria turcica*, *Exserohilum turcicum* = *Helminthosporium furcicum*, *Cochhoholus carbonum*,
- 15 *Bipolaris zeicola* = *Helminthosporium carbonum*, *Penicillium* spp., *P. chrysogenum*, *P. expansum*, *P. oxalicum*, *Phaeocytostroma ambiguum*, *Phaeocylosporella zeae*, *Phaeosphaeria maydis* = *Sphaerulina maydis*, *Botryosphaeria festucae* = *Physalospora zeicola* (anamorph: *Diplodia fumenfi*), *Herniparasitic bacteria and fungi* *Pyrenochaeta Phoma terrestris* = *Pyrenochaeta terrestris*, *Pythium* spp., *P. arrhenomanes*, *P. graminicola*, *Pythium*
- 20 *aphanidermatum* = *P. hutleri* L., *Rhizoctonia zeae* (teleomorph: *Waitea circinata*), *Rhizoctonia solani*, minor *A Iternaria alternata*, *Cercospora sorghi*, *Dictochaetafritilis*, *Fusarium acuminatum* (teleomorph *Gibberella acuminata*), *E. equiseti* (teleomorph: *G. intricans*), *E. oxysporum*, *E. pallidroseum*, *E. poae*, *E. roseum*, *G. cyanogena* (anamorph: *E. sulphureum*), *Microdochium holleyi*, *Mucor* sp., *Periconia circinata*, *Phytophthora cactorum*,
- 25 *P. drechsleri*, *P. nicotianae* var. *parasitica*, *Rhizopus arrhizus*, *Setosphaeria rostrata*, *Exserohilum rostratum* = *Helminthosporium rostratum*, *Puccinia sorghi*, *Physopella pallescens*, *P. zeae*, *Sclerotium rofsii* Sacc. (teleomorph- *Athelia rotfsii*), *Bipolaris sorokiniana*, *B. zeicola* = *Helminthosporium carbonum*, *Diplodia maydis*, *Exserohilum pedicellatum*, *Exserohilum furcicum* = *Helminthosporium turcicum*, *Fusarium avenaceum*, *E.*
- 30 *culmorum*, *E. moniliforme*, *Gibberella zeae* (anamorph - *E. graminearum*), *Macrophominaphaseolina*, *Penicillium* spp., *Phomopsis* sp., *Pythium* spp., *Rhizoctonia solani*, *R. zeae*, *Sclerotium rolfsii*, *Spicaria* sp., *Selenophoma* sp., *Gaeumannomyces graminis*, *Myrothecium gramineum*, *Monascus purpureus*, *M. ruber* Smut, *Ustilago zeae* = *U. maydis*

Smut, *Ustilaginoidea virens* Smut, *Sphacelotheca reiliana* = *Sporisorium holci*, *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis* = *Helminthosporium maydis*), *Stenocarpella macrospora* = *Diplodia macrospora*, *Cercospora sorghi*, *Fusarium episphaeria*, *E. merismoides*, *F. oxysporum* Schlechtend, *E. poae*, *E. roseum*, *E. solani* (teleomorph: *Nectria haematococca*), *F. tricinctum*, *Mariannaea elegans*, *Mucor* sp., *Rhopographus zeae*, *Spicaria* sp., *Aspergillus* spp., *Penicillium* spp., *Trichoderma viride* = *T lignorum* teleomorph: *Hypocrea* sp., *Stenocarpella maydis* = *Diplodia zeae*, *Ascochyta ischaemi*, *Phyllosticta maydis* (telomorph: *Mycosphaerella zeae-maydis*), and *Gloeocercospora sorghi*.

Parasitic nematodes include but are not limited to *Awl Dolichodorus* spp., *D. heterocephalus* Bulb and stem (Europe), *Ditylenchus dipsaci* Burrowing Radopholus similis Cyst Heterodera avenae, *H. zeae*, *Punctodera chalcoensis* Dagger *Xiphinema* spp., *X. americanum*, *X. mediterraneum* False root-knot *Nacobbus dorsalis* Lance, *Columbia Hoplolaimus columbus* Lance *Hoplolaimus* spp., *H. galeatus* Lesion *Pratylenchus* spp., *P. brachyurus*, *P. crenatus*, *P. hexincisus*, *P. neglectus*, *P. penetrans*, *P. scribneri*, *P. thornei*, *P. zeae* Needle Longidorus spp., *L. breviannulatus* Ring *Criconebella* spp., *C. ornata* Root-knot *Meloidogyne* spp., *M. chitwoodi*, *M. incognita*, *M. javanica* Spiral *Helicotylenchus* spp., *Belonolaimus* spp., *B. longicaudatus* Stubby-root *Paratrichodorus* spp., *P. christiei*, *P. minor*, *Ouinisulcius aculus*, and *Trichodorus* spp.

"Promoter" refers to a nucleotide sequence, usually upstream (5') to its coding sequence, which controls the expression of the coding sequence by providing the recognition for RNA polymerase and other factors required for proper transcription. "Promoter" includes a minimal promoter that is a short DNA sequence comprised of a TATA box and other sequences that serve to specify the site of transcription initiation, to which regulatory elements are added for control of expression. "Promoter" also refers to a nucleotide sequence that includes a minimal promoter plus regulatory elements that is capable of controlling the expression of a coding sequence or functional RNA. This type of promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an "enhancer" is a DNA sequence which can stimulate promoter activity and may be an innate element of the promoter or a heterologous element inserted to enhance the level or tissue specificity of a promoter. It is capable of operating in both orientations (normal or flipped), and is capable of functioning even when moved either upstream or downstream from the promoter. Both enhancers and other upstream promoter elements bind sequence-specific DNA-binding proteins that mediate their effects. Promoters

may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even be comprised of synthetic DNA segments. A promoter may also contain DNA sequences that are involved in the binding of protein factors which control the effectiveness of transcription initiation in response to physiological or developmental conditions.

The "initiation site" is the position surrounding the first nucleotide that is part of the transcribed sequence, which is also defined as position +1. With respect to this site all other sequences of the gene and its controlling regions are numbered. Downstream sequences (i.e., further protein encoding sequences in the 3' direction) are denominated positive, while upstream sequences (mostly of the controlling regions in the 5' direction) are denominated negative.

Promoter elements, particularly a TATA element, that are inactive or that have greatly reduced promoter activity in the absence of upstream activation are referred to as "minimal or core promoters." In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription. A "minimal or core promoter" thus consists only of all basal elements needed for transcription initiation, e.g., a TATA box and/or an initiator.

"Constitutive expression" refers to expression using a constitutive or regulated promoter. "Conditional" and "regulated expression" refer to expression controlled by a regulated promoter.

"Constitutive promoter" refers to a promoter that is able to express the open reading frame (ORF) that it controls in all or nearly all of the plant tissues during all or nearly all developmental stages of the plant. Each of the transcription-activating elements do not exhibit an absolute tissue-specificity, but mediate transcriptional activation in most plant parts at a level of $\geq 1\%$ of the level reached in the part of the plant in which transcription is most active.

"Regulated promoter" refers to promoters that direct gene expression not constitutively, but in a temporally- and/or spatially-regulated manner, and includes both tissue-specific and inducible promoters. It includes natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. Different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. New promoters of various types useful in plant cells are constantly being discovered, numerous examples may be found in the compilation by Okamuro et al. (1989). Typical regulated promoters useful in plants include but are not limited to safener-inducible promoters, promoters derived from the tetracycline-

inducible system, promoters derived from salicylate-inducible systems, promoters derived from alcohol-inducible systems, promoters derived from glucocorticoid-inducible system, promoters derived from pathogen-inducible systems, and promoters derived from ecdysome-inducible systems.

5 "Tissue-specific promoter" refers to regulated promoters that are not expressed in all plant cells but only in one or more cell types in specific organs (such as leaves or seeds), specific tissues (such as embryo or cotyledon), or specific cell types (such as leaf parenchyma or seed storage cells). These also include promoters that are temporally regulated, such as in early or late embryogenesis, during fruit ripening in developing seeds or fruit, in fully
10 differentiated leaf, or at the onset of senescence.

"Inducible promoter" refers to those regulated promoters that can be turned on in one or more cell types by an external stimulus, such as a chemical, light, hormone, stress, or a pathogen.

"Operably-linked" refers to the association of nucleic acid sequences on single nucleic
15 acid fragment so that the function of one is affected by the other. For example, a regulatory DNA sequence is said to be "operably linked to" or "associated with" a DNA sequence that codes for an RNA or a polypeptide if the two sequences are situated such that the regulatory DNA sequence affects expression of the coding DNA sequence (i.e., that the coding sequence or functional RNA is under the transcriptional control of the promoter). Coding sequences can
20 be operably-linked to regulatory sequences in sense or antisense orientation.

"Expression" refers to the transcription and/or translation of an endogenous gene, ORF or portion thereof, or a transgene in plants. For example, in the case of antisense constructs, expression may refer to the transcription of the antisense DNA only. In addition, expression refers to the transcription and stable accumulation of sense (mRNA) or functional RNA.
25 Expression may also refer to the production of protein.

"Specific expression" is the expression of gene products which is limited to one or a few plant tissues (spatial limitation) and/or to one or a few plant developmental stages (temporal limitation). It is acknowledged that hardly a true specificity exists: promoters seem to be preferably switch on in some tissues, while in other tissues there can be no or only little
30 activity. This phenomenon is known as leaky expression. However, with specific expression in this invention is meant preferable expression in one or a few plant tissues.

The "expression pattern" of a promoter (with or without enhancer) is the pattern of expression levels which shows where in the plant and in what developmental stage

transcription is initiated by said promoter. Expression patterns of a set of promoters are said to be complementary when the expression pattern of one promoter shows little overlap with the expression pattern of the other promoter. The level of expression of a promoter can be determined by measuring the 'steady state' concentration of a standard transcribed reporter mRNA. This measurement is indirect since the concentration of the reporter mRNA is dependent not only on its synthesis rate, but also on the rate with which the mRNA is degraded. Therefore, the steady state level is the product of synthesis rates and degradation rates.

The rate of degradation can however be considered to proceed at a fixed rate when the transcribed sequences are identical, and thus this value can serve as a measure of synthesis rates. When promoters are compared in this way techniques available to those skilled in the art are hybridization S1-RNase analysis, northern blots and competitive RT-PCR. This list of techniques in no way represents all available techniques, but rather describes commonly used procedures used to analyze transcription activity and expression levels of mRNA.

The analysis of transcription start points in practically all promoters has revealed that there is usually no single base at which transcription starts, but rather a more or less clustered set of initiation sites, each of which accounts for some start points of the mRNA. Since this distribution varies from promoter to promoter the sequences of the reporter mRNA in each of the populations would differ from each other. Since each mRNA species is more or less prone to degradation, no single degradation rate can be expected for different reporter mRNAs. It has been shown for various eukaryotic promoter sequences that the sequence surrounding the initiation site ('initiator') plays an important role in determining the level of RNA expression directed by that specific promoter. This includes also part of the transcribed sequences. The direct fusion of promoter to reporter sequences would therefore lead to suboptimal levels of transcription.

A commonly used procedure to analyze expression patterns and levels is through determination of the 'steady state' level of protein accumulation in a cell. Commonly used candidates for the reporter gene, known to those skilled in the art are β -glucuronidase (GUS), chloramphenicol acetyl transferase (CAT) and proteins with fluorescent properties, such as green fluorescent protein (GFP) from *Aequora victoria*. In principle, however, many more proteins are suitable for this purpose, provided the protein does not interfere with essential plant functions. For quantification and determination of localization a number of tools are suited. Detection systems can readily be created or are available which are based on, e.g.,

immunochemical, enzymatic, fluorescent detection and quantification. Protein levels can be determined in plant tissue extracts or in intact tissue using *in situ* analysis of protein expression.

Generally, individual transformed lines with one chimeric promoter reporter construct will vary in their levels of expression of the reporter gene. Also frequently observed is the phenomenon that such transformants do not express any detectable product (RNA or protein). The variability in expression is commonly ascribed to 'position effects', although the molecular mechanisms underlying this inactivity are usually not clear.

The term "average expression" is used here as the average level of expression found in all lines that do express detectable amounts of reporter gene, so leaving out of the analysis plants that do not express any detectable reporter mRNA or protein.

"Root expression level" indicates the expression level found in protein extracts of complete plant roots. Likewise, leaf, and stem expression levels, are determined using whole extracts from leaves and stems. It is acknowledged however, that within each of the plant parts just described, cells with variable functions may exist, in which promoter activity may vary.

"Non-specific expression" refers to constitutive expression or low level, basal ('leaky') expression in undesired cells or tissues from a 'regulated promoter'.

"Altered levels" refers to the level of expression in transgenic organisms that differs from that of normal or untransformed organisms.

"Overexpression" refers to the level of expression in transgenic cells or organisms that exceeds levels of expression in normal or untransformed (nontransgenic) cells or organisms.

"Antisense inhibition" refers to the production of antisense RNA transcripts capable of suppressing the expression of protein from an endogenous gene or a transgene.

"Co-suppression" and "transwitch" each refer to the production of sense RNA transcripts capable of suppressing the expression of identical or substantially similar transgene or endogenous genes (U.S. Patent No. 5,231,020).

"Gene silencing" refers to homology-dependent suppression of viral genes, transgenes, or endogenous nuclear genes. Gene silencing may be transcriptional, when the suppression is due to decreased transcription of the affected genes, or post-transcriptional, when the suppression is due to increased turnover (degradation) of RNA species homologous to the affected genes (English et al., 1996). Gene silencing includes virus-induced gene silencing (Ruiz et al. 1998).

"Silencing suppressor" gene refers to a gene whose expression leads to counteracting gene silencing and enhanced expression of silenced genes. Silencing suppressor genes may be of plant, non-plant, or viral origin. Examples include, but are not limited to HC-Pro, P1-HC-Pro, and 2b proteins. Other examples include one or more genes in TGMV-B genome.

5 The terms "heterologous DNA sequence," "exogenous DNA segment" or "heterologous nucleic acid," as used herein, each refer to a sequence that originates from a source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include
10 non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the terms refer to a DNA segment that is foreign or heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides. A "homologous" DNA sequence is a DNA sequence that is naturally associated with a host cell
15 into which it is introduced.

"Homologous to" in the context of nucleotide sequence identity refers to the similarity between the nucleotide sequence of two nucleic acid molecules or between the amino acid sequences of two protein molecules. Estimates of such homology are provided by either DNA-DNA or DNA-RNA hybridization under conditions of stringency as is well understood
20 by those skilled in the art (as described in Haines and Higgins (eds.), Nucleic Acid Hybridization, IRL Press, Oxford, U.K.), or by the comparison of sequence similarity between two nucleic acids or proteins.

The term "substantially similar" refers to nucleotide and amino acid sequences that represent functional and/or structural equivalents of *Arabidopsis* sequences disclosed herein.
25 For example, altered nucleotide sequences which simply reflect the degeneracy of the genetic code but nonetheless encode amino acid sequences that are identical to a particular amino acid sequence are substantially similar to the particular sequences. In addition, amino acid sequences that are substantially similar to a particular sequence are those wherein overall amino acid identity is at least 65% or greater to the instant sequences. Modifications that
30 result in equivalent nucleotide or amino acid sequences are well within the routine skill in the art. Moreover, the skilled artisan recognizes that equivalent nucleotide sequences encompassed by this invention can also be defined by their ability to hybridize, under low, moderate and/or stringent conditions (e.g., 0.1X SSC, 0.1% SDS, 65°C), with the nucleotide

sequences that are within the literal scope of the instant claims.

"Target gene" refers to a gene on the replicon that expresses the desired target coding sequence, functional RNA, or protein. The target gene is not essential for replicon replication. Additionally, target genes may comprise native non-viral genes inserted into a non-native organism, or chimeric genes, and will be under the control of suitable regulatory sequences. Thus, the regulatory sequences in the target gene may come from any source, including the virus. Target genes may include coding sequences that are either heterologous or homologous to the genes of a particular plant to be transformed. However, target genes do not include native viral genes. Typical target genes include, but are not limited to genes encoding a structural protein, a seed storage protein, a protein that conveys herbicide resistance, and a protein that conveys insect resistance. Proteins encoded by target genes are known as "foreign proteins". The expression of a target gene in a plant will typically produce an altered plant trait.

The term "altered plant trait" means any phenotypic or genotypic change in a transgenic plant relative to the wild-type or non-transgenic plant host.

"Transcription Stop Fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as polyadenylation signal sequences, capable of terminating transcription. Examples include the 3' non-regulatory regions of genes encoding nopaline synthase and the small subunit of ribulose biphosphate carboxylase.

"Replication gene" refers to a gene encoding a viral replication protein. In addition to the ORF of the replication protein, the replication gene may also contain other overlapping or non-overlapping ORF(s), as are found in viral sequences in nature. While not essential for replication, these additional ORFs may enhance replication and/or viral DNA accumulation. Examples of such additional ORFs are AC3 and AL3 in ACMV and TGMV geminiviruses, respectively.

"Chimeric *trans*-acting replication gene" refers either to a replication gene in which the coding sequence of a replication protein is under the control of a regulated plant promoter other than that in the native viral replication gene, or a modified native viral replication gene, for example, in which a site specific sequence(s) is inserted in the 5' transcribed but untranslated region. Such chimeric genes also include insertion of the known sites of

replication protein binding between the promoter and the transcription start site that attenuate transcription of viral replication protein gene.

"Chromosomally-integrated" refers to the integration of a foreign gene or DNA construct into the host DNA by covalent bonds. Where genes are not "chromosomally integrated" they may be "transiently expressed." Transient expression of a gene refers to the
5 expression of a gene that is not integrated into the host chromosome but functions independently, either as part of an autonomously replicating plasmid or expression cassette, for example, or as part of another biological system such as a virus.

"Production tissue" refers to mature, harvestable tissue consisting of non-dividing,
10 terminally-differentiated cells. It excludes young, growing tissue consisting of germline, meristematic, and not-fully-differentiated cells.

"Germline cells" refer to cells that are destined to be gametes and whose genetic material is heritable.

"*Trans*-activation" refers to switching on of gene expression or replicon replication by
15 the expression of another (regulatory) gene in *trans*.

The term "transformation" refers to the transfer of a nucleic acid fragment into the genome of a host cell, resulting in genetically stable inheritance. Host cells containing the transformed nucleic acid fragments are referred to as "transgenic" cells, and organisms comprising transgenic cells are referred to as "transgenic organisms". Examples of methods of
20 transformation of plants and plant cells include *Agrobacterium*-mediated transformation (De Blaere et al., 1987) and particle bombardment technology (Klein et al. 1987; U.S. Patent No. 4,945,050). Whole plants may be regenerated from transgenic cells by methods well known to the skilled artisan (see, for example, Fromm et al., 1990).

"Transformed," "transgenic," and "recombinant" refer to a host organism such as a
25 bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome generally known in the art and are disclosed in Sambrook et al., 1989. See also Innis et al., 1995 and Gelfand, 1995; and Innis and Gelfand, 1999. Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific
30 primers, vector-specific primers, partially mismatched primers, and the like. For example, "transformed," "transformant," and "transgenic" plants or calli have been through the transformation process and contain a foreign gene integrated into their chromosome. The term "untransformed" refers to normal plants that have not been through the transformation process.

"Transiently transformed" refers to cells in which transgenes and foreign DNA have been introduced (for example, by such methods as *Agrobacterium*-mediated transformation or biolistic bombardment), but not selected for stable maintenance.

5 "Stably transformed" refers to cells that have been selected and regenerated on a selection media following transformation.

"Transient expression" refers to expression in cells in which a virus or a transgene is introduced by viral infection or by such methods as *Agrobacterium*-mediated transformation, electroporation, or biolistic bombardment, but not selected for its stable maintenance.

10 "Genetically stable" and "heritable" refer to chromosomally-integrated genetic elements that are stably maintained in the plant and stably inherited by progeny through successive generations.

"Primary transformant" and "T0 generation" refer to transgenic plants that are of the same genetic generation as the tissue which was initially transformed (i.e., not having gone through meiosis and fertilization since transformation).

15 "Secondary transformants" and the "T1, T2, T3, etc. generations" refer to transgenic plants derived from primary transformants through one or more meiotic and fertilization cycles. They may be derived by self-fertilization of primary or secondary transformants or crosses of primary or secondary transformants with other transformed or untransformed plants.

"Wild-type" refers to a virus or organism found in nature without any known mutation.

20 "Genome" refers to the complete genetic material of an organism.

The term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, composed of monomers (nucleotides) containing a sugar, phosphate and a base which is either a purine or pyrimidine. Unless specifically limited, the term encompasses nucleic acids containing known analogs of natural
25 nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may
30 be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzner et al., 1991; Ohtsuka et al., 1985; Rossolini et al. 1994). A "nucleic acid fragment" is a fraction of a given nucleic acid molecule. In higher plants, deoxyribonucleic acid (DNA) is the genetic material

while ribonucleic acid (RNA) is involved in the transfer of information contained within DNA into proteins. The term "nucleotide sequence" refers to a polymer of DNA or RNA which can be single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases capable of incorporation into DNA or RNA polymers. The terms "nucleic acid" or
5 "nucleic acid sequence" may also be used interchangeably with gene, cDNA, DNA and RNA encoded by a gene.

The invention encompasses isolated or substantially purified nucleic acid or protein compositions. In the context of the present invention, an "isolated" or "purified" DNA molecule or an "isolated" or "purified" polypeptide is a DNA molecule or polypeptide that, by
10 the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or polypeptide may exist in a purified form or may exist in a non-native environment such as, for example, a transgenic host cell. For example, an "isolated" or "purified" nucleic acid molecule or protein, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by
15 recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. Preferably, an "isolated" nucleic acid is free of sequences (preferably protein encoding sequences) that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can
20 contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A protein that is substantially free of cellular material includes preparations of protein or polypeptide having less than about 30%, 20%, 10%, 5%, (by dry weight) of contaminating protein. When the protein of the invention, or biologically active
25 portion thereof, is recombinantly produced, preferably culture medium represents less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-protein of interest chemicals.

The nucleotide sequences of the invention include both the naturally occurring sequences as well as mutant (variant) forms. Such variants will continue to possess the desired
30 activity, i.e., either promoter activity or the activity of the product encoded by the open reading frame of the non-variant nucleotide sequence.

Thus, by "variants" is intended substantially similar sequences. For nucleotide sequences comprising an open reading frame, variants include those sequences that, because of

the degeneracy of the genetic code, encode the identical amino acid sequence of the native protein. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques. Variant nucleotide sequences also include synthetically
5 derived nucleotide sequences, such as those generated, for example, by using site-directed mutagenesis and for open reading frames, encode the native protein, as well as those that encode a polypeptide having amino acid substitutions relative to the native protein. Generally, nucleotide sequence variants of the invention will have at least 40, 50, 60, to 70%, e.g., preferably 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, to 79%, generally at least 80%, e.g.,
10 81%-84%, at least 85%, e.g., 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, to 98% and 99% nucleotide sequence identity to the native (wild type or endogenous) nucleotide sequence.

"Conservatively modified variations" of a particular nucleic acid sequence refers to those nucleic acid sequences that encode identical or essentially identical amino acid
15 sequences, or where the nucleic acid sequence does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given polypeptide. For instance the codons CGT, CGC, CGA, CGG, AGA, and AGG all encode the amino acid arginine. Thus, at every position where an arginine is specified by a codon, the codon can be altered to any of the
20 corresponding codons described without altering the encoded protein. Such nucleic acid variations are "silent variations" which are one species of "conservatively modified variations." Every nucleic acid sequence described herein which encodes a polypeptide also describes every possible silent variation, except where otherwise noted. One of skill will recognize that each codon in a nucleic acid (except ATG, which is ordinarily the only codon
25 for methionine) can be modified to yield a functionally identical molecule by standard techniques. Accordingly, each "silent variation" of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

The nucleic acid molecules of the invention can be "optimized" for enhanced expression in plants of interest. See, for example, EPA 035472; WO 91/16432; Perlak et al.,
30 1991; and Murray et al., 1989. In this manner, the open reading frames in genes or gene fragments can be synthesized utilizing plant-preferred codons. See, for example, Campbell and Gowri, 1990 for a discussion of host-preferred codon usage. Thus, the nucleotide sequences can be optimized for expression in any plant. It is recognized that all or any part of

the gene sequence may be optimized or synthetic. That is, synthetic or partially optimized sequences may also be used. Variant nucleotide sequences and proteins also encompass sequences and protein derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different coding sequences can be manipulated
5 to create a new polypeptide possessing the desired properties. In this manner, libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer, 1994; Stemmer, 1994; Cramer et al., 1997; Moore et
10 al., 1997; Zhang et al., 1997; Cramer et al., 1998; and U.S. Patent Nos. 5,605,793 and 5,837,458.

By "variant" polypeptide is intended a polypeptide derived from the native protein by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or
15 more sites in the native protein; or substitution of one or more amino acids at one or more sites in the native protein. Such variants may result from, for example, genetic polymorphism or from human manipulation. Methods for such manipulations are generally known in the art.

Thus, the polypeptides may be altered in various ways including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are
20 generally known in the art. For example, amino acid sequence variants of the polypeptides can be prepared by mutations in the DNA. Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel, 1985; Kunkel et al., 1987; U. S. Patent No. 4,873,192; Walker and Gaastra, 1983 and the references cited therein. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of
25 interest may be found in the model of Dayhoff et al. (1978). Conservative substitutions, such as exchanging one amino acid with another having similar properties, are preferred.

Individual substitutions deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids (typically less than 5%, more typically less than 1%) in an encoded sequence are "conservatively modified variations," where the alterations result
30 in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. The following five groups each contain amino acids that are conservative substitutions for one another: Aliphatic: Glycine (G), Alanine (A), Valine (V), Leucine (L), Isoleucine (I);

Aromatic: Phenylalanine (F), Tyrosine (Y), Tryptophan (W); Sulfur-containing: Methionine (M), Cysteine (C); Basic: Arginine I, Lysine (K), Histidine (H); Acidic: Aspartic acid (D), Glutamic acid (E), Asparagine (N), Glutamine (Q). See also, Creighton, 1984. In addition, individual substitutions, deletions or additions which alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence are also "conservatively modified variations."

"Expression cassette" as used herein means a DNA sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operably linked to the nucleotide sequence of interest which is operably linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. The expression of the nucleotide sequence in the expression cassette may be under the control of a constitutive promoter or of an inducible promoter which initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, the promoter can also be specific to a particular tissue or organ or stage of development.

"Vector" is defined to include, inter alia, any plasmid, cosmid, phage or *Agrobacterium* binary vector in double or single stranded linear or circular form which may or may not be self transmissible or mobilizable, and which can transform prokaryotic or eukaryotic host either by integration into the cellular genome or exist extrachromosomally (e.g. autonomous replicating plasmid with an origin of replication).

Specifically included are shuttle vectors by which is meant a DNA vehicle capable, naturally or by design, of replication in two different host organisms, which may be selected from actinomycetes and related species, bacteria and eukaryotic (e.g. higher plant, mammalian, yeast or fungal cells).

Preferably the nucleic acid in the vector is under the control of, and operably linked to, an appropriate promoter or other regulatory elements for transcription in a host cell such as a microbial, e.g. bacterial, or plant cell. The vector may be a bi-functional expression vector

which functions in multiple hosts. In the case of genomic DNA, this may contain its own promoter or other regulatory elements and in the case of cDNA this may be under the control of an appropriate promoter or other regulatory elements for expression in the host cell.

"Cloning vectors" typically contain one or a small number of restriction endonuclease recognition sites at which foreign DNA sequences can be inserted in a determinable fashion without loss of essential biological function of the vector, as well as a marker gene that is suitable for use in the identification and selection of cells transformed with the cloning vector. Marker genes typically include genes that provide tetracycline resistance, hygromycin resistance or ampicillin resistance.

10 A "transgenic plant" is a plant having one or more plant cells that contain an expression vector.

"Plant tissue" includes differentiated and undifferentiated tissues or plants, including but not limited to roots, stems, shoots, leaves, pollen, seeds, tumor tissue and various forms of cells and culture such as single cells, protoplast, embryos, and callus tissue. The plant tissue
15 may be in plants or in organ, tissue or cell culture.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence identity", and (e) "substantial identity".

(a) As used herein, "reference sequence" is a defined sequence used as a basis for
20 sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full length cDNA or gene sequence, or the complete cDNA or gene sequence.

(b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the
25 comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide
30 sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well known in the art. Thus, the determination of percent identity between any two sequences can be accomplished using a mathematical algorithm. Preferred, non-limiting examples of such mathematical algorithms

are the algorithm of Myers and Miller, 1988; the local homology algorithm of Smith et al. 1981; the homology alignment algorithm of Needleman and Wunsch 1970; the search-for-similarity-method of Pearson and Lipman 1988; the algorithm of Karlin and Altschul, 1990, modified as in Karlin and Altschul, 1993.

5 Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from
10 Genetics Computer Group (GCG), 575 Science Drive, Madison, Wisconsin, USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins et al. 1988; Higgins et al. 1989; Corpet et al. 1988; Huang et al. 1992; and Pearson et al. 1994. The ALIGN program is based on the algorithm of Myers and Miller, *supra*. The BLAST programs of Altschul et al., 1990, are
15 based on the algorithm of Karlin and Altschul *supra*.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when
20 aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the
25 parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more
30 negative-scoring residue alignments, or the end of either sequence is reached.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul (1993). One measure of similarity provided by the BLAST algorithm is the smallest

sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul et al. 1997. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul et al., *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g. BLASTN for nucleotide sequences, BLASTX for proteins) can be used. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989). See <http://www.ncbi.nlm.nih.gov>. Alignment may also be performed manually by inspection.

For purposes of the present invention, comparison of nucleotide sequences for determination of percent sequence identity to the promoter sequences disclosed herein is preferably made using the BlastN program (version 1.4.7 or later) with its default parameters or any equivalent program. By "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the preferred program.

(c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences makes reference to the residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the

substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity." Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California).

(d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, or 79%, preferably at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, and most preferably at least 95%, 96%, 97%, 98%, or 99% sequence identity, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 70%, more preferably at least 80%, 90%, and most preferably at least 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions (see below). Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1°C to about 20°C, depending upon the desired

degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two
5 nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

(e)(ii) The term "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, or
10 79%, preferably 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, or even more preferably, 95%, 96%, 97%, 98% or 99%, sequence identity to the reference sequence over a specified comparison window. Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch (1970). An indication that two peptide sequences are substantially
15 identical is that one peptide is immunologically reactive with antibodies raised against the second peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference
20 sequences are input into a computer, subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

As noted above, another indication that two nucleic acid sequences are substantially
25 identical is that the two molecules hybridize to each other under stringent conditions. The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA. "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target
30 nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

“Stringent hybridization conditions” and “stringent hybridization wash conditions” in the context of nucleic acid hybridization experiments such as Southern and Northern hybridization are sequence dependent, and are different under different environmental parameters. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, 1984; $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, $\%GC$ is the percentage of guanosine and cytosine nucleotides in the DNA, $\% \text{ form}$ is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with $>90\%$ identity are sought, the T_m can be decreased 10°C . Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point T_m for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point T_m ; moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point T_m ; low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point T_m . Using the equation, hybridization and wash compositions, and desired T_m , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen, 1993. Generally, highly stringent hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point T_m for the specific sequence at a defined ionic strength and pH.

An example of highly stringent wash conditions is 0.15 M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2X SSC wash at 65°C for 15 minutes (see, Sambrook, *infra*, for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium

stringency wash for a duplex of, e.g., more than 100 nucleotides, is 1X SSC at 45°C for 15 minutes. An example low stringency wash for a duplex of, e.g., more than 100 nucleotides, is 4-6X SSC at 40°C for 15 minutes. For short probes (e.g., about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.5 M, more preferably about 0.01 to 1.0 M, Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C and at least about 60°C for long robes (e.g., >50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2X (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or Northern blot is 50% formamide, e.g., hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C.

The following are examples of sets of hybridization/wash conditions that may be used to clone orthologous nucleotide sequences that are substantially identical to reference nucleotide sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X

SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

“DNA shuffling” is a method to introduce mutations or rearrangements, preferably randomly, in a DNA molecule or to generate exchanges of DNA sequences between two or more DNA molecules, preferably randomly. The DNA molecule resulting from DNA shuffling is a shuffled DNA molecule that is a non-naturally occurring DNA molecule derived from at least one template DNA molecule. The shuffled DNA preferably encodes a variant polypeptide modified with respect to the polypeptide encoded by the template DNA, and may have an altered biological activity with respect to the polypeptide encoded by the template DNA.

“Recombinant DNA molecule” is a combination of DNA sequences that are joined together using recombinant DNA technology and procedures used to join together DNA sequences as described, for example, in Sambrook et al., 1989.

The word “plant” refers to any plant, particularly to seed plant, and “plant cell” is a structural and physiological unit of the plant, which comprises a cell wall but may also refer to a protoplast. The plant cell may be in form of an isolated single cell or a cultured cell, or as a part of higher organized unit such as, for example, a plant tissue, or a plant organ.

“Significant increase” is an increase that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater.

“Significantly less” means that the decrease is larger than the margin of error inherent in the measurement technique, preferably a decrease by about 2-fold or greater.

II. DNA Sequences for Transformation

Virtually any DNA composition may be used for delivery to recipient plant cells, e.g., monocotyledonous cells, to ultimately produce fertile transgenic plants in accordance with the present invention. For example, DNA segments in the form of vectors and plasmids, or linear DNA fragments, in some instances containing only the DNA element to be expressed in the plant, and the like, may be employed. The construction of vectors which may be employed in conjunction with the present invention will be known to those of skill of the art in light of the present disclosure (see, e.g., Sambrook et al., 1989; Gelvin et al., 1990).

Vectors, plasmids, cosmids, YACs (yeast artificial chromosomes), BACs (bacterial artificial chromosomes) and DNA segments for use in transforming such cells will, of course, generally comprise the cDNA, gene or genes which one desires to introduce into the cells. These DNA constructs can further include structures such as promoters, enhancers,

polylinkers, or even regulatory genes as desired. The DNA segment or gene chosen for cellular introduction will often encode a protein which will be expressed in the resultant recombinant cells, such as will result in a screenable or selectable trait and/or which will impart an improved phenotype to the regenerated plant. However, this may not always be the case, and the present invention also encompasses transgenic plants incorporating non-expressed transgenes.

In certain embodiments, it is contemplated that one may wish to employ replication-competent viral vectors in monocot transformation. Such vectors include, for example, wheat dwarf virus (WDV) "shuttle" vectors, such as pW1-11 and PW1-GUS (Ugaki et al., 1991). These vectors are capable of autonomous replication in maize cells as well as *E. coli*, and as such may provide increased sensitivity for detecting DNA delivered to transgenic cells. A replicating vector may also be useful for delivery of genes flanked by DNA sequences from transposable elements such as Ac, Ds, or Mu. It has been proposed (Laufs et al., 1990) that transposition of these elements within the maize genome requires DNA replication. It is also contemplated that transposable elements would be useful for introducing DNA fragments lacking elements necessary for selection and maintenance of the plasmid vector in bacteria, e.g., antibiotic resistance genes and origins of DNA replication. It is also proposed that use of a transposable element such as Ac, Ds, or Mu would actively promote integration of the desired DNA and hence increase the frequency of stably transformed cells. The use of a transposable element such as Ac, Ds, or Mu may actively promote integration of the DNA of interest and hence increase the frequency of stably transformed cells. Transposable elements may be useful to allow separation of genes of interest from elements necessary for selection and maintenance of a plasmid vector in bacteria or selection of a transformant. By use of a transposable element, desirable and undesirable DNA sequences may be transposed apart from each other in the genome, such that through genetic segregation in progeny, one may identify plants with either the desirable undesirable DNA sequences.

DNA useful for introduction into plant cells includes that which has been derived or isolated from any source, that may be subsequently characterized as to structure, size and/or function, chemically altered, and later introduced into plants. An example of DNA "derived" from a source, would be a DNA sequence that is identified as a useful fragment within a given organism, and which is then chemically synthesized in essentially pure form. An example of such DNA "isolated" from a source would be a useful DNA sequence that is excised or removed from said source by chemical means, e.g., by the use of restriction endonucleases, so

that it can be further manipulated, e.g., amplified, for use in the invention, by the methodology of genetic engineering. Such DNA is commonly referred to as "recombinant DNA."

Therefore useful DNA includes completely synthetic DNA, semi-synthetic DNA, DNA isolated from biological sources, and DNA derived from introduced RNA. Generally, the introduced DNA is not originally resident in the plant genotype which is the recipient of the DNA, but it is within the scope of the invention to isolate a gene from a given plant genotype, and to subsequently introduce multiple copies of the gene into the same genotype, e.g., to enhance production of a given gene product such as a storage protein or a protein that confers tolerance or resistance to water deficit.

The introduced DNA includes but is not limited to, DNA from plant genes, and non-plant genes such as those from bacteria, yeasts, animals or viruses. The introduced DNA can include modified genes, portions of genes, or chimeric genes, including genes from the same or different maize genotype. The term "chimeric gene" or "chimeric DNA" is defined as a gene or DNA sequence or segment comprising at least two DNA sequences or segments from species which do not combine DNA under natural conditions, or which DNA sequences or segments are positioned or linked in a manner which does not normally occur in the native genome of untransformed plant.

The introduced DNA used for transformation herein may be circular or linear, double-stranded or single-stranded. Generally, the DNA is in the form of chimeric DNA, such as plasmid DNA, that can also contain coding regions flanked by regulatory sequences which promote the expression of the recombinant DNA present in the resultant plant. For example, the DNA may itself comprise or consist of a promoter that is active in a plant which is derived from a source other than that plant, or may utilize a promoter already present in a plant genotype that is the transformation target.

Generally, the introduced DNA will be relatively small, i.e., less than about 30 kb to minimize any susceptibility to physical, chemical, or enzymatic degradation which is known to increase as the size of the DNA increases. As noted above, the number of proteins, RNA transcripts or mixtures thereof which is introduced into the plant genome is preferably preselected and defined, e.g., from one to about 5-10 such products of the introduced DNA may be formed.

Two principal methods for the control of expression are known, viz.: overexpression and underexpression. Overexpression can be achieved by insertion of one or more than one extra copy of the selected gene. It is, however, not unknown for plants or their progeny,

originally transformed with one or more than one extra copy of a nucleotide sequence, to exhibit the effects of underexpression as well as overexpression. For underexpression there are two principle methods which are commonly referred to in the art as “antisense downregulation” and “sense downregulation” (sense downregulation is also referred to as “cosuppression”). Generically these processes are referred to as “gene silencing”. Both of these methods lead to an inhibition of expression of the target gene.

Obtaining sufficient levels of transgene expression in the appropriate plant tissues is an important aspect in the production of genetically engineered crops. Expression of heterologous DNA sequences in a plant host is dependent upon the presence of an operably linked promoter that is functional within the plant host. Choice of the promoter sequence will determine when and where within the organism the heterologous DNA sequence is expressed.

Furthermore, it is contemplated that promoters combining elements from more than one promoter may be useful. For example, U.S. Patent No. 5,491,288 discloses combining a Cauliflower Mosaic Virus promoter with a histone promoter. Thus, the elements from the promoters disclosed herein may be combined with elements from other promoters.

Promoters which are useful for plant transgene expression include those that are inducible, viral, synthetic, constitutive (Odell et al., 1985), temporally regulated, spatially regulated, tissue-specific, and spatio-temporally regulated.

Where expression in specific tissues or organs is desired, tissue-specific promoters may be used. In contrast, where gene expression in response to a stimulus is desired, inducible promoters are the regulatory elements of choice. Where continuous expression is desired throughout the cells of a plant, constitutive promoters are utilized. Additional regulatory sequences upstream and/or downstream from the core promoter sequence may be included in expression constructs of transformation vectors to bring about varying levels of expression of heterologous nucleotide sequences in a transgenic plant.

A. Transcription Regulatory Sequences

1. Promoters

The choice of promoter will vary depending on the temporal and spatial requirements for expression, and also depending on the target species. In some cases, expression in multiple tissues is desirable. While in others, tissue-specific, e.g., leaf-specific, seed-specific, petal-specific, anther-specific, or pith-specific, expression is desirable. Although many promoters from dicotyledons have been shown to be operational in monocotyledons and *vice versa*, ideally dicotyledonous promoters are selected for expression

in dicotyledons, and monocotyledonous promoters for expression in monocotyledons.

However, there is no restriction to the provenance of selected promoters; it is sufficient that they are operational in driving the expression of the nucleotide sequences in the desired cell.

These promoters include, but are not limited to, constitutive, inducible, temporally
5 regulated, developmentally regulated, spatially-regulated, chemically regulated, stress-
responsive, tissue-specific, viral and synthetic promoters. Promoter sequences are known to be
strong or weak. A strong promoter provides for a high level of gene expression, whereas a
weak promoter provides for a very low level of gene expression. An inducible promoter is a
promoter that provides for the turning on and off of gene expression in response to an
10 exogenously added agent, or to an environmental or developmental stimulus. A bacterial
promoter such as the P_{tac} promoter can be induced to varying levels of gene expression
depending on the level of isothiopyrogalactoside added to the transformed bacterial cells.
An isolated promoter sequence that is a strong promoter for heterologous nucleic acid is
advantageous because it provides for a sufficient level of gene expression to allow for easy
15 detection and selection of transformed cells and provides for a high level of gene expression
when desired.

Within a plant promoter region there are several domains that are necessary for full
function of the promoter. The first of these domains lies immediately upstream of the
structural gene and forms the "core promoter region" containing consensus sequences,
20 normally 70 base pairs immediately upstream of the gene. The core promoter region contains
the characteristic CAAT and TATA boxes plus surrounding sequences, and represents a
transcription initiation sequence that defines the transcription start point for the structural gene.

The presence of the core promoter region defines a sequence as being a promoter: if the
region is absent, the promoter is non-functional. Furthermore, the core promoter region is
25 insufficient to provide full promoter activity. A series of regulatory sequences upstream of the
core constitute the remainder of the promoter. The regulatory sequences determine expression
level, the spatial and temporal pattern of expression and, for an important subset of promoters,
expression under inductive conditions (regulation by external factors such as light,
temperature, chemicals, hormones).

30 A range of naturally-occurring promoters are known to be operative in plants and have
been used to drive the expression of heterologous (both foreign and endogenous) genes in
plants: for example, the constitutive 35S cauliflower mosaic virus (CaMV) promoter, the
ripening-enhanced tomato polygalacturonase promoter (Bird et al., 1988), the E8 promoter

(Diekman & Fischer, 1988) and the fruit specific 2A1 promoter (Pear et al., 1989) and many others, e.g., U2 and U5 snRNA promoters from maize, the promoter from alcohol dehydrogenase, the Z4 promoter from a gene encoding the Z4 22 kD zein protein, the Z10 promoter from a gene encoding a 10 kD zein protein, a Z27 promoter from a gene encoding a 27 kD zein protein, the A20 promoter from the gene encoding a 19 kD -zein protein, inducible promoters, such as the light inducible promoter derived from the pea *rbcS* gene and the actin promoter from rice, e.g., the actin 2 promoter (WO 00/70067); seed specific promoters, such as the phaseolin promoter from beans, may also be used. The nucleotide sequences of this invention can also be expressed under the regulation of promoters that are chemically regulated. This enables the nucleic acid sequence or encoded polypeptide to be synthesized only when the crop plants are treated with the inducing chemicals. Chemical induction of gene expression is detailed in EP 0 332 104 (to Ciba-Geigy) and U.S. Patent 5,614,395. A preferred promoter for chemical induction is the tobacco PR-1a promoter.

Examples of some constitutive promoters which have been described include the rice actin 1 (Wang et al., 1992; U.S. Patent No. 5,641,876), CaMV 35S (Odell et al., 1985), CaMV 19S (Lawton et al., 1987), *nos*, *Adh*, sucrose synthase; and the ubiquitin promoters.

Examples of tissue specific promoters which have been described include the lectin (Vodkin, 1983; Lindstrom et al., 1990) corn alcohol dehydrogenase 1 (Vogel et al., 1989; Dennis et al., 1984), corn light harvesting complex (Simpson, 1986; Bansal et al., 1992), corn heat shock protein (Odell et al., 1985), pea small subunit RuBP carboxylase (Poulsen et al., 1986), Ti plasmid mannopine synthase (Langridge et al., 1989), Ti plasmid nopaline synthase (Langridge et al., 1989), petunia chalcone isomerase (vanTunen et al., 1988), bean glycine rich protein 1 (Keller et al., 1989), truncated CaMV 35s (Odell et al., 1985), potato patatin (Wenzler et al., 1989), root cell (Yamamoto et al., 1990), maize zein (Reina et al., 1990; Kriz et al., 1987; Wandelt et al., 1989; Langridge et al., 1983; Reina et al., 1990), globulin-1 (Belanger et al., 1991), α -tubulin, *cab* (Sullivan et al., 1989), PEPCase (Hudspeth & Grula, 1989), R gene complex-associated promoters (Chandler et al., 1989), histone, and chalcone synthase promoters (Franken et al., 1991). Tissue specific enhancers are described in Fromm et al. (1989).

Inducible promoters that have been described include the ABA- and turgor-inducible promoters, the promoter of the auxin-binding protein gene (Schwob et al., 1993), the UDP glucose flavonoid glycosyl-transferase gene promoter (Ralston et al., 1988), the MPI

proteinase inhibitor promoter (Cordero et al., 1994), and the glyceraldehyde-3-phosphate dehydrogenase gene promoter (Kohler et al., 1995; Quigley et al., 1989; Martinez et al., 1989).

Several other tissue-specific regulated genes and/or promoters have been reported in plants. These include genes encoding the seed storage proteins (such as napin, cruciferin, beta-conglycinin, and phaseolin) zein or oil body proteins (such as oleosin), or genes involved in fatty acid biosynthesis (including acyl carrier protein, stearoyl-ACP desaturase. And fatty acid desaturases (fad 2-1)), and other genes expressed during embryo development (such as Bce4, see, for example, EP 255378 and Kridl et al., 1991). Particularly useful for seed-specific expression is the pea vicilin promoter (Czako et al., 1992). (See also U.S. Pat. No. 5,625,136, herein incorporated by reference.) Other useful promoters for expression in mature leaves are those that are switched on at the onset of senescence, such as the SAG promoter from *Arabidopsis* (Gan et al., 1995).

A class of fruit-specific promoters expressed at or during antithesis through fruit development, at least until the beginning of ripening, is discussed in U.S. 4,943,674. cDNA clones that are preferentially expressed in cotton fiber have been isolated (John et al., 1992). cDNA clones from tomato displaying differential expression during fruit development have been isolated and characterized (Mansson et al., 1985, Slater et al., 1985). The promoter for polygalacturonase gene is active in fruit ripening. The polygalacturonase gene is described in U.S. Patent No. 4,535,060, U.S. Patent No. 4,769,061, U.S. Patent No. 4,801,590, and U.S. Patent No. 5,107,065, which disclosures are incorporated herein by reference.

Other examples of tissue-specific promoters include those that direct expression in leaf cells following damage to the leaf (for example, from chewing insects), in tubers (for example, patatin gene promoter), and in fiber cells (an example of a developmentally-regulated fiber cell protein is E6 (John et al., 1992). The E6 gene is most active in fiber, although low levels of transcripts are found in leaf, ovule and flower.

The tissue-specificity of some "tissue-specific" promoters may not be absolute and may be tested by one skilled in the art using the diphtheria toxin sequence. One can also achieve tissue-specific expression with "leaky" expression by a combination of different tissue-specific promoters (Beals et al., 1997). Other tissue-specific promoters can be isolated by one skilled in the art (see U.S. 5,589,379). Several inducible promoters ("gene switches") have been reported. Many are described in the review by Gatz (1996) and Gatz (1997). These include tetracycline repressor system, *Lac* repressor system, copper-inducible systems, salicylate-inducible systems (such as the PR1a system), glucocorticoid- (Aoyama et al., 1997) and

ecdysome-inducible systems. Also included are the benzene sulphonamide- (U.S. Patent No. 5,364,780) and alcohol-(WO 97/06269 and WO 97/06268) inducible systems and glutathione S-transferase promoters. Other studies have focused on genes inducibly regulated in response to environmental stress or stimuli such as increased salinity. Drought, pathogen and wounding. (Graham et al., 1985; Graham et al., 1985, Smith et al., 1986). Accumulation of metallocarboxypeptidase-inhibitor protein has been reported in leaves of wounded potato plants (Graham et al., 1981). Other plant genes have been reported to be induced methyl jasmonate, elicitors, heat-shock, anaerobic stress, or herbicide safeners.

Regulated expression of the chimeric transacting viral replication protein can be further regulated by other genetic strategies. For example, *Cre*-mediated gene activation as described by Odell et al. 1990. Thus, a DNA fragment containing 3' regulatory sequence bound by lox sites between the promoter and the replication protein coding sequence that blocks the expression of a chimeric replication gene from the promoter can be removed by *Cre*-mediated excision and result in the expression of the *trans*-acting replication gene. In this case, the chimeric *Cre* gene, the chimeric *trans*-acting replication gene, or both can be under the control of tissue- and developmental- specific or inducible promoters. An alternate genetic strategy is the use of tRNA suppressor gene. For example, the regulated expression of a tRNA suppressor gene can conditionally control expression of a *trans*-acting replication protein coding sequence containing an appropriate termination codon as described by Ulmasov et al. 1997. Again, either the chimeric tRNA suppressor gene, the chimeric transacting replication gene, or both can be under the control of tissue- and developmental-specific or inducible promoters.

Frequently it is desirable to have continuous or inducible expression of a DNA sequence throughout the cells of an organism in a tissue-independent manner. For example, increased resistance of a plant to infection by soil- and airborne-pathogens might be accomplished by genetic manipulation of the plant's genome to comprise a continuous promoter operably linked to a heterologous pathogen-resistance gene such that pathogen-resistance proteins are continuously expressed throughout the plant's tissues.

Alternatively, it might be desirable to inhibit expression of a native DNA sequence within a plant's tissues to achieve a desired phenotype. In this case, such inhibition might be accomplished with transformation of the plant to comprise a constitutive, tissue-independent promoter operably linked to an antisense nucleotide sequence, such that constitutive

expression of the antisense sequence produces an RNA transcript that interferes with translation of the mRNA of the native DNA sequence.

To define a minimal promoter region, a DNA segment representing the promoter region is removed from the 5' region of the gene of interest and operably linked to the coding sequence of a marker (reporter) gene by recombinant DNA techniques well known to the art. The reporter gene is operably linked downstream of the promoter, so that transcripts initiating at the promoter proceed through the reporter gene. Reporter genes generally encode proteins which are easily measured, including, but not limited to, chloramphenicol acetyl transferase (CAT), beta-glucuronidase (GUS), green fluorescent protein (GFP), beta-galactosidase (beta-GAL), and luciferase.

The construct containing the reporter gene under the control of the promoter is then introduced into an appropriate cell type by transfection techniques well known to the art. To assay for the reporter protein, cell lysates are prepared and appropriate assays, which are well known in the art, for the reporter protein are performed. For example, if CAT were the reporter gene of choice, the lysates from cells transfected with constructs containing CAT under the control of a promoter under study are mixed with isotopically labeled chloramphenicol and acetyl-coenzyme A (acetyl-CoA). The CAT enzyme transfers the acetyl group from acetyl-CoA to the 2- or 3-position of chloramphenicol. The reaction is monitored by thin-layer chromatography, which separates acetylated chloramphenicol from unreacted material. The reaction products are then visualized by autoradiography.

The level of enzyme activity corresponds to the amount of enzyme that was made, which in turn reveals the level of expression from the promoter of interest. This level of expression can be compared to other promoters to determine the relative strength of the promoter under study. In order to be sure that the level of expression is determined by the promoter, rather than by the stability of the mRNA, the level of the reporter mRNA can be measured directly, such as by Northern blot analysis.

Once activity is detected, mutational and/or deletional analyses may be employed to determine the minimal region and/or sequences required to initiate transcription. Thus, sequences can be deleted at the 5' end of the promoter region and/or at the 3' end of the promoter region, and nucleotide substitutions introduced. These constructs are then introduced to cells and their activity determined.

In one embodiment, the promoter may be a gamma zein promoter, an oleosin ole16 promoter, a globulinI promoter, an actin I promoter, an actin cl promoter, a sucrose synthetase

promoter, an INOPS promoter, an EXM5 promoter, a globulin2 promoter, a b-32, ADPG-pyrophosphorylase promoter, an LtpI promoter, an Ltp2 promoter, an oleosin ole17 promoter, an oleosin ole18 promoter, an actin 2 promoter, a pollen-specific protein promoter, a pollen-specific pectate lyase promoter, an anther-specific protein promoter (Huffman), an anther-specific gene RTS2 promoter, a pollen-specific gene promoter, a tapetum-specific gene promoter, tapetum-specific gene RAB24 promoter, a anthranilate synthase alpha subunit promoter, an alpha zein promoter, an anthranilate synthase beta subunit promoter, a dihydrodipicolinate synthase promoter, a Thil promoter, an alcohol dehydrogenase promoter, a cab binding protein promoter, an H3C4 promoter, a RUBISCO SS starch branching enzyme promoter, an ACCase promoter, an actin3 promoter, an actin7 promoter, a regulatory protein GF14-12 promoter, a ribosomal protein L9 promoter, a cellulose biosynthetic enzyme promoter, an S-adenosyl-L-homocysteine hydrolase promoter, a superoxide dismutase promoter, a C-kinase receptor promoter, a phosphoglycerate mutase promoter, a root-specific RCc3 mRNA promoter, a glucose-6 phosphate isomerase promoter, a pyrophosphate-fructose 6-phosphatetphosphotransferase promoter, an ubiquitin promoter, a beta-ketoacyl-ACP synthase promoter, a 33 kDa photosystem 11 promoter, an oxygen evolving protein promoter, a 69 kDa vacuolar ATPase subunit promoter, a metallothionein-like protein promoter, a glyceraldehyde-3-phosphate dehydrogenase promoter, an ABA- and ripening-inducible-like protein promoter, a phenylalanine ammonia lyase promoter, an adenosine triphosphatase S-adenosyl-L-homocysteine hydrolase promoter, an a-tubulin promoter, a cab promoter, a PEPCase promoter, an R gene promoter, a lectin promoter, a light harvesting complex promoter, a heat shock protein promoter, a chalcone synthase promoter, a zein promoter, a globulin-1 promoter, an ABA promoter, an auxin-binding protein promoter, a UDP glucose flavonoid glycosyl-transferase gene promoter, an NTI promoter, an actin promoter, an opaque 2 promoter, a b70 promoter, an oleosin promoter, a CaMV 35S promoter, a CaMV 19S promoter, a histone promoter, a turgor-inducible promoter, a pea small subunit RuBP carboxylase promoter, a Ti plasmid mannopine synthase promoter, Ti plasmid nopaline synthase promoter, a petunia chalcone isomerase promoter, a bean glycine rich protein I promoter, a CaMV 35S transcript promoter, a potato patatin promoter, or a S-E9 small subunit RuBP carboxylase promoter.

2. Other Regulatory Elements

In addition to promoters, a variety of 5' and 3' transcriptional regulatory sequences are also available for use in the present invention. Transcriptional terminators are responsible

for the termination of transcription and correct mRNA polyadenylation. The 3N nontranslated regulatory DNA sequence preferably includes from about 50 to about 1,000, more preferably about 100 to about 1,000, nucleotide base pairs and contains plant transcriptional and translational termination sequences. Appropriate transcriptional terminators and those which are known to function in plants include the CaMV 35S terminator, the *tml* terminator, the nopaline synthase terminator, the pea *rbcS* E9 terminator, the terminator for the T7 transcript from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3N end of the protease inhibitor I or II genes from potato or tomato, although other 3N elements known to those of skill in the art can also be employed. Alternatively, one also could use a gamma coixin, oleosin 3 or other terminator from the genus *Coix*.

Preferred 3' elements include those from the nopaline synthase gene of *Agrobacterium tumefaciens* (Bevan et al., 1983), the terminator for the T7 transcript from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3' end of the protease inhibitor I or II genes from potato or tomato.

As the DNA sequence between the transcription initiation site and the start of the coding sequence, i.e., the untranslated leader sequence, can influence gene expression, one may also wish to employ a particular leader sequence. Preferred leader sequences are contemplated to include those which include sequences predicted to direct optimum expression of the attached gene, i.e., to include a preferred consensus leader sequence which may increase or maintain mRNA stability and prevent inappropriate initiation of translation. The choice of such sequences will be known to those of skill in the art in light of the present disclosure. Sequences that are derived from genes that are highly expressed in plants will be most preferred.

Other sequences that have been found to enhance gene expression in transgenic plants include intron sequences (e.g., from *Adh1*, *bronzel*, *actin1*, *actin 2* (WO 00/760067), or the sucrose synthase intron) and viral leader sequences (e.g., from TMV, MCMV and AMV). For example, a number of non-translated leader sequences derived from viruses are known to enhance expression. Specifically, leader sequences from Tobacco Mosaic Virus (TMV), Maize Chlorotic Mottle Virus (MCMV), and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (e.g., Gallie et al., 1987; Skuzeski et al., 1990). Other leaders known in the art include but are not limited to: Picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5 noncoding region) (Elroy-Stein et al., 1989); Potyvirus leaders, for example, TEV leader (Tobacco Etch Virus); MDMV leader (Maize Dwarf Mosaic

Virus); Human immunoglobulin heavy-chain binding protein (BiP) leader, (Macejak et al., 1991); Untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), (Jobling et al., 1987; Tobacco mosaic virus leader (TMV), (Gallie et al., 1989; and Maize Chlorotic Mottle Virus leader (MCMV) (Lommel et al., 1991. See also, Della-Cioppa et al., 1987.

Regulatory elements such as Adh intron 1 (Callis et al., 1987), sucrose synthase intron (Vasil et al., 1989) or TMV omega element (Gallie, et al., 1989), may further be included where desired.

Examples of enhancers include elements from the CaMV 35S promoter, octopine synthase genes (Ellis et al., 1987), the rice actin I gene, the maize alcohol dehydrogenase gene (Callis et al., 1987), the maize shrunken I gene (Vasil et al., 1989), TMV Omega element (Gallie et al., 1989) and promoters from non-plant eukaryotes (e.g. yeast; Ma et al., 1988).

Vectors for use in accordance with the present invention may be constructed to include the ocs enhancer element. This element was first identified as a 16 bp palindromic enhancer from the octopine synthase (ocs) gene of utilane (Ellis et al., 1987), and is present in at least 10 other promoters (Bouchez et al., 1989). The use of an enhancer element, such as the ocs element and particularly multiple copies of the element, will act to increase the level of transcription from adjacent promoters when applied in the context of monocot transformation.

Ultimately, the most desirable DNA segments for introduction into for example a monocot genome may be homologous genes or gene families which encode a desired trait (e.g., increased yield per acre) and which are introduced under the control of novel promoters or enhancers, etc., or perhaps even homologous or tissue specific (e.g., root-, collar/sheath-, whorl-, stalk-, earshank-, kernel- or leaf-specific) promoters or control elements. Indeed, it is envisioned that a particular use of the present invention will be the targeting of a gene in a constitutive manner or a root-specific manner. For example, insect resistant genes may be expressed specifically in the whorl and collar/sheath tissues which are targets for the first and second broods, respectively, of ECB. Likewise, genes encoding proteins with particular activity against rootworm may be targeted directly to root tissues.

Vectors for use in tissue-specific targeting of genes in transgenic plants will typically include tissue-specific promoters and may also include other tissue-specific control elements such as enhancer sequences. Promoters which direct specific or enhanced expression in certain plant tissues will be known to those of skill in the art in light of the present disclosure. These include, for example, the rbcS promoter, specific for green tissue; the ocs, nos and mas

promoters which have higher activity in roots or wounded leaf tissue; a truncated (-90 to +8) 35S promoter which directs enhanced expression in roots, an alpha-tubulin gene that directs expression in roots and promoters derived from zein storage protein genes which direct expression in endosperm. It is particularly contemplated that one may advantageously use the 16 bp ocs enhancer element from the octopine synthase (ocs) gene (Ellis et al., 1987; Bouchez et al., 1989), especially when present in multiple copies, to achieve enhanced expression in roots.

Tissue specific expression may be functionally accomplished by introducing a constitutively expressed gene (all tissues) in combination with an antisense gene that is expressed only in those tissues where the gene product is not desired. For example, a gene coding for the crystal toxin protein from *B. thuringiensis* (Bt) may be introduced such that it is expressed in all tissues using the 35S promoter from Cauliflower Mosaic Virus. Expression of an antisense transcript of the Bt gene in a maize kernel, using for example a zein promoter, would prevent accumulation of the Bt protein in seed. Hence the protein encoded by the introduced gene would be present in all tissues except the kernel.

Expression of some genes in transgenic plants will be desired only under specified conditions. For example, it is proposed that expression of certain genes that confer resistance to environmental stress factors such as drought will be desired only under actual stress conditions. It is contemplated that expression of such genes throughout a plants development may have detrimental effects. It is known that a large number of genes exist that respond to the environment. For example, expression of some genes such as *rbcS*, encoding the small subunit of ribulose biphosphate carboxylase, is regulated by light as mediated through phytochrome. Other genes are induced by secondary stimuli. For example, synthesis of abscisic acid (ABA) is induced by certain environmental factors, including but not limited to water stress. A number of genes have been shown to be induced by ABA (Skriver and Mundy, 1990). It is also anticipated that expression of genes conferring resistance to insect predation would be desired only under conditions of actual insect infestation. Therefore, for some desired traits inducible expression of genes in transgenic plants will be desired.

Expression of a gene in a transgenic plant will be desired only in a certain time period during the development of the plant. Developmental timing is frequently correlated with tissue specific gene expression. For example, expression of zein storage proteins is initiated in the endosperm about 15 days after pollination.

Additionally, vectors may be constructed and employed in the intracellular targeting of a specific gene product within the cells of a transgenic plant or in directing a protein to the extracellular environment. This will generally be achieved by joining a DNA sequence encoding a transit or signal peptide sequence to the coding sequence of a particular gene. The resultant transit, or signal, peptide will transport the protein to a particular intracellular, or extracellular destination, respectively, and will then be post-translationally removed. Transit or signal peptides act by facilitating the transport of proteins through intracellular membranes, e.g., vacuole, vesicle, plastid and mitochondrial membranes, whereas signal peptides direct proteins through the extracellular membrane.

A particular example of such a use concerns the direction of a herbicide resistance gene, such as the EPSPS gene, to a particular organelle such as the chloroplast rather than to the cytoplasm. This is exemplified by the use of the rbcS transit peptide which confers plastid-specific targeting of proteins. In addition, it is proposed that it may be desirable to target certain genes responsible for male sterility to the mitochondria, or to target certain genes for resistance to phytopathogenic organisms to the extracellular spaces, or to target proteins to the vacuole.

By facilitating the transport of the protein into compartments inside and outside the cell, these sequences may increase the accumulation of gene product protecting them from proteolytic degradation. These sequences also allow for additional mRNA sequences from highly expressed genes to be attached to the coding sequence of the genes. Since mRNA being translated by ribosomes is more stable than naked mRNA, the presence of translatable mRNA in front of the gene may increase the overall stability of the mRNA transcript from the gene and thereby increase synthesis of the gene product. Since transit and signal sequences are usually post-translationally removed from the initial translation product, the use of these sequences allows for the addition of extra translated sequences that may not appear on the final polypeptide. Targeting of certain proteins may be desirable in order to enhance the stability of the protein (U.S. Patent No. 5,545,818).

It may be useful to target DNA itself within a cell. For example, it may be useful to target introduced DNA to the nucleus as this may increase the frequency of transformation. Within the nucleus itself it would be useful to target a gene in order to achieve site specific integration. For example, it would be useful to have an gene introduced through transformation replace an existing gene in the cell.

Other elements include those that can be regulated by endogenous or exogenous agents, e.g., by zinc finger proteins, including naturally occurring zinc finger proteins or chimeric zinc finger proteins (see, e.g., U.S. Patent No. 5,789,538, WO 99/48909; WO 99/45132; WO 98/53060; WO 98/53057; WO 98/53058; WO 00/23464; WO 95/19431; and WO 98/54311) or myb-like transcription factors. For example, a chimeric zinc finger protein may include amino acid sequences which bind to a specific DNA sequence (the zinc finger) and amino acid sequences that activate (e.g., GAL 4 sequences) or repress the transcription of the sequences linked to the specific DNA sequence.

3. Preferred Nucleic Acid Molecules of the Invention

The invention relates to an isolated plant, e.g., *Arabidopsis*, *Chenopodium* and rice, nucleic acid molecule comprising a gene having an open reading frame, the expression of which is altered in response to pathogen infection, as well as the endogenous plant promoters for those genes. However, the expression of these genes may also be altered in response to non-pathogens, e.g., in response to environmental stimuli. The nucleic acid molecules can be used in pathogen control strategies, e.g., by overexpressing nucleic acid molecules which can confer tolerance to a cell, or by altering the expression of host genes which are required for pathogen infection, e.g., by "knocking out" the expression of at least one genomic copy of the gene. Plants having genetic disruptions in host genes may be less susceptible to infection, e.g., due to a decrease or absence of a host protein needed for infection, or, alternatively, hypersusceptible to infection. Plants that are hypersusceptible to infection may be useful to prepare transgenic plants as the expression of the gene(s) which was disrupted may be related to gene silencing.

Preferred sources from which the nucleic acid molecules of the invention can be obtained or isolated include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*),

tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea utilane*), fig (*Ficus casica*),
 guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica*
papaya), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond
 (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, duckweed
 5 (*Lemna*), barley, vegetables, ornamentals, and conifers.

Duckweed (*Lemna*, see WO 00/07210) includes members of the family *Lemnaceae*.
 There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L.*
aequinoctialis, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L.*
obscura, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S.*
 10 *intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. Angusta*, *Wa. Arrhiza*, *Wa.*
Australina, *Wa. Borealis*, *Wa. Brasiliensis*, *Wa. Columbiana*, *Wa. Elongata*, *Wa. Globosa*, *Wa.*
Microscopica, *Wa. Neglecta*) and genus *Wofliella* (*Wl. utila*, *Wl. utilane* n, *Wl. gladiata*, *Wl.*
utila, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*). Any other genera or
 species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*,
 15 *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula*
 being most preferred. *Lemna* species can be classified using the taxonomic scheme described
 by Landolt, Biosystematic Investigation on the Family of Duckweeds: The family of
Lemnaceae – A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich
 (1986)).

20 Vegetables from which to obtain or isolate the nucleic acid molecules of the invention
 include, but are not limited to, tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca*
sativa), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus*
 spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C.*
cantalupensis), and musk melon (*C. melo*). Ornamentals from which to obtain or isolate the
 25 nucleic acid molecules of the invention include, but are not limited to, azalea (*Rhododendron*
 spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa*
 spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation
 (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers
 that may be employed in practicing the present invention include, for example, pines such as
 30 loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*),
 lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga*
menziesii); Western hemlock (*Tsuga utilane*); Sitka spruce (*Picea glauca*); redwood (*Sequoia*
sempervirens); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*);

and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants from which the nucleic acid molecules of the invention can be isolated or obtained include, but are not limited to, beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, and the like. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo.

Papaya, garlic, pea, peach, pepper, petunia, strawberry, sorghum, sweet potato, turnip, safflower, corn, pea, endive, gourd, grape, snap bean, chicory, cotton, tobacco, aubergine, beet, buckwheat, broad bean, nectarine, avocado, mango, banana, groundnut, potato, peanut, lettuce, pineapple, spinach, squash, sugarbeet, sugarcane, sweet corn, chrysanthemum.

Other preferred sources of the nucleic acid molecules of the invention include *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, utilan sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, utilane, and zucchini.

Yet other sources of nucleic acid molecules are ornamental plants including, but not limited to, impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia, and plants such as those shown in Table 1.

Table 1

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Cucurbitaceae	<i>Cucumis sativus</i>	Cucumber		http://www.cucurbit.org/
	<i>Cucumis melo</i>	Melon		http://genome.cornell.edu/cgc/
	<i>Citrullus lanatus</i>	Watermelon		
	<i>Cucurbita pepo</i>	Squash – summer		
	<i>Cucurbita maxima</i>	Squash – winter		
	<i>Cucurbita moschata</i>	Pumpkin /butternut		
Total				http://www.nal.usda.gov/pgdic/Map_proj/

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Solanaceae	<i>Lycopersicon esculentum</i>	Tomato	<ul style="list-style-type: none"> 15x BAC on variety Heinz 1706 order from Clemson Genome center (www.genome.clemson.edu) 11.6x BAC of L. cheesmanii (originates from J. Giovannoni) available from Clemson genome center (www.genome.clemson.edu) EST collection from TIGR (www.tigr.org/tdb/lgi/index.html) EST collection from Clemson Genome Center (www.genome.clemson.edu) TAG 99:254-271, 1999 (esculentum x pennelli) TAG 89:1007-1013, 1994 (peruvianum) Plant Cell Reports 12:293-297, 1993 (RAPDs) Genetics 132:1141-1160, 1992 (potato x tomato) Genetics 120:1095-1105, 1988 (RFLP potato and tomato) Genetics 115:387-393, 1986 (esculentum x pennelli isozyme and cDNAs) 	genome.cornell.edu/solgenes http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=solgenes http://genome.cornell.edu/tgc/ http://tgrc.ucdavis.edu/
	<i>Capsicum annuum</i>	Pepper		http://neptune.netimages.com/~chile/science.html
	<i>Capsicum frutescens</i>	Chile pepper		
	<i>Solanum melongena</i>	Eggplant		

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
	<i>(Nicotiana tabacum)</i>	(Tobacco)		
	<i>(Solanum tuberosum)</i>	(Potato)		
	<i>(Petunia x hybrida hort. Ex E. Vilm.)</i>	(Petunia)	4x BAC of Petunia hybrida 7984 available from Clemson genome center (www.genome.clemson.edu)	
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Brassicaceae	<i>Brassica oleracea</i> L. var. <i>italica</i>	Broccoli		http://res.agr.ca/ecorc/cwmt/crucifer/traits/index.htm http://geneous.cit.cornell.edu/cabbage/abotutcab.html
	<i>Brassica oleracea</i> L. var. <i>capitata</i>	Cabbage		
	<i>Brassica rapa</i>	Chinese Cabbage		
	<i>Brassica oleracea</i> L. var. <i>botrytis</i>	Cauliflower		
	<i>Raphanus sativus</i> var. <i>niger</i>	Daikon		
	<i>(Brassica napus)</i>	(Oilseed rape)		http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=brassicadb
		Arabidopsis	12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=agr

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Umbelliferae	<i>Daucus carota</i>	Carrot		
Compositae	<i>Lactuca sativa</i>	Lettuce		
	<i>Helianthus annuus</i>	(Sunflower)		
Total				
Chenopodiaceae	<i>Spinacia oleracea</i>	Spinach		
	(<i>Beta vulgaris</i>)	(Sugar Beet)		
Total				
Leguminosae	<i>Phaseolus vulgaris</i>	Bean	4.3x BAC available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=beanengenes
	<i>Pisum sativum</i>	Pea		
	(<i>Glycine max</i>)	(Soybean)	7.5x and 7.9x BACs available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase
Total			http://www.nal.usda.gov/pgdic/Map_proj/	
Gramineae	<i>Zea mays</i>	Sweet Corn	Novartis BACs for Mo17 and B73 have been donated to Clemson Genome Center (www.genome.clemson.edu)	
	(<i>Zea mays</i>)	(Field Corn)		http://www.agron.missouri.edu/mnl/

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Total			http://www.nal.usda.gov/pgdic/Map_proj/	
Liliaceae	<i>Allium cepa</i>	Onion		
		Leek		
		(Garlic)		
		(Asparagus)		
Total			http://www.nal.usda.gov/pgdic/Map_proj/	

Preferred forage and turf grass nucleic acid sources for the nucleic acid molecules of the invention include, but are not limited to, alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop. Yet other preferred sources include, but are not limited to, crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean, barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, oat, rye, rape, wheat, millet, tobacco, and the like), and even more preferably corn, rice and soybean.

According to one embodiment, the present invention is directed to a nucleic acid molecule comprising a nucleotide sequence isolated or obtained from any plant which encodes a polypeptide having at least 70% amino acid sequence identity to a polypeptide encoded by a gene comprising any one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737, or a gene comprising SEQ ID NOs:2137-2661 or 4738-6813. Based on the *Arabidopsis*, *Chenopodium* and rice nucleic acid sequences of the present invention, orthologs may be identified or isolated from the genome of any desired organism, preferably from another plant, according to well known techniques based on their sequence similarity to the *Arabidopsis*, *Chenopodium* and rice nucleic acid sequences, e.g., hybridization, PCR or computer generated sequence comparisons. For example, all or a portion of a particular *Arabidopsis*, *Chenopodium* and rice nucleic acid sequence is used as a probe that selectively hybridizes to other gene sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen source organism. Further, suitable genomic and cDNA libraries may be prepared from any cell or tissue of an organism. Such techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, e.g., Sambrook et al., 1989) and amplification by PCR using oligonucleotide primers

preferably corresponding to sequence domains conserved among related polypeptide or subsequences of the nucleotide sequences provided herein (see, e.g., Innis et al., 1990). These methods are particularly well suited to the isolation of gene sequences from organisms closely related to the organism from which the probe sequence is derived. The application of these methods using the *Arabidopsis* sequences as probes is well suited for the isolation of gene sequences from any source organism, preferably other plant species. In a PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted from any plant of interest. Methods for designing PCR primers and PCR cloning are generally known in the art.

In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ^{32}P , or any other detectable marker. Thus, for example, probes for hybridization can be made by labeling synthetic oligonucleotides based on the sequence of the invention. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook et al. (1989). In general, sequences that hybridize to the sequences disclosed herein will have at least 40% to 50%, about 60% to 70% and even about 80% 85%, 90%, 95% to 98% or more identity with the disclosed sequences. That is, the sequence similarity of sequences may range, sharing at least about 40% to 50%, about 60% to 70%, and even about 80%, 85%, 90%, 95% to 98% sequence similarity.

The nucleic acid molecules of the invention can also be identified by, for example, a search of known databases for genes encoding polypeptides having a specified amino acid sequence identity or DNA having a specified nucleotide sequence identity. Methods of alignment of sequences for comparison are well known in the art and are described hereinabove.

4. Methods for Mutagenizing DNA

It is specifically contemplated by the inventors that one could mutagenize DNA having a promoter or open reading frame to, for example, potentially improve the utility of the DNA for expression of transgenes in plants. The mutagenesis can be carried out at random and the mutagenized sequences screened for activity in a trial-by-error procedure. Alternatively,

particular sequences which provide the promoter with desirable expression characteristics, or a promoter with expression enhancement activity, could be identified and these or similar sequences introduced into the sequences via mutation. It is further contemplated that one could mutagenize these sequences in order to enhance their expression of transgenes in a particular species.

The means for mutagenizing a DNA segment of the current invention are well-known to those of skill in the art. As indicated, modifications may be made by random or site-specific mutagenesis procedures. The DNA may be modified by altering its structure through the addition or deletion of one or more nucleotides from the sequence which encodes the corresponding un-modified sequences.

Mutagenesis may be performed in accordance with any of the techniques known in the art, such as, and not limited to, synthesizing an oligonucleotide having one or more mutations within the sequence of a particular regulatory region. In particular, site-specific mutagenesis is a technique useful in the preparation of promoter mutants, through specific mutagenesis of the underlying DNA. The technique further provides a ready ability to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA. Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Typically, a primer of about 17 to about 75 nucleotides or more in length is preferred, with about 10 to about 25 or more residues on both sides of the junction of the sequence being altered.

In general, the technique of site-specific mutagenesis is well known in the art, as exemplified by various publications. As will be appreciated, the technique typically employs a phage vector which exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially available and their use is generally well known to those skilled in the art.

Double stranded plasmids also are routinely employed in site directed mutagenesis which eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double stranded vector which includes within its sequence a DNA sequence which encodes the promoter. An

oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation.

This heteroduplex vector is then used to transform or transfect appropriate cells, such as *E. coli* cells, and cells are selected which include recombinant vectors bearing the mutated sequence arrangement. Vector DNA can then be isolated from these cells and used for plant transformation. A genetic selection scheme was devised by Kunkel et al. (1987) to enrich for clones incorporating mutagenic oligonucleotides. Alternatively, the use of PCR with commercially available thermostable enzymes such as Taq polymerase may be used to incorporate a mutagenic oligonucleotide primer into an amplified DNA fragment that can then be cloned into an appropriate cloning or expression vector. The PCR-mediated mutagenesis procedures of Tomic et al. (1990) and Upender et al. (1995) provide two examples of such protocols. A PCR employing a thermostable ligase in addition to a thermostable polymerase also may be used to incorporate a phosphorylated mutagenic oligonucleotide into an amplified DNA fragment that may then be cloned into an appropriate cloning or expression vector. The mutagenesis procedure described by Michael (1994) provides an example of one such protocol.

The preparation of sequence variants of DNA segments using site-directed mutagenesis is provided as a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of DNA sequences may be obtained. For example, recombinant vectors encoding the desired promoter sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants.

In addition, an unmodified or modified nucleotide sequence of the present invention can be varied by shuffling the sequence of the invention. To test for a function of variant DNA sequences according to the invention, the sequence of interest is operably linked to a selectable or screenable marker gene and expression of the marker gene is tested in transient expression assays with protoplasts or in stably transformed plants. It is known to the skilled artisan that DNA sequences capable of driving expression of an associated nucleotide sequence are build in a modular way. Accordingly, expression levels from shorter DNA fragments may be different than the one from the longest fragment and may be different from each other. For

example, deletion of a down-regulating upstream element will lead to an increase in the expression levels of the associated nucleotide sequence while deletion of an up-regulating element will decrease the expression levels of the associated nucleotide sequence. It is also known to the skilled artisan that deletion of development-specific or a tissue-specific element
5 will lead to a temporally or spatially altered expression profile of the associated nucleotide sequence.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in
10 the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" also is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template-dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the
15 sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (see, for example, Watson and Rarnstad, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U.S. Patent No.
20 4,237,224. A number of template dependent processes are available to amplify the target sequences of interest present in a sample, such methods being well known in the art and specifically disclosed herein below.

Where a clone comprising a promoter has been isolated in accordance with the instant invention, one may wish to delimit the essential promoter regions within the clone. One
25 efficient, targeted means for preparing mutagenizing promoters relies upon the identification of putative regulatory elements within the promoter sequence. This can be initiated by comparison with promoter sequences known to be expressed in similar tissue-specific or developmentally unique manner. Sequences which are shared among promoters with similar expression patterns are likely candidates for the binding of transcription factors and are thus
30 likely elements which confer expression patterns. Confirmation of these putative regulatory elements can be achieved by deletion analysis of each putative regulatory region followed by functional analysis of each deletion construct by assay of a reporter gene which is functionally

attached to each construct. As such, once a starting promoter sequence is provided, any of a number of different deletion mutants of the starting promoter could be readily prepared.

As indicated above, deletion mutants, deletion mutants of the promoter of the invention also could be randomly prepared and then assayed. With this strategy, a series of constructs are prepared, each containing a different portion of the clone (a subclone), and these constructs are then screened for activity. A suitable means for screening for activity is to attach a deleted promoter or intron construct which contains a deleted segment to a selectable or screenable marker, and to isolate only those cells expressing the marker gene. In this way, a number of different, deleted promoter constructs are identified which still retain the desired, or even enhanced, activity. The smallest segment which is required for activity is thereby identified through comparison of the selected constructs. This segment may then be used for the construction of vectors for the expression of exogenous genes.

B. Marker Genes

In order to improve the ability to identify transformants, one may desire to employ a selectable or screenable marker gene as, or in addition to, the expressible gene of interest. "Marker genes" are genes that impart a distinct phenotype to cells expressing the marker gene and thus allow such transformed cells to be distinguished from cells that do not have the marker. Such genes may encode either a selectable or screenable marker, depending on whether the marker confers a trait which one can 'select' for by chemical means, i.e., through the use of a selective agent (e.g., a herbicide, antibiotic, or the like), or whether it is simply a trait that one can identify through observation or testing, i.e., by 'screening' (e.g., the R-locus trait, the green fluorescent protein (GFP)). Of course, many examples of suitable marker genes are known to the art and can be employed in the practice of the invention.

Included within the terms selectable or screenable marker genes are also genes which encode a "secretable marker" whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected by their catalytic activity. Secretable proteins fall into a number of classes, including small, diffusible proteins detectable, e.g., by ELISA; small active enzymes detectable in extracellular solution (e.g., alpha-amylase, beta-lactamase, phosphinothricin acetyltransferase); and proteins that are inserted or trapped in the cell wall (e.g., proteins that include a leader sequence such as that found in the expression unit of extensin or tobacco PR-S).

With regard to selectable secretable markers, the use of a gene that encodes a protein that becomes sequestered in the cell wall, and which protein includes a unique epitope is considered to be particularly advantageous. Such a secreted antigen marker would ideally employ an epitope sequence that would provide low background in plant tissue, a promoter-
5 leader sequence that would impart efficient expression and targeting across the plasma membrane, and would produce protein that is bound in the cell wall and yet accessible to antibodies. A normally secreted wall protein modified to include a unique epitope would satisfy all such requirements.

One example of a protein suitable for modification in this manner is extensin, or
10 hydroxyproline rich glycoprotein (HPRG). For example, the maize HPRG (Steifel et al., 1990) molecule is well characterized in terms of molecular biology, expression and protein structure. However, any one of a variety of utilane and/or glycine-rich wall proteins (Keller et al., 1989) could be modified by the addition of an antigenic site to create a screenable marker.

One exemplary embodiment of a secretable screenable marker concerns the use of a
15 maize sequence encoding the wall protein HPRG, modified to include a 15 residue epitope from the pro-region of murine interleukin, however, virtually any detectable epitope may be employed in such embodiments, as selected from the extremely wide variety of antigen-antibody combinations known to those of skill in the art. The unique extracellular epitope can then be straightforwardly detected using antibody labeling in conjunction with chromogenic or
20 fluorescent adjuncts.

Elements of the present disclosure may be exemplified in detail through the use of the bar and/or GUS genes, and also through the use of various other markers. Of course, in light of this disclosure, numerous other possible selectable and/or screenable marker genes will be apparent to those of skill in the art in addition to the one set forth hereinbelow. Therefore, it
25 will be understood that the following discussion is exemplary rather than exhaustive. In light of the techniques disclosed herein and the general recombinant techniques which are known in the art, the present invention renders possible the introduction of any gene, including marker genes, into a recipient cell to generate a transformed plant.

1. Selectable Markers

30 Possible selectable markers for use in connection with the present invention include, but are not limited to, a *neo* gene which codes for kanamycin resistance and can be selected for using kanamycin, G418, paromomycin, and the like; a *bar* gene which codes for bialaphos or phosphinothricin resistance; a gene which encodes an altered EPSP synthase protein (Hinchee

et al., 1988) thus conferring glyphosate resistance; a nitrilase gene such as *bxn* from *Klebsiella ozaenae* which confers resistance to bromoxynil (Stalker et al., 1988); a mutant acetolactate synthase gene (ALS) which confers resistance to imidazolinone, sulfonylurea or other ALS-inhibiting chemicals (European Patent Application 154,204, 1985); a methotrexate-resistant DHFR gene (Thillet et al., 1988); a dalapon dehalogenase gene that confers resistance to the herbicide dalapon; a mutated anthranilate synthase gene that confers resistance to 5-methyl tryptophan. Preferred selectable marker genes encode phosphinothricin acetyltransferase; glyphosate resistant EPSPS, aminoglycoside phosphotransferase; hygromycin phosphotransferase, or neomycin phosphotransferase. Where a mutant EPSP synthase gene is employed, additional benefit may be realized through the incorporation of a suitable chloroplast transit peptide, CTP (European Patent Application 0,218,571, 1987).

An illustrative embodiment of a selectable marker gene capable of being used in systems to select transformants is the genes that encode the enzyme phosphinothricin acetyltransferase, such as the *bar* gene from *Streptomyces hygroscopicus* or the *pat* gene from *Streptomyces viridochromogenes*. The enzyme phosphinothricin acetyl transferase (PAT) inactivates the active ingredient in the herbicide bialaphos, phosphinothricin (PPT). PPT inhibits glutamine synthetase, (Murakami et al., 1986; Twell et al., 1989) causing rapid accumulation of ammonia and cell death. The success in using this selective system in conjunction with monocots was particularly surprising because of the major difficulties which have been reported in transformation of cereals.

Where one desires to employ a bialaphos resistance gene in the practice of the invention, a particularly useful gene for this purpose is the *bar* or *pat* genes obtainable from species of *Streptomyces* (e.g., ATCC No. 21,705). The cloning of the *bar* gene has been described (Murakami et al., 1986; Thompson et al., 1987) as has the use of the *bar* gene in the context of plants other than monocots (De Block et al., 1987; De Block et al., 1989).

Selection markers resulting in positive selection, such as a phosphomannose isomerase gene, as described in patent application WO 93/05163, may also be used. Alternative genes to be used for positive selection are described in WO 94/20627 and encode xyloisomerases and phosphomanno-isomerases such as mannose-6-phosphate isomerase and mannose-1-phosphate isomerase; phosphomanno mutase; mannose epimerases such as those which convert carbohydrates to mannose or mannose to carbohydrates such as glucose or galactose; phosphatases such as mannose or xylose phosphatase, mannose-6-phosphatase and mannose-1-phosphatase, and permeases which are involved in the transport of mannose, or a

derivative, or a precursor thereof into the cell. Transformed cells are identified without damaging or killing the non-transformed cells in the population and without co-introduction of antibiotic or herbicide resistance genes. As described in WO 93/05163, in addition to the fact that the need for antibiotic or herbicide resistance genes is eliminated, it has been shown that the positive selection method is often far more efficient than traditional negative selection.

2. Screenable Markers

Screenable markers that may be employed include, but are not limited to, a beta-glucuronidase (GUS) or *uidA* gene which encodes an enzyme for which various chromogenic substrates are known; an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues (Dellaporta et al., 1988); a beta-lactamase gene (Sutcliffe, 1978), which encodes an enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a *xylE* gene (Zukowsky et al., 1983) which encodes a catechol dioxygenase that can convert chromogenic catechols; an α -amylase gene (Ikuta et al., 1990); a tyrosinase gene (Katz et al., 1983) which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to form the easily detectable compound melanin; a β -galactosidase gene, which encodes an enzyme for which there are chromogenic substrates; a luciferase (*lux*) gene (Ow et al., 1986), which allows for bioluminescence detection; or even an aequorin gene (Prasher et al., 1985), which may be employed in calcium-sensitive bioluminescence detection, or a green fluorescent protein gene (Niedz et al., 1995).

Genes from the maize R gene complex are contemplated to be particularly useful as screenable markers. The R gene complex in maize encodes a protein that acts to regulate the production of anthocyanin pigments in most seed and plant tissue. A gene from the R gene complex was applied to maize transformation, because the expression of this gene in transformed cells does not harm the cells. Thus, an R gene introduced into such cells will cause the expression of a red pigment and, if stably incorporated, can be visually scored as a red sector. If a maize line carries dominant alleles for genes encoding the enzymatic intermediates in the anthocyanin biosynthetic pathway (C2, A1, A2, Bz1 and Bz2) (Roth et al., 1990), but carries a recessive allele at the R locus, transformation of any cell from that line with R will result in red pigment formation. Exemplary lines include Wisconsin 22 which contains the *rg*-Stadler allele and TR112, a K55 derivative which is *r-g, b, P1*. Alternatively any genotype of maize can be utilized if the C1 and R alleles are introduced together.

It is further proposed that R gene regulatory regions may be employed in chimeric constructs in order to provide mechanisms for controlling the expression of chimeric genes. More diversity of phenotypic expression is known at the R locus than at any other locus (Coe et al., 1988). It is contemplated that regulatory regions obtained from regions 5' to the structural R gene would be valuable in directing the expression of genes, e.g., insect resistance, drought resistance, herbicide tolerance or other protein coding regions. For the purposes of the present invention, it is believed that any of the various R gene family members may be successfully employed (e.g., P, S, Lc, etc.). However, the most preferred will generally be Sn (particularly Sn:bol3). Sn is a dominant member of the R gene complex and is functionally similar to the R and B loci in that Sn controls the tissue specific deposition of anthocyanin pigments in certain seedling and plant cells, therefore, its phenotype is similar to R.

A further screenable marker contemplated for use in the present invention is firefly luciferase, encoded by the *lux* gene. The presence of the *lux* gene in transformed cells may be detected using, for example, X-ray film, scintillation counting, fluorescent spectrophotometry, low-light video cameras, photon counting cameras or multiwell luminometry. It is also envisioned that this system may be developed for populational screening for bioluminescence, such as on tissue culture plates, or even for whole plant screening. Where use of a screenable marker gene such as *lux* or GFP is desired, benefit may be realized by creating a gene fusion between the screenable marker gene and a selectable marker gene, for example, a GFP-NPTII gene fusion. This could allow, for example, selection of transformed cells followed by screening of transgenic plants or seeds.

C. Exogenous Genes for Modification of Plant Phenotypes

Genes of interest are reflective of the commercial markets and interests of those involved in the development of the crop. Crops and markets of interest changes, and as developing nations open up world markets, new crops and technologies will also emerge. In addition, as the understanding of agronomic traits and characteristics such as yield and heterosis increase, the choice of genes for transformation will change accordingly. General categories of genes of interest include, for example, those genes involved in information, such as zinc fingers, those involved in communication, such as kinases, and those involved in housekeeping, such as heat shock proteins. More specific categories of transgenes, for example, include genes encoding important traits for agronomics, insect resistance, disease resistance, herbicide resistance, sterility, grain characteristics, and commercial products. Genes of interest include, generally, those involved in starch, oil, carbohydrate, or nutrient

metabolism, as well as those affecting kernel size, sucrose loading, zinc finger proteins, see, e.g., U.S. Patent No. 5,789,538, WO 99/48909; WO 99/45132; WO 98/53060; WO 98/53057; WO 98/53058; WO 00/23464; WO 95/19431; and WO 98/54311, and the like.

One skilled in the art recognizes that the expression level and regulation of a transgene
5 in a plant can vary significantly from line to line. Thus, one has to test several lines to find one with the desired expression level and regulation. Once a line is identified with the desired regulation specificity of a chimeric Cre transgene, it can be crossed with lines carrying different inactive replicons or inactive transgene for activation.

Other sequences which may be linked to the gene of interest which encodes a
10 polypeptide are those which can target to a specific organelle, e.g., to the mitochondria, nucleus, or plastid, within the plant cell. Targeting can be achieved by providing the polypeptide with an appropriate targeting peptide sequence, such as a secretory signal peptide (for secretion or cell wall or membrane targeting, a plastid transit peptide, a chloroplast transit peptide, e.g., the chlorophyll a/b binding protein, a mitochondrial target peptide, a vacuole
15 targeting peptide, or a nuclear targeting peptide, and the like. For example, the small subunit of ribulose biphosphate carboxylase transit peptide, the EPSPS transit peptide or the dihydrodipicolinic acid synthase transit peptide may be used. For examples of plastid organelle targeting sequences (see WO 00/12732). Plastids are a class of plant organelles derived from proplastids and include chloroplasts, leucoplasts, aravloplast, and chromoplasts.
20 The plastids are major sites of biosynthesis in plants. In addition to photosynthesis in the chloroplast, plastids are also sites of lipid biosynthesis, nitrate reduction to ammonium, and starch storage. And while plastids contain their own circular genome, most of the proteins localized to the plastids are encoded by the nuclear genome and are imported into the organelle from the cytoplasm.

25 Transgenes used with the present invention will often be genes that direct the expression of a particular protein or polypeptide product, but they may also be non-expressible DNA segments, e.g., transposons such as Ds that do not direct their own transposition. As used herein, an "expressible gene" is any gene that is capable of being transcribed into RNA (e.g., mRNA, antisense RNA, etc.) or translated into a protein, expressed as a trait of interest, or the
30 like, etc., and is not limited to selectable, screenable or non-selectable marker genes. The invention also contemplates that, where both an expressible gene that is not necessarily a marker gene is employed in combination with a marker gene, one may employ the separate

genes on either the same or different DNA segments for transformation. In the latter case, the different vectors are delivered concurrently to recipient cells to maximize cotransformation.

The choice of the particular DNA segments to be delivered to the recipient cells will often depend on the purpose of the transformation. One of the major purposes of transformation of crop plants is to add some commercially desirable, agronomically important traits to the plant. Such traits include, but are not limited to, herbicide resistance or tolerance; insect resistance or tolerance; disease resistance or tolerance (viral, bacterial, fungal, nematode); stress tolerance and/or resistance, as exemplified by resistance or tolerance to drought, heat, chilling, freezing, excessive moisture, salt stress; oxidative stress; increased yields; food content and makeup; physical appearance; male sterility; drydown; standability; prolificacy; starch properties; oil quantity and quality; and the like. One may desire to incorporate one or more genes conferring any such desirable trait or traits, such as, for example, a gene or genes encoding pathogen resistance.

In certain embodiments, the present invention contemplates the transformation of a recipient cell with more than one advantageous transgene. Two or more transgenes can be supplied in a single transformation event using either distinct transgene-encoding vectors, or using a single vector incorporating two or more gene coding sequences. For example, plasmids bearing the *bar* and *aroA* expression units in either convergent, divergent, or colinear orientation, are considered to be particularly useful. Further preferred combinations are those of an insect resistance gene, such as a *Bt* gene, along with a protease inhibitor gene such as *pinII*, or the use of *bar* in combination with either of the above genes. Of course, any two or more transgenes of any description, such as those conferring herbicide, insect, disease (viral, bacterial, fungal, nematode) or drought resistance, male sterility, drydown, standability, prolificacy, starch properties, oil quantity and quality, or those increasing yield or nutritional quality may be employed as desired.

1. Herbicide Resistance

The genes encoding phosphinothricin acetyltransferase (*bar* and *pat*), glyphosate tolerant EPSP synthase genes, the glyphosate degradative enzyme gene *gox* encoding glyphosate oxidoreductase, *deh* (encoding a dehalogenase enzyme that inactivates dalapon), herbicide resistant (e.g., sulfonylurea and imidazolinone) acetolactate synthase, and *bxn* genes (encoding a nitrilase enzyme that degrades bromoxynil) are good examples of herbicide resistant genes for use in transformation. The *bar* and *pat* genes code for an enzyme, phosphinothricin acetyltransferase (PAT), which inactivates the herbicide phosphinothricin

and prevents this compound from inhibiting glutamine synthetase enzymes. The enzyme 5-enolpyruvylshikimate 3-phosphate synthase (EPSP Synthase), is normally inhibited by the herbicide N-(phosphonomethyl)glycine (glyphosate). However, genes are known that encode glyphosate-resistant EPSP Synthase enzymes.

5 These genes are particularly contemplated for use in monocot transformation. The *deh* gene encodes the enzyme dalapon dehalogenase and confers resistance to the herbicide dalapon. The *bxn* gene codes for a specific nitrilase enzyme that converts bromoxynil to a non-herbicidal degradation product.

2. Insect Resistance

10 An important aspect of the present invention concerns the introduction of insect resistance-conferring genes into plants. Potential insect resistance genes which can be introduced include *Bacillus thuringiensis* crystal toxin genes or *Bt* genes (Watrud et al., 1985). *Bt* genes may provide resistance to lepidopteran or coleopteran pests such as European Corn Borer (ECB) and corn rootworm (CRW). Preferred *Bt* toxin genes for use in such
15 embodiments include the CryIA(b) and CryIA(c) genes. Endotoxin genes from other species of *B. thuringiensis* which affect insect growth or development may also be employed in this regard.

 The poor expression of *Bt* toxin genes in plants is a well-documented phenomenon, and the use of different promoters, fusion proteins, and leader sequences has not led to significant
20 increases in *Bt* protein expression (Vaeck et al., 1989; Barton et al., 1987). It is therefore contemplated that the most advantageous *Bt* genes for use in the transformation protocols disclosed herein will be those in which the coding sequence has been modified to effect increased expression in plants, and more particularly, those in which maize preferred codons have been used. Examples of such modified *Bt* toxin genes include the variant *Bt* CryIA(b)
25 gene termed Iab6 (Perlak et al., 1991) and the synthetic CryIA(c) genes termed 1800a and 1800b.

 Protease inhibitors may also provide insect resistance (Johnson et al., 1989), and will thus have utility in plant transformation. The use of a protease inhibitor II gene, *pinII*, from tomato or potato is envisioned to be particularly useful. Even more advantageous is the use of
30 a *pinII* gene in combination with a *Bt* toxin gene, the combined effect of which has been discovered by the present inventors to produce synergistic insecticidal activity. Other genes which encode inhibitors of the insects' digestive system, or those that encode enzymes or co-

factors that facilitate the production of inhibitors, may also be useful. This group may be exemplified by oryzacystatin and amylase inhibitors, such as those from wheat and barley.

Also, genes encoding lectins may confer additional or alternative insecticide properties. Lectins (originally termed phytohemagglutinins) are multivalent carbohydrate-binding proteins which have the ability to agglutinate red blood cells from a range of species. Lectins have been identified recently as insecticidal agents with activity against weevils, ECB and rootworm (Murdock et al., 1990; Czapla and Lang, 1990). Lectin genes contemplated to be useful include, for example, barley and wheat germ agglutinin (WGA) and rice lectins (Gatehouse et al., 1984), with WGA being preferred.

Genes controlling the production of large or small polypeptides active against insects when introduced into the insect pests, such as, e.g., lytic peptides, peptide hormones and toxins and venoms, form another aspect of the invention. For example, it is contemplated that the expression of juvenile hormone esterase, directed towards specific insect pests, may also result in insecticidal activity, or perhaps cause cessation of metamorphosis (Hammock et al., 1990).

Transgenic plants expressing genes which encode enzymes that affect the integrity of the insect cuticle form yet another aspect of the invention. Such genes include those encoding, e.g., chitinase, proteases, lipases and also genes for the production of nikkomycin, a compound that inhibits chitin synthesis, the introduction of any of which is contemplated to produce insect resistant maize plants. Genes that code for activities that affect insect molting, such as those affecting the production of ecdysteroid UDP-glucosyl transferase, also fall within the scope of the useful transgenes of the present invention.

Genes that code for enzymes that facilitate the production of compounds that reduce the nutritional quality of the host plant to insect pests are also encompassed by the present invention. It may be possible, for instance, to confer insecticidal activity on a plant by altering its sterol composition. Sterols are obtained by insects from their diet and are used for hormone synthesis and membrane stability. Therefore alterations in plant sterol composition by expression of novel genes, e.g., those that directly promote the production of undesirable sterols or those that convert desirable sterols into undesirable forms, could have a negative effect on insect growth and/or development and hence endow the plant with insecticidal activity. Lipxygenases are naturally occurring plant enzymes that have been shown to exhibit anti-nutritional effects on insects and to reduce the nutritional quality of their diet. Therefore, further embodiments of the invention concern transgenic plants with enhanced lipxygenase activity which may be resistant to insect feeding.

The present invention also provides methods and compositions by which to achieve qualitative or quantitative changes in plant secondary metabolites. One example concerns transforming plants to produce DIMBOA which, it is contemplated, will confer resistance to European corn borer, rootworm and several other maize insect pests. Candidate genes that are particularly considered for use in this regard include those genes at the *bx* locus known to be involved in the synthetic DIMBOA pathway (Dunn et al., 1981). The introduction of genes that can regulate the production of maysin, and genes involved in the production of dhurrin in sorghum, is also contemplated to be of use in facilitating resistance to earworm and rootworm, respectively.

Tripsacum dactyloides is a species of grass that is resistant to certain insects, including corn root worm. It is anticipated that genes encoding proteins that are toxic to insects or are involved in the biosynthesis of compounds toxic to insects will be isolated from *Tripsacum* and that these novel genes will be useful in conferring resistance to insects. It is known that the basis of insect resistance in *Tripsacum* is genetic, because said resistance has been transferred to *Zea mays* via sexual crosses (Branson and Guss, 1972).

Further genes encoding proteins characterized as having potential insecticidal activity may also be used as transgenes in accordance herewith. Such genes include, for example, the cowpea trypsin inhibitor (CpTI; Hilder et al., 1987) which may be used as a rootworm deterrent; genes encoding avermectin (Campbell, 1989; Ikeda et al., 1987) which may prove particularly useful as a corn rootworm deterrent; ribosome inactivating protein genes; and even genes that regulate plant structures. Transgenic maize including anti-insect antibody genes and genes that code for enzymes that can covert a non-toxic insecticide (pro-insecticide) applied to the outside of the plant into an insecticide inside the plant are also contemplated.

3. Environment or Stress Resistance

Improvement of a plant's ability to tolerate various environmental stresses such as, but not limited to, drought, excess moisture, chilling, freezing, high temperature, salt, and oxidative stress, can also be effected through expression of heterologous, or overexpression of homologous genes. Benefits may be realized in terms of increased resistance to freezing temperatures through the introduction of an "antifreeze" protein such as that of the Winter Flounder (Cutler et al., 1989) or synthetic gene derivatives thereof. Improved chilling tolerance may also be conferred through increased expression of glycerol-3-phosphate acetyltransferase in chloroplasts (Murata et al., 1992; Wolter et al., 1992). Resistance to oxidative stress (often exacerbated by conditions such as chilling temperatures in combination

with high light intensities) can be conferred by expression of superoxide dismutase (Gupta et al., 1993), and may be improved by glutathione reductase (Bowler et al., 1992). Such strategies may allow for tolerance to freezing in newly emerged fields as well as extending later maturity higher yielding varieties to earlier relative maturity zones.

5 Expression of novel genes that favorably effect plant water content, total water potential, osmotic potential, and turgor can enhance the ability of the plant to tolerate drought. As used herein, the terms "drought resistance" and "drought tolerance" are used to refer to a plants increased resistance or tolerance to stress induced by a reduction in water availability, as compared to normal circumstances, and the ability of the plant to function and survive in
10 lower-water environments, and perform in a relatively superior manner. In this aspect of the invention it is proposed, for example, that the expression of a gene encoding the biosynthesis of osmotically-active solutes can impart protection against drought. Within this class of genes are DNAs encoding mannitol dehydrogenase (Lee and Saier, 1982) and trehalose-6-phosphate synthase (Kaasen et al., 1992). Through the subsequent action of native phosphatases in the
15 cell or by the introduction and coexpression of a specific phosphatase, these introduced genes will result in the accumulation of either mannitol or trehalose, respectively, both of which have been well documented as protective compounds able to mitigate the effects of stress. Mannitol accumulation in transgenic tobacco has been verified and preliminary results indicate that plants expressing high levels of this metabolite are able to tolerate an applied osmotic stress
20 (Tarczynski et al., cited supra (1992), 1993).

 Similarly, the efficacy of other metabolites in protecting either enzyme function (e.g. alanopine or propionic acid) or membrane integrity (e.g., alanopine) has been documented (Loomis et al., 1989), and therefore expression of gene encoding the biosynthesis of these compounds can confer drought resistance in a manner similar to or complimentary to mannitol.
25 Other examples of naturally occurring metabolites that are osmotically active and/or provide some direct protective effect during drought and/or desiccation include sugars and sugar derivatives such as fructose, erythritol (Coxson et al., 1992), sorbitol, dulcitol (Karsten et al., 1992), glucosylglycerol (Reed et al., 1984; Erdmann et al., 1992), sucrose, stachyose (Koster and Leopold, 1988; Blackman et al., 1992), ononitol and pinitol (Vernon and Bohnert, 1992),
30 and raffinose (Bernal-Lugo and Leopold, 1992). Other osmotically active solutes which are not sugars include, but are not limited to, proline and glycine-betaine (Wyn-Jones and Storey, 1981). Continued canopy growth and increased reproductive fitness during times of stress can be augmented by introduction and expression of genes such as those controlling the

osmotically active compounds discussed above and other such compounds, as represented in one exemplary embodiment by the enzyme myoinositol 0-methyltransferase.

It is contemplated that the expression of specific proteins may also increase drought tolerance. Three classes of Late Embryogenic Proteins have been assigned based on structural similarities (see Dure et al., 1989). All three classes of these proteins have been demonstrated in maturing (i.e., desiccating) seeds. Within these 3 types of proteins, the Type-II (dehydrin-type) have generally been implicated in drought and/or desiccation tolerance in vegetative plant parts (i.e. Mundy and Chua, 1988; Piatkowski et al., 1990; Yamaguchi-Shinozaki et al., 1992). Recently, expression of a Type-III LEA (HVA-1) in tobacco was found to influence plant height, maturity and drought tolerance (Fitzpatrick, 1993). Expression of structural genes from all three groups may therefore confer drought tolerance. Other types of proteins induced during water stress include thiol proteases, aldolases and transmembrane transporters (Guerrero et al., 1990), which may confer various protective and/or repair-type functions during drought stress. The expression of a gene that effects lipid biosynthesis and hence membrane composition can also be useful in conferring drought resistance on the plant.

Many genes that improve drought resistance have complementary modes of action. Thus, combinations of these genes might have additive and/or synergistic effects in improving drought resistance in maize. Many of these genes also improve freezing tolerance (or resistance); the physical stresses incurred during freezing and drought are similar in nature and may be mitigated in similar fashion. Benefit may be conferred via constitutive expression of these genes, but the preferred means of expressing these novel genes may be through the use of a turgor-induced promoter (such as the promoters for the turgor-induced genes described in Guerrero et al. 1990 and Shagan et al., 1993). Spatial and temporal expression patterns of these genes may enable maize to better withstand stress.

Expression of genes that are involved with specific morphological traits that allow for increased water extractions from drying soil would be of benefit. For example, introduction and expression of genes that alter root characteristics may enhance water uptake. Expression of genes that enhance reproductive fitness during times of stress would be of significant value. For example, expression of DNAs that improve the synchrony of pollen shed and receptiveness of the female flower parts, i.e., silks, would be of benefit. In addition, expression of genes that minimize kernel abortion during times of stress would increase the amount of grain to be harvested and hence be of value. Regulation of cytokinin levels in monocots, such as maize, by introduction and expression of an isopentenyl transferase gene with appropriate regulatory

sequences can improve monocot stress resistance and yield (Gan et al., Science, 270:1986 (1995)).

Given the overall role of water in determining yield, it is contemplated that enabling plants to utilize water more efficiently, through the introduction and expression of novel genes, will improve overall performance even when soil water availability is not limiting. By introducing genes that improve the ability of plants to maximize water usage across a full range of stresses relating to water availability, yield stability or consistency of yield performance may be realized.

4. Disease Resistance

It is proposed that increased resistance to diseases may be realized through introduction of genes into plants period. It is possible to produce resistance to diseases caused by viruses, bacteria, fungi, root pathogens, insects and nematodes. It is also contemplated that control of mycotoxin producing organisms may be realized through expression of introduced genes.

Resistance to viruses may be produced through expression of novel genes. For example, it has been demonstrated that expression of a viral coat protein in a transgenic plant can impart resistance to infection of the plant by that virus and perhaps other closely related viruses (Cuozzo et al., 1988, Hemenway et al., 1988, Abel et al., 1986). It is contemplated that expression of antisense genes targeted at essential viral functions may impart resistance to said virus. For example, an antisense gene targeted at the gene responsible for replication of viral nucleic acid may inhibit said replication and lead to resistance to the virus. It is believed that interference with other viral functions through the use of antisense genes may also increase resistance to viruses. Further it is proposed that it may be possible to achieve resistance to viruses through other approaches, including, but not limited to the use of satellite viruses.

It is proposed that increased resistance to diseases caused by bacteria and fungi may be realized through introduction of novel genes. It is contemplated that genes encoding so-called "peptide antibiotics," pathogenesis related (PR) proteins, toxin resistance, and proteins affecting host-pathogen interactions such as morphological characteristics will be useful. Peptide antibiotics are polypeptide sequences which are inhibitory to growth of bacteria and other microorganisms. For example, the classes of peptides referred to as cecropins and magainins inhibit growth of many species of bacteria and fungi. It is proposed that expression of PR proteins in plants may be useful in conferring resistance to bacterial disease. These genes are induced following pathogen attack on a host plant and have been divided into at least five classes of proteins (Bol et al., 1990). Included amongst the PR proteins are beta-1,3-

glucanases, chitinases, and osmotin and other proteins that are believed to function in plant resistance to disease organisms. Other genes have been identified that have antifungal properties, e.g., UDA (stinging nettle lectin) and hevein (Broakgert et al., 1989; Barkai-Golan et al., 1978). It is known that certain plant diseases are caused by the production of
5 phytotoxins. Resistance to these diseases could be achieved through expression of a novel gene that encodes an enzyme capable of degrading or otherwise inactivating the phytotoxin. Expression novel genes that alter the interactions between the host plant and pathogen may be useful in reducing the ability the disease organism to invade the tissues of the host plant, e.g., an increase in the waxiness of the leaf cuticle or other morphological characteristics.

10 Plant parasitic nematodes are a cause of disease in many plants. It is proposed that it would be possible to make the plant resistant to these organisms through the expression of novel genes. It is anticipated that control of nematode infestations would be accomplished by altering the ability of the nematode to recognize or attach to a host plant and/or enabling the plant to produce nematocidal compounds, including but not limited to proteins.

15 5. Mycotoxin Reduction/Elimination

Production of mycotoxins, including aflatoxin and fumonisin, by fungi associated with plants is a significant factor in rendering the grain not useful. These fungal organisms do not cause disease symptoms and/or interfere with the growth of the plant, but they produce chemicals (mycotoxins) that are toxic to animals. Inhibition of the growth of these fungi
20 would reduce the synthesis of these toxic substances and, therefore, reduce grain losses due to mycotoxin contamination. Novel genes may be introduced into plants that would inhibit synthesis of the mycotoxin without interfering with fungal growth. Expression of a novel gene which encodes an enzyme capable of rendering the mycotoxin nontoxic would be useful in order to achieve reduced mycotoxin contamination of grain. The result of any of the above
25 mechanisms would be a reduced presence of mycotoxins on grain.

6. Grain Composition or Quality

Genes may be introduced into plants, particularly commercially important cereals such as maize, wheat or rice, to improve the grain for which the cereal is primarily grown. A wide range of novel transgenic plants produced in this manner may be envisioned depending on the
30 particular end use of the grain.

For example, the largest use of maize grain is for feed or food. Introduction of genes that alter the composition of the grain may greatly enhance the feed or food value. The primary components of maize grain are starch, protein, and oil. Each of these primary

components of maize grain may be improved by altering its level or composition. Several examples may be mentioned for illustrative purposes but in no way provide an exhaustive list of possibilities.

The protein of many cereal grains is suboptimal for feed and food purposes especially when fed to pigs, poultry, and humans. The protein is deficient in several amino acids that are essential in the diet of these species, requiring the addition of supplements to the grain. Limiting essential amino acids may include lysine, methionine, tryptophan, threonine, valine, arginine, and histidine. Some amino acids become limiting only after the grain is supplemented with other inputs for feed formulations. For example, when the grain is supplemented with soybean meal to meet lysine requirements, methionine becomes limiting. The levels of these essential amino acids in seeds and grain may be elevated by mechanisms which include, but are not limited to, the introduction of genes to increase the biosynthesis of the amino acids, decrease the degradation of the amino acids, increase the storage of the amino acids in proteins, or increase transport of the amino acids to the seeds or grain.

One mechanism for increasing the biosynthesis of the amino acids is to introduce genes that deregulate the amino acid biosynthetic pathways such that the plant can no longer adequately control the levels that are produced. This may be done by deregulating or bypassing steps in the amino acid biosynthetic pathway which are normally regulated by levels of the amino acid end product of the pathway. Examples include the introduction of genes that encode deregulated versions of the enzymes aspartokinase or dihydrodipicolinic acid (DHDP)-synthase for increasing lysine and threonine production, and anthranilate synthase for increasing tryptophan production. Reduction of the catabolism of the amino acids may be accomplished by introduction of DNA sequences that reduce or eliminate the expression of genes encoding enzymes that catalyse steps in the catabolic pathways such as the enzyme lysine-ketoglutarate reductase.

The protein composition of the grain may be altered to improve the balance of amino acids in a variety of ways including elevating expression of native proteins, decreasing expression of those with poor composition, changing the composition of native proteins, or introducing genes encoding entirely new proteins possessing superior composition. DNA may be introduced that decreases the expression of members of the zein family of storage proteins. This DNA may encode ribozymes or antisense sequences directed to impairing expression of zein proteins or expression of regulators of zein expression such as the opaque-2 gene product. The protein composition of the grain may be modified through the phenomenon of

cosuppression, i.e., inhibition of expression of an endogenous gene through the expression of an identical structural gene or gene fragment introduced through transformation (Goring et al., 1991). Additionally, the introduced DNA may encode enzymes which degrade seines. The decreases in zein expression that are achieved may be accompanied by increases in proteins with more desirable amino acid composition or increases in other major seed constituents such as starch. Alternatively, a chimeric gene may be introduced that comprises a coding sequence for a native protein of adequate amino acid composition such as for one of the globulin proteins or 10 kD zein of maize and a promoter or other regulatory sequence designed to elevate expression of said protein. The coding sequence of said gene may include additional or replacement codons for essential amino acids. Further, a coding sequence obtained from another species, or, a partially or completely synthetic sequence encoding a completely unique peptide sequence designed to enhance the amino acid composition of the seed may be employed.

The introduction of genes that alter the oil content of the grain may be of value. Increases in oil content may result in increases in metabolizable energy content and density of the seeds for uses in feed and food. The introduced genes may encode enzymes that remove or reduce rate-limitations or regulated steps in fatty acid or lipid biosynthesis. Such genes may include, but are not limited to, those that encode acetyl-CoA carboxylase, ACP-acyltransferase, beta-ketoacyl-ACP synthase, plus other well known fatty acid biosynthetic activities. Other possibilities are genes that encode proteins that do not possess enzymatic activity such as acyl carrier protein. Additional examples include 2-acetyltransferase, oleosin pyruvate dehydrogenase complex, acetyl CoA synthetase, ATP citrate lyase, ADP-glucose pyrophosphorylase and genes of the carnitine-CoA- acetyl-CoA shuttles. It is anticipated that expression of genes related to oil biosynthesis will be targeted to the plastid, using a plastid transit peptide sequence and preferably expressed in the seed embryo. Genes may be introduced that alter the balance of fatty acids present in the oil providing a more healthful or nutritive feedstuff. The introduced DNA may also encode sequences that block expression of enzymes involved in fatty acid biosynthesis, altering the proportions of fatty acids present in the grain such as described below.

Genes may be introduced that enhance the nutritive value of the starch component of the grain, for example by increasing the degree of branching, resulting in improved utilization of the starch in cows by delaying its metabolism.

Besides affecting the major constituents of the grain, genes may be introduced that affect a variety of other nutritive, processing, or other quality aspects of the grain as used for feed or food. For example, pigmentation of the grain may be increased or decreased. Enhancement and stability of yellow pigmentation is desirable in some animal feeds and may be achieved by introduction of genes that result in enhanced production of xanthophylls and carotenes by eliminating rate-limiting steps in their production. Such genes may encode altered forms of the enzymes phytoene synthase, phytoene desaturase, or lycopene synthase. Alternatively, unpigmented white corn is desirable for production of many food products and may be produced by the introduction of DNA which blocks or eliminates steps in pigment production pathways.

Feed or food comprising some cereal grains possesses insufficient quantities of vitamins and must be supplemented to provide adequate nutritive value. Introduction of genes that enhance vitamin biosynthesis in seeds may be envisioned including, for example, vitamins A, E, B₁₂, choline, and the like. For example, maize grain also does not possess sufficient mineral content for optimal nutritive value. Genes that affect the accumulation or availability of compounds containing phosphorus, sulfur, calcium, manganese, zinc, and iron among others would be valuable. An example may be the introduction of a gene that reduced phytic acid production or encoded the enzyme phytase which enhances phytic acid breakdown. These genes would increase levels of available phosphate in the diet, reducing the need for supplementation with mineral phosphate.

Numerous other examples of improvement of cereals for feed and food purposes might be described. The improvements may not even necessarily involve the grain, but may, for example, improve the value of the grain for silage. Introduction of DNA to accomplish this might include sequences that alter lignin production such as those that result in the "brown midrib" phenotype associated with superior feed value for cattle.

In addition to direct improvements in feed or food value, genes may also be introduced which improve the processing of grain and improve the value of the products resulting from the processing. The primary method of processing certain grains such as maize is via wetmilling. Maize may be improved through the expression of novel genes that increase the efficiency and reduce the cost of processing such as by decreasing steeping time.

Improving the value of wetmilling products may include altering the quantity or quality of starch, oil, corn gluten meal, or the components of corn gluten feed. Elevation of starch may be achieved through the identification and elimination of rate limiting steps in starch

biosynthesis or by decreasing levels of the other components of the grain resulting in proportional increases in starch. An example of the former may be the introduction of genes encoding ADP-glucose pyrophosphorylase enzymes with altered regulatory activity or which are expressed at higher level. Examples of the latter may include selective inhibitors of, for
5 example, protein or oil biosynthesis expressed during later stages of kernel development.

The properties of starch may be beneficially altered by changing the ratio of amylose to amylopectin, the size of the starch molecules, or their branching pattern. Through these changes a broad range of properties may be modified which include, but are not limited to, changes in gelatinization temperature, heat of gelatinization, clarity of films and pastes,
10 Theological properties, and the like. To accomplish these changes in properties, genes that encode granule-bound or soluble starch synthase activity or branching enzyme activity may be introduced alone or combination. DNA such as antisense constructs may also be used to decrease levels of endogenous activity of these enzymes. The introduced genes or constructs may possess regulatory sequences that time their expression to specific intervals in starch
15 biosynthesis and starch granule development. Furthermore, it may be advisable to introduce and express genes that result in the *in vivo* derivatization, or other modification, of the glucose moieties of the starch molecule. The covalent attachment of any molecule may be envisioned, limited only by the existence of enzymes that catalyze the derivatizations and the accessibility of appropriate substrates in the starch granule. Examples of important derivations may include
20 the addition of functional groups such as amines, carboxyls, or phosphate groups which provide sites for subsequent *in vitro* derivatizations or affect starch properties through the introduction of ionic charges. Examples of other modifications may include direct changes of the glucose units such as loss of hydroxyl groups or their oxidation to aldehyde or carboxyl groups.

25 Oil is another product of wetmilling of corn and other grains, the value of which may be improved by introduction and expression of genes. The quantity of oil that can be extracted by wetmilling may be elevated by approaches as described for feed and food above. Oil properties may also be altered to improve its performance in the production and use of cooking oil, shortenings, lubricants or other oil-derived products or improvement of its health attributes
30 when used in the food-related applications. Novel fatty acids may also be synthesized which upon extraction can serve as starting materials for chemical syntheses. The changes in oil properties may be achieved by altering the type, level, or lipid arrangement of the fatty acids present in the oil. This in turn may be accomplished by the addition of genes that encode

enzymes that catalyze the synthesis of novel fatty acids and the lipids possessing them or by increasing levels of native fatty acids while possibly reducing levels of precursors.

Alternatively DNA sequences may be introduced which slow or block steps in fatty acid biosynthesis resulting in the increase in precursor fatty acid intermediates. Genes that might be added include desaturases, epoxidases, hydratases, dehydratases, and other enzymes that catalyze reactions involving fatty acid intermediates. Representative examples of catalytic steps that might be blocked include the desaturations from stearic to oleic acid and oleic to linolenic acid resulting in the respective accumulations of stearic and oleic acids.

Improvements in the other major cereal wetmilling products, gluten meal and gluten feed, may also be achieved by the introduction of genes to obtain novel plants. Representative possibilities include but are not limited to those described above for improvement of food and feed value.

In addition it may further be considered that the plant be used for the production or manufacturing of useful biological compounds that were either not produced at all, or not produced at the same level, in the plant previously. The novel plants producing these compounds are made possible by the introduction and expression of genes by transformation methods. The possibilities include, but are not limited to, any biological compound which is presently produced by any organism such as proteins, nucleic acids, primary and intermediary metabolites, carbohydrate polymers, etc. The compounds may be produced by the plant, extracted upon harvest and/or processing, and used for any presently recognized useful purpose such as pharmaceuticals, fragrances, industrial enzymes to name a few.

Further possibilities to exemplify the range of grain traits or properties potentially encoded by introduced genes in transgenic plants include grain with less breakage susceptibility for export purposes or larger grit size when processed by dry milling through introduction of genes that enhance gamma-zein synthesis, popcorn with improved popping quality and expansion volume through genes that increase pericarp thickness, corn with whiter grain for food uses through introduction of genes that effectively block expression of enzymes involved in pigment production pathways, and improved quality of alcoholic beverages or sweet corn through introduction of genes which affect flavor such as the shrunken gene (encoding sucrose synthase) for sweet corn.

7. Plant Agronomic Characteristics

Two of the factors determining where plants can be grown are the average daily temperature during the growing season and the length of time between frosts. Within the areas

where it is possible to grow a particular plant, there are varying limitations on the maximal time it is allowed to grow to maturity and be harvested. The plant to be grown in a particular area is selected for its ability to mature and dry down to harvestable moisture content within the required period of time with maximum possible yield. Therefore, plant of varying

5 maturities are developed for different growing locations. Apart from the need to dry down sufficiently to permit harvest is the desirability of having maximal drying take place in the field to minimize the amount of energy required for additional drying post-harvest. Also the more readily the grain can dry down, the more time there is available for growth and kernel fill. Genes that influence maturity and/or dry down can be identified and introduced into plant

10 lines using transformation techniques to create new varieties adapted to different growing locations or the same growing location but having improved yield to moisture ratio at harvest. Expression of genes that are involved in regulation of plant development may be especially useful, e.g., the liguleless and rough sheath genes that have been identified in plants.

Genes may be introduced into plants that would improve standability and other plant

15 growth characteristics. For example, expression of novel genes which confer stronger stalks, improved root systems, or prevent or reduce ear droppage would be of great value to the corn farmer. Introduction and expression of genes that increase the total amount of photoassimilate available by, for example, increasing light distribution and/or interception would be advantageous. In addition the expression of genes that increase the efficiency of

20 photosynthesis and/or the leaf canopy would further increase gains in productivity. Such approaches would allow for increased plant populations in the field.

Delay of late season vegetative senescence would increase the flow of assimilate into the grain and thus increase yield. Overexpression of genes within plants that are associated with "stay green" or the expression of any gene that delays senescence would achieve be

25 advantageous. For example, a non-yellowing mutant has been identified in *Festuca pratensis* (Davies et al., 1990). Expression of this gene as well as others may prevent premature breakdown of chlorophyll and thus maintain canopy function.

8. Nutrient Utilization

The ability to utilize available nutrients and minerals may be a limiting factor in growth

30 of many plants. It is proposed that it would be possible to alter nutrient uptake, tolerate pH extremes, mobilization through the plant, storage pools, and availability for metabolic activities by the introduction of novel genes. These modifications would allow a plant to more efficiently utilize available nutrients. It is contemplated that an increase in the activity of, for

example, an enzyme that is normally present in the plant and involved in nutrient utilization would increase the availability of a nutrient. An example of such an enzyme would be phytase. It is also contemplated that expression of a novel gene may make a nutrient source available that was previously not accessible, e.g., an enzyme that releases a component of nutrient value
5 from a more complex molecule, perhaps a macromolecule.

9. Male Sterility

Male sterility is useful in the production of hybrid seed. It is proposed that male sterility may be produced through expression of novel genes. For example, it has been shown that expression of genes that encode proteins that interfere with development of the male
10 inflorescence and/or gametophyte result in male sterility. Chimeric ribonuclease genes that express in the anthers of transgenic tobacco and oilseed rape have been demonstrated to lead to male sterility (Mariani et al, 1990).

For example, a number of mutations were discovered in maize that confer cytoplasmic male sterility. One mutation in particular, referred to as T cytoplasm, also correlates with
15 sensitivity to Southern corn leaf blight. A DNA sequence, designated TURF-13 (Levings, 1990), was identified that correlates with T cytoplasm. It would be possible through the introduction of TURF-13 via transformation to separate male sterility from disease sensitivity. As it is necessary to be able to restore male fertility for breeding purposes and for grain production, it is proposed that genes encoding restoration of male fertility may also be
20 introduced.

10. Negative Selectable Markers

Introduction of genes encoding traits that can be selected against may be useful for eliminating undesirable linked genes. When two or more genes are introduced together by cotransformation, the genes will be linked together on the host chromosome. For example, a
25 gene encoding a *Bt* gene that confers insect resistance on the plant may be introduced into a plant together with a *bar* gene that is useful as a selectable marker and confers resistance to the herbicide Ignite® on the plant. However, it may not be desirable to have an insect resistant plant that is also resistant to the herbicide Ignite®. It is proposed that one could also introduce an antisense *bar* gene that is expressed in those tissues where one does not want expression of
30 the *bar* gene, e.g., in whole plant parts. Hence, although the *bar* gene is expressed and is useful as a selectable marker, it is not useful to confer herbicide resistance on the whole plant. The *bar* antisense gene is a negative selectable marker.

Negative selection is necessary in order to screen a population of transformants for rare homologous recombinants generated through gene targeting. For example, a homologous recombinant may be identified through the inactivation of a gene that was previously expressed in that cell. The antisense gene to neomycin phosphotransferase II (*nptII*) has been
5 investigated as a negative selectable marker in tobacco (*Nicotiana tabacum*) and *Arabidopsis thaliana* (Xiang and Guerra, 1993). In this example both sense and antisense *nptII* genes are introduced into a plant through transformation and the resultant plants are sensitive to the antibiotic kanamycin. An introduced gene that integrates into the host cell chromosome at the site of the antisense *nptII* gene, and inactivates the antisense gene, will make the plant resistant
10 to kanamycin and other aminoglycoside antibiotics. Therefore, rare site specific recombinants may be identified by screening for antibiotic resistance. Similarly, any gene, native to the plant or introduced through transformation, that when inactivated confers resistance to a compound, may be useful as a negative selectable marker.

It is contemplated that negative selectable markers may also be useful in other ways.
15 One application is to construct transgenic lines in which one could select for transposition to unlinked sites. In the process of tagging it is most common for the transposable element to move to a genetically linked site on the same chromosome. A selectable marker for recovery of rare plants in which transposition has occurred to an unlinked locus would be useful. For example, the enzyme cytosine deaminase may be useful for this purpose (Stouggard, 1993). In
20 the presence of this enzyme the compound 5-fluorocytosine is converted to 5-fluoruracil which is toxic to plant and animal cells. If a transposable element is linked to the gene for the enzyme cytosine deaminase, one may select for transposition to unlinked sites by selecting for transposition events in which the resultant plant is now resistant to 5-fluorocytosine. The parental plants and plants containing transpositions to linked sites will remain sensitive to 5-
25 fluorocytosine. Resistance to 5-fluorocytosine is due to loss of the cytosine deaminase gene through genetic segregation of the transposable element and the cytosine deaminase gene. Other genes that encode proteins that render the plant sensitive to a certain compound will also be useful in this context. For example, T-DNA gene 2 from *Agrobacterium tumefaciens* encodes a protein that catalyzes the conversion of alpha-naphthalene acetamide (NAM) to
30 alpha-naphthalene acetic acid (NAA) renders plant cells sensitive to high concentrations of NAM (Depicker et al., 1988).

It is also contemplated that negative selectable markers may be useful in the construction of transposon tagging lines. For example, by marking an autonomous

transposable element such as Ac, Master Mu, or En/Spn with a negative selectable marker, one could select for transformants in which the autonomous element is not stably integrated into the genome. This would be desirable, for example, when transient expression of the autonomous element is desired to activate in *trans* the transposition of a defective transposable element, such as Ds, but stable integration of the autonomous element is not desired. The presence of the autonomous element may not be desired in order to stabilize the defective element, i.e., prevent it from further transposing. However, it is proposed that if stable integration of an autonomous transposable element is desired in a plant the presence of a negative selectable marker may make it possible to eliminate the autonomous element during the breeding process.

11. Non-Protein-Expressing Sequences

a. RNA-Expressing

DNA may be introduced into plants for the purpose of expressing RNA transcripts that function to affect plant phenotype yet are not translated into protein. Two examples are antisense RNA and RNA with ribozyme activity. Both may serve possible functions in reducing or eliminating expression of native or introduced plant genes.

Genes may be constructed or isolated, which when transcribed, produce antisense RNA that is complementary to all or part(s) of a targeted messenger RNA(s). The antisense RNA reduces production of the polypeptide product of the messenger RNA. The polypeptide product may be any protein encoded by the plant genome. The aforementioned genes will be referred to as antisense genes. An antisense gene may thus be introduced into a plant by transformation methods to produce a novel transgenic plant with reduced expression of a selected protein of interest. For example, the protein may be an enzyme that catalyzes a reaction in the plant. Reduction of the enzyme activity may reduce or eliminate products of the reaction which include any enzymatically synthesized compound in the plant such as fatty acids, amino acids, carbohydrates, nucleic acids and the like. Alternatively, the protein may be a storage protein, such as a zein, or a structural protein, the decreased expression of which may lead to changes in seed amino acid composition or plant morphological changes respectively. The possibilities cited above are provided only by way of example and do not represent the full range of applications.

Genes may also be constructed or isolated, which when transcribed produce RNA enzymes, or ribozymes, which can act as endoribonucleases and catalyze the cleavage of RNA molecules with selected sequences. The cleavage of selected messenger RNA's can result in

the reduced production of their encoded polypeptide products. These genes may be used to prepare novel transgenic plants which possess them. The transgenic plants may possess reduced levels of polypeptides including but not limited to the polypeptides cited above that may be affected by antisense RNA.

- 5 It is also possible that genes may be introduced to produce novel transgenic plants which have reduced expression of a native gene product by a mechanism of cosuppression. It has been demonstrated in tobacco, tomato, and petunia (Goring et al, 1991; Smith et al., 1990; Napoli et al., 1990; van der Krol et al., 1990) that expression of the sense transcript of a native gene will reduce or eliminate expression of the native gene in a manner similar to that
10 observed for antisense genes. The introduced gene may encode all or part of the targeted native protein but its translation may not be required for reduction of levels of that native protein.

b. Non-RNA-Expressing

- For example, DNA elements including those of transposable elements such as Ds, Ac, or Mu, may be inserted into a gene and cause mutations. These DNA elements may be
15 inserted in order to inactivate (or activate) a gene and thereby "tag" a particular trait. In this instance the transposable element does not cause instability of the tagged mutation, because the utility of the element does not depend on its ability to move in the genome. Once a desired trait is tagged, the introduced DNA sequence may be used to clone the corresponding gene,
20 e.g., using the introduced DNA sequence as a PCR primer together with PCR gene cloning techniques (Shapiro, 1983; Dellaporta et al., 1988). Once identified, the entire gene(s) for the particular trait, including control or regulatory regions where desired may be isolated, cloned and manipulated as desired. The utility of DNA elements introduced into an organism for purposed of gene tagging is independent of the DNA sequence and does not depend on any
25 biological activity of the DNA sequence, i.e., transcription into RNA or translation into protein. The sole function of the DNA element is to disrupt the DNA sequence of a gene.

- It is contemplated that unexpressed DNA sequences, including novel synthetic sequences could be introduced into cells as proprietary "labels" of those cells and plants and seeds thereof. It would not be necessary for a label DNA element to disrupt the function of a
30 gene endogenous to the host organism, as the sole function of this DNA would be to identify the origin of the organism. For example, one could introduce a unique DNA sequence into a plant and this DNA element would identify all cells, plants, and progeny of these cells as having arisen from that labeled source. It is proposed that inclusion of label DNAs would

enable one to distinguish proprietary germplasm or germplasm derived from such, from unlabelled germplasm.

Another possible element which may be introduced is a matrix attachment region element (MAR), such as the chicken lysozyme A element (Stief et al., 1989), which can be positioned around an expressible gene of interest to effect an increase in overall expression of the gene and diminish position dependant effects upon incorporation into the plant genome (Stief et al., 1989; Phi-Van et al., 1990).

III. Transformed (Transgenic) Plants of the Invention and Methods of Preparation

Plant species may be transformed with the DNA construct of the present invention by the DNA-mediated transformation of plant cell protoplasts and subsequent regeneration of the plant from the transformed protoplasts in accordance with procedures well known in the art.

Any plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a vector of the present invention. The term "organogenesis," as used herein, means a process by which shoots and roots are developed sequentially from meristematic centers; the term "embryogenesis," as used herein, means a process by which shoots and roots develop together in a concerted fashion (not sequentially), whether from somatic cells or gametes. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristems, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and utilane meristem).

Plants of the present invention may take a variety of forms. The plants may be chimeras of transformed cells and non-transformed cells; the plants may be clonal transformants (e.g., all cells transformed to contain the expression cassette); the plants may comprise grafts of transformed and untransformed tissues (e.g., a transformed root stock grafted to an untransformed scion in citrus species). The transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, first generation (or T1) transformed plants may be selfed to give homozygous second generation (or T2) transformed plants, and the T2 plants further propagated through classical breeding techniques. A dominant selectable marker (such as npt II) can be associated with the expression cassette to assist in breeding.

Thus, the present invention provides a transformed (transgenic) plant cell, *in planta* or *ex planta*, including a transformed plastid or other organelle, e.g., nucleus, mitochondria or chloroplast. The present invention may be used for transformation of any plant species, including, but not limited to, cells from corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*,
 5 *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*),
 10 tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea utiliane*), fig (*Ficus casica*), guava (*Psidium*
 15 *guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, duckweed (*Lemna*), barley, vegetables, ornamentals, and conifers.

Duckweed (*Lemna*, see WO 00/07210) includes members of the family *Lemnaceae*.
 20 There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. Angusta*, *Wa. Arrhiza*, *Wa. Australina*, *Wa. Borealis*, *Wa. Brasiliensis*, *Wa. Columbiana*, *Wa. Elongata*, *Wa. Globosa*, *Wa.*
 25 *Microscopica*, *Wa. Neglecta*) and genus *Wofliella* (*W1. utila*, *W1. utilanen*, *W1. gladiata*, *W1. utila*, *W1. lingulata*, *W1. repunda*, *W1. rotunda*, and *W1. neotropica*). Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described
 30 by Landolt, Biosystematic Investigation on the Family of Duckweeds: The family of *Lemnaceae* – A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)).

Vegetables within the scope of the invention include tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*).

- 5 Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus*
- 10 *elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga utilane*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants
- 15 include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil,
- 20 lens, e.g., lentil, and false indigo. Preferred forage and turf grass for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop.

- Papaya, garlic, pea, peach, pepper, petunia, strawberry, sorghum, sweet potato, turnip, safflower, corn, pea, endive, gourd, grape, snap bean, chicory, cotton, tobacco, aubergine, beet,
- 25 buckwheat, broad bean, nectarine, avocado, mango, banana, groundnut, potato, peanut, lettuce, pineapple, spinach, squash, sugarbeet, sugarcane, sweet corn, chrysanthemum.

- Other plants within the scope of the invention include *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon,
- 30 plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, ultilan sprouts, onion, carrot, leek, beet,

broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, utilane, and zucchini.

Ornamental plants within the scope of the invention include impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, 5 Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia. Other plants within the scope of the invention are shown in Table 1 (above).

Preferably, transgenic plants of the present invention are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean, barley, soybean, 10 sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.), and even more preferably corn, rice and soybean.

Transformation of plants can be undertaken with a single DNA molecule or multiple DNA molecules (i.e., co-transformation), and both these techniques are suitable for use with the expression cassettes of the present invention. Numerous transformation vectors are 15 available for plant transformation, and the expression cassettes of this invention can be used in conjunction with any such vectors. The selection of vector will depend upon the preferred transformation technique and the target species for transformation.

A variety of techniques are available and known to those skilled in the art for introduction of constructs into a plant cell host. These techniques generally include 20 transformation with DNA employing *A. tumefaciens* or *A. rhizogenes* as the transforming agent, liposomes, PEG precipitation, electroporation, DNA injection, direct DNA uptake, microprojectile bombardment, particle acceleration, and the like (See, for example, EP 295959 and EP 138341) (see below). However, cells other than plant cells may be transformed with the expression cassettes of the invention. The general descriptions of plant expression vectors and reporter genes, and *Agrobacterium* and *Agrobacterium*-mediated gene transfer, can be 25 found in Gruber et al. (1993).

Expression vectors containing genomic or synthetic fragments can be introduced into protoplasts or into intact tissues or isolated cells. Preferably expression vectors are introduced into intact tissue. General methods of culturing plant tissues are provided for example by 30 Maki et al., (1993); and by Phillips et al. (1988). Preferably, expression vectors are introduced into maize or other plant tissues using a direct gene transfer method such as microprojectile-mediated delivery, DNA injection, electroporation and the like. More preferably expression vectors are introduced into plant tissues using the microprojectile media delivery with the

biolistic device. See, for example, Tomes et al. (1995). The vectors of the invention can not only be used for expression of structural genes but may also be used in exon-trap cloning, or promoter trap procedures to detect differential gene expression in varieties of tissues, (Lindsey et al., 1993; Auch & Reth et al.).

5 It is particularly preferred to use the binary type vectors of Ti and Ri plasmids of *Agrobacterium spp.* Ti-derived vectors transform a wide variety of higher plants, including monocotyledonous and dicotyledonous plants, such as soybean, cotton, rape, tobacco, and rice (Pacciotti et al., 1985; Byrne et al., 1987; Sukhapinda et al., 1987; Park et al., 1985; Hiei et al., 1994). The use of T-DNA to transform plant cells has received extensive study and is amply
10 described (EP 120516; Hoekema, 1985; Knauf, et al., 1983; and An et al., 1985). For introduction into plants, the chimeric genes of the invention can be inserted into binary vectors as described in the examples.

Other transformation methods are available to those skilled in the art, such as direct uptake of foreign DNA constructs (see EP 295959), techniques of electroporation (Fromm et
15 al., 1986) or high velocity ballistic bombardment with metal particles coated with the nucleic acid constructs (Kline et al., 1987, and U.S. Patent No. 4,945,050). Once transformed, the cells can be regenerated by those skilled in the art. Of particular relevance are the recently described methods to transform foreign genes into commercially important crops, such as rapeseed (De Block et al., 1989), sunflower (Everett et al., 1987), soybean (McCabe et al.,
20 1988; Hinchey et al., 1988; Chee et al., 1989; Christou et al., 1989; EP 301749), rice (Hiei et al., 1994), and corn (Gordon Kamm et al., 1990; Fromm et al., 1990).

Those skilled in the art will appreciate that the choice of method might depend on the type of plant, i.e., monocotyledonous or dicotyledonous, targeted for transformation. Suitable methods of transforming plant cells include, but are not limited to, microinjection (Crossway
25 et al., 1986), electroporation (Riggs et al., 1986), *Agrobacterium*-mediated transformation (Hinchey et al., 1988), direct gene transfer (Paszkowski et al., 1984), and ballistic particle acceleration using devices available from Agracetus, Inc., Madison, Wis. And BioRad, Hercules, Calif. (see, for example, Sanford et al., U.S. Pat. No. 4,945,050; and McCabe et al., 1988). Also see, Weissinger et al., 1988; Sanford et al., 1987 (onion); Christou et al., 1988
30 (soybean); McCabe et al., 1988 (soybean); Datta et al., 1990 (rice); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Fromm et al., 1990 (maize); and Gordon-Kamm et al., 1990 (maize); Svab et al., 1990 (tobacco chloroplast); Koziel et al., 1993 (maize); Shimamoto et al., 1989 (rice); Christou et al., 1991 (rice); European Patent

Application EP 0 332 581 (orchardgrass and other Pooideae); Vasil et al., 1993 (wheat); Weeks et al., 1993 (wheat). In one embodiment, the protoplast transformation method for maize is employed (European Patent Application EP 0 292 435, U. S. Pat. No. 5,350,689).

In another embodiment, a nucleotide sequence of the present invention is directly
5 transformed into the plastid genome. Plastid transformation technology is extensively described in U.S. Patent Nos. 5,451,513, 5,545,817, and 5,545,818, in PCT application no. WO 95/16783, and in McBride et al., 1994. The basic technique for chloroplast transformation involves introducing regions of cloned plastid DNA flanking a selectable marker together with the gene of interest into a suitable target tissue, e.g., using biolistics or protoplast
10 transformation (e.g., calcium chloride or PEG mediated transformation). The 1 to 1.5 kb flanking regions, termed targeting sequences, facilitate orthologous recombination with the plastid genome and thus allow the replacement or modification of specific regions of the plastome. Initially, point mutations in the chloroplast 16S rRNA and *rps12* genes conferring resistance to spectinomycin and/or streptomycin are utilized as selectable markers for
15 transformation (Svab et al., 1990; Staub et al., 1992). This resulted in stable homoplasmic transformants at a frequency of approximately one per 100 bombardments of target leaves. The presence of cloning sites between these markers allowed creation of a plastid targeting vector for introduction of foreign genes (Staub et al., 1993). Substantial increases in transformation frequency are obtained by replacement of the recessive rRNA or r-protein
20 antibiotic resistance genes with a dominant selectable marker, the bacterial *aadA* gene encoding the spectinomycin-detoxifying enzyme aminoglycoside-3N-adenyltransferase (Svab et al., 1993). Other selectable markers useful for plastid transformation are known in the art and encompassed within the scope of the invention. Typically, approximately 15-20 cell division cycles following transformation are required to reach a homoplastidic state. Plastid
25 expression, in which genes are inserted by orthologous recombination into all of the several thousand copies of the circular plastid genome present in each plant cell, takes advantage of the enormous copy number advantage over nuclear-expressed genes to permit expression levels that can readily exceed 10% of the total soluble plant protein. In a preferred embodiment, a nucleotide sequence of the present invention is inserted into a plastid targeting
30 vector and transformed into the plastid genome of a desired plant host. Plants homoplasmic for plastid genomes containing a nucleotide sequence of the present invention are obtained, and are preferentially capable of high expression of the nucleotide sequence.

Agrobacterium tumefaciens cells containing a vector comprising an expression cassette of the present invention, wherein the vector comprises a Ti plasmid, are useful in methods of making transformed plants. Plant cells are infected with an *Agrobacterium tumefaciens* as described above to produce a transformed plant cell, and then a plant is regenerated from the transformed plant cell. Numerous *Agrobacterium* vector systems useful in carrying out the present invention are known.

For example, vectors are available for transformation using *Agrobacterium tumefaciens*. These typically carry at least one T-DNA border sequence and include vectors such as pBIN19 (Bevan, 1984). In one preferred embodiment, the expression cassettes of the present invention may be inserted into either of the binary vectors pCIB200 and pCIB2001 for use with *Agrobacterium*. These vector cassettes for *Agrobacterium*-mediated transformation wear constructed in the following manner. PTJS75kan was created by NarI digestion of pTJS75 (Schmidhauser & Helinski, 1985) allowing excision of the tetracycline-resistance gene, followed by insertion of an AccI fragment from pUC4K carrying an NPTII (Messing & Vierra, 1982; Bevan et al., 1983; McBride et al., 1990). XhoI linkers were ligated to the EcoRV fragment of pCIB7 which contains the left and right T-DNA borders, a plant selectable nos/nptII chimeric gene and the pUC polylinker (Rothstein et al., 1987), and the XhoI-digested fragment was cloned into SalI-digested pTJS75kan to create pCIB200 (see also EP 0 332 104, example 19). PCIB200 contains the following unique polylinker restriction sites: EcoRI, SstI, KpnI, BglII, XbaI, and SalI. The plasmid pCIB2001 is a derivative of pCIB200 which was created by the insertion into the polylinker of additional restriction sites. Unique restriction sites in the polylinker of pCIB2001 are EcoRI, SstI, KpnI, BglII, XbaI, SalI, MluI, BclI, AvrII, ApaI, HpaI, and StuI. PCIB2001, in addition to containing these unique restriction sites also has plant and bacterial kanamycin selection, left and right T-DNA borders for *Agrobacterium*-mediated transformation, the RK2-derived trfA function for mobilization between *E. coli* and other hosts, and the OriT and OriV functions also from RK2. The pCIB2001 polylinker is suitable for the cloning of plant expression cassettes containing their own regulatory signals.

An additional vector useful for *Agrobacterium*-mediated transformation is the binary vector pCIB 10, which contains a gene encoding kanamycin resistance for selection in plants, T-DNA right and left border sequences and incorporates sequences from the wide host-range plasmid pRK252 allowing it to replicate in both *E. coli* and *Agrobacterium*. Its construction is described by Rothstein et al., 1987. Various derivatives of pCIB10 have been constructed

which incorporate the gene for hygromycin B phosphotransferase described by Gritz et al., 1983. These derivatives enable selection of transgenic plant cells on hygromycin only (pCIB743), or hygromycin and kanamycin (pCIB715, pCIB717).

5 Methods using either a form of direct gene transfer or *Agrobacterium*-mediated transfer usually, but not necessarily, are undertaken with a selectable marker which may provide resistance to an antibiotic (e.g., kanamycin, hygromycin or methotrexate) or a herbicide (e.g., phosphinothricin). The choice of selectable marker for plant transformation is not, however, critical to the invention.

For certain plant species, different antibiotic or herbicide selection markers may be preferred. Selection markers used routinely in transformation include the nptII gene which 10 confers resistance to kanamycin and related antibiotics (Messing & Vierra, 1982; Bevan et al., 1983), the bar gene which confers resistance to the herbicide phosphinothricin (White et al., 1990, Spencer et al., 1990), the hph gene which confers resistance to the antibiotic hygromycin (Blochinger & Diggelmann), and the dhfr gene, which confers resistance to methotrexate 15 (Bourouis et al., 1983).

One such vector useful for direct gene transfer techniques in combination with selection by the herbicide Basta (or phosphinothricin) is pCIB3064. This vector is based on the plasmid pCIB246, which comprises the CaMV 35S promoter in operational fusion to the E. coli GUS gene and the CaMV 35S transcriptional terminator and is described in the PCT 20 published application WO 93/07278, herein incorporated by reference. One gene useful for conferring resistance to phosphinothricin is the bar gene from *Streptomyces viridochromogenes* (Thompson et al., 1987). This vector is suitable for the cloning of plant expression cassettes containing their own regulatory signals.

An additional transformation vector is pSOG35 which utilizes the *E. coli* gene 25 dihydrofolate reductase (DHFR) as a selectable marker conferring resistance to methotrexate. PCR was used to amplify the 35S promoter (about 800 bp), intron 6 from the maize Adh1 gene (about 550 bp) and 18 bp of the GUS untranslated leader sequence from pSOG10. A 250 bp fragment encoding the *E. coli* dihydrofolate reductase type II gene was also amplified by PCR and these two PCR fragments were assembled with a SacI-PstI fragment from pBI221 30 (Clontech) which comprised the pUC19 vector backbone and the nopaline synthase terminator. Assembly of these fragments generated pSOG19 which contains the 35S promoter in fusion with the intron 6 sequence, the GUS leader, the DHFR gene and the nopaline synthase terminator. Replacement of the GUS leader in pSOG19 with the leader sequence from Maize

Chlorotic Mottle Virus check (MCMV) generated the vector pSOG35. pSOG19 and pSOG35 carry the pUC-derived gene for ampicillin resistance and have HindIII, SphI, PstI and EcoRI sites available for the cloning of foreign sequences.

IV. Production and Characterization of Stably Transformed Plants

5 Transgenic plant cells are then placed in an appropriate selective medium for selection of transgenic cells which are then grown to callus. Shoots are grown from callus and plantlets generated from the shoot by growing in rooting medium. The various constructs normally will be joined to a marker for selection in plant cells. Conveniently, the marker may be resistance to a biocide (particularly an antibiotic, such as kanamycin, G418, bleomycin, hygromycin,
10 chloramphenicol, herbicide, or the like). The particular marker used will allow for selection of transformed cells as compared to cells lacking the DNA which has been introduced. Components of DNA constructs including transcription cassettes of this invention may be prepared from sequences which are native (endogenous) or foreign (exogenous) to the host. By "foreign" it is meant that the sequence is not found in the wild-type host into which the
15 construct is introduced. Heterologous constructs will contain at least one region which is not native to the gene from which the transcription-initiation-region is derived.

To confirm the presence of the transgenes in transgenic cells and plants, a variety of assays may be performed. Such assays include, for example, "molecular biological" assays well known to those of skill in the art, such as Southern and Northern blotting, *in situ*
20 hybridization and nucleic acid-based amplification methods such as PCR or RT-PCR; "biochemical" assays, such as detecting the presence of a protein product, e.g., by immunological means (ELISAs and Western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the phenotype of the whole regenerated plant, e.g., for disease or pest resistance.

25 DNA may be isolated from cell lines or any plant parts to determine the presence of the preselected nucleic acid segment through the use of techniques well known to those skilled in the art. Note that intact sequences will not always be present, presumably due to rearrangement or deletion of sequences in the cell.

The presence of nucleic acid elements introduced through the methods of this invention
30 may be determined by polymerase chain reaction (PCR). Using this technique discreet fragments of nucleic acid are amplified and detected by gel electrophoresis. This type of analysis permits one to determine whether a preselected nucleic acid segment is present in a stable transformant, but does not prove integration of the introduced preselected nucleic acid

segment into the host cell genome. In addition, it is not possible using PCR techniques to determine whether transformants have exogenous genes introduced into different sites in the genome, i.e., whether transformants are of independent origin. It is contemplated that using PCR techniques it would be possible to clone fragments of the host genomic DNA adjacent to an introduced preselected DNA segment.

Positive proof of DNA integration into the host genome and the independent identities of transformants may be determined using the technique of Southern hybridization. Using this technique specific DNA sequences that were introduced into the host genome and flanking host DNA sequences can be identified. Hence the Southern hybridization pattern of a given transformant serves as an identifying characteristic of that transformant. In addition it is possible through Southern hybridization to demonstrate the presence of introduced preselected DNA segments in high molecular weight DNA, i.e., confirm that the introduced preselected DNA segment has been integrated into the host cell genome. The technique of Southern hybridization provides information that is obtained using PCR, e.g., the presence of a preselected DNA segment, but also demonstrates integration into the genome and characterizes each individual transformant.

It is contemplated that using the techniques of dot or slot blot hybridization which are modifications of Southern hybridization techniques one could obtain the same information that is derived from PCR, e.g., the presence of a preselected DNA segment.

Both PCR and Southern hybridization techniques can be used to demonstrate transmission of a preselected DNA segment to progeny. In most instances the characteristic Southern hybridization pattern for a given transformant will segregate in progeny as one or more Mendelian genes (Spencer et al., 1992); Laursen et al., 1994) indicating stable inheritance of the gene. The nonchimeric nature of the callus and the parental transformants (R_0) was suggested by germline transmission and the identical Southern blot hybridization patterns and intensities of the transforming DNA in callus, R_0 plants and R_1 progeny that segregated for the transformed gene.

Whereas DNA analysis techniques may be conducted using DNA isolated from any part of a plant, RNA may only be expressed in particular cells or tissue types and hence it will be necessary to prepare RNA for analysis from these tissues. PCR techniques may also be used for detection and quantitation of RNA produced from introduced preselected DNA segments. In this application of PCR it is first necessary to reverse transcribe RNA into DNA, using enzymes such as reverse transcriptase, and then through the use of conventional PCR

techniques amplify the DNA. In most instances PCR techniques, while useful, will not demonstrate integrity of the RNA product. Further information about the nature of the RNA product may be obtained by Northern blotting. This technique will demonstrate the presence of an RNA species and give information about the integrity of that RNA. The presence or
5 absence of an RNA species can also be determined using dot or slot blot Northern hybridizations. These techniques are modifications of Northern blotting and will only demonstrate the presence or absence of an RNA species.

While Southern blotting and PCR may be used to detect the preselected DNA segment in question, they do not provide information as to whether the preselected DNA segment is
10 being expressed. Expression may be evaluated by specifically identifying the protein products of the introduced preselected DNA segments or evaluating the phenotypic changes brought about by their expression.

Assays for the production and identification of specific proteins may make use of physical-chemical, structural, functional, or other properties of the proteins. Unique physical-
15 chemical or structural properties allow the proteins to be separated and identified by electrophoretic procedures, such as native or denaturing gel electrophoresis or isoelectric focusing, or by chromatographic techniques such as ion exchange or gel exclusion chromatography. The unique structures of individual proteins offer opportunities for use of specific antibodies to detect their presence in formats such as an ELISA assay. Combinations
20 of approaches may be employed with even greater specificity such as Western blotting in which antibodies are used to locate individual gene products that have been separated by electrophoretic techniques. Additional techniques may be employed to absolutely confirm the identity of the product of interest such as evaluation by amino acid sequencing following purification. Although these are among the most commonly employed, other procedures may
25 be additionally used.

Assay procedures may also be used to identify the expression of proteins by their functionality, especially the ability of enzymes to catalyze specific chemical reactions involving specific substrates and products. These reactions may be followed by providing and
quantifying the loss of substrates or the generation of products of the reactions by physical or
30 chemical procedures. Examples are as varied as the enzyme to be analyzed.

Very frequently the expression of a gene product is determined by evaluating the phenotypic results of its expression. These assays also may take many forms including but not limited to analyzing changes in the chemical composition, morphology, or physiological

properties of the plant. Morphological changes may include greater stature or thicker stalks. Most often changes in response of plants or plant parts to imposed treatments are evaluated under carefully controlled conditions termed bioassays.

V. Uses of Transgenic Plants

5 Once an expression cassette of the invention has been transformed into a particular plant species, it may be propagated in that species or moved into other varieties of the same species, particularly including commercial varieties, using traditional breeding techniques. Particularly preferred plants of the invention include the agronomically important crops listed above. The genetic properties engineered into the transgenic seeds and plants described above
10 are passed on by sexual reproduction and can thus be maintained and propagated in progeny plants. The present invention also relates to a transgenic plant cell, tissue, organ, seed or plant part obtained from the transgenic plant. Also included within the invention are transgenic descendants of the plant as well as transgenic plant cells, tissues, organs, seeds and plant parts obtained from the descendants.

15 Preferably, the expression cassette in the transgenic plant is sexually transmitted. In one preferred embodiment, the coding sequence is sexually transmitted through a complete normal sexual cycle of the R0 plant to the R1 generation. Additionally preferred, the expression cassette is expressed in the cells, tissues, seeds or plant of a transgenic plant in an amount that is different than the amount in the cells, tissues, seeds or plant of a plant which
20 only differs in that the expression cassette is absent.

 The transgenic plants produced herein are thus expected to be useful for a variety of commercial and research purposes. Transgenic plants can be created for use in traditional agriculture to possess traits beneficial to the grower (e.g., agronomic traits such as resistance to water deficit, pest resistance, herbicide resistance or increased yield), beneficial to the
25 consumer of the grain harvested from the plant (e.g., improved nutritive content in human food or animal feed; increased vitamin, amino acid, and antioxidant content; the production of antibodies (passive immunization) and nutraceuticals), or beneficial to the food processor (e.g., improved processing traits). In such uses, the plants are generally grown for the use of their grain in human or animal foods. Additionally, the use of root-specific promoters in transgenic
30 plants can provide beneficial traits that are localized in the consumable (by animals and humans) roots of plants such as carrots, parsnips, and beets. However, other parts of the plants, including stalks, husks, vegetative parts, and the like, may also have utility, including use as part of animal silage or for ornamental purposes. Often, chemical constituents (e.g., oils

or starches) of maize and other crops are extracted for foods or industrial use and transgenic plants may be created which have enhanced or modified levels of such components.

Transgenic plants may also find use in the commercial manufacture of proteins or other molecules, where the molecule of interest is extracted or purified from plant parts, seeds, and the like. Cells or tissue from the plants may also be cultured, grown *in vitro*, or fermented to manufacture such molecules.

The transgenic plants may also be used in commercial breeding programs, or may be crossed or bred to plants of related crop species. Improvements encoded by the expression cassette may be transferred, e.g., from maize cells to cells of other species, e.g., by protoplast fusion.

The transgenic plants may have many uses in research or breeding, including creation of new mutant plants through insertional mutagenesis, in order to identify beneficial mutants that might later be created by traditional mutation and selection. An example would be the introduction of a recombinant DNA sequence encoding a transposable element that may be used for generating genetic variation. The methods of the invention may also be used to create plants having unique "signature sequences" or other marker sequences which can be used to identify proprietary lines or varieties.

Thus, the transgenic plants and seeds according to the invention can be used in plant breeding which aims at the development of plants with improved properties conferred by the expression cassette, such as tolerance of drought, disease, or other stresses. The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate descendant plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, utilane breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines which for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can be

obtained which, due to their optimized genetic "equipment", yield harvested product of better quality than products which were not able to tolerate comparable adverse developmental conditions.

VI. A Computer Readable Medium

5 The invention also provides a computer readable medium having stored thereon a data structure containing nucleic acid sequences having at least 70% sequence identity to a nucleic acid sequence selected from those listed in SEQ ID Nos: 1-953, 2137-2661, 1954-1966, 2000-2129, 2662-4737 and 4738-6813, as well as complementary, ortholog, and variant sequences thereof. Storage and use of nucleic acid sequences on a computer readable medium is well
10 known in the art. (See for example U.S. Patent Nos. 6,023,659; 5,867,402; 5,795,716) Examples of such medium include, but are not limited to, magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory. Accordingly, the nucleic acid sequences contained on the computer readable medium may be compared through use of a module that receives the sequence information and compares it to
15 other sequence information. Examples of other sequences to which the nucleic acid sequences of the invention may be compared include those maintained by the National Center for Biotechnology Information (NCBI)(<http://www.ncbi.nlm.nih.gov/>) and the Swiss Protein Data Bank. A computer is an example of such a module that can read and compare nucleic acid sequence information. Accordingly, the invention also provides the method of comparing a
20 nucleic acid sequence of the invention to another sequence. For example, a sequence of the invention may be submitted to the NCBI for a Blast search as described herein where the sequence is compared to sequence information contained within the NCBI database and a comparison is returned. The invention also provides nucleic acid sequence information in a computer readable medium that allows the encoded polypeptide to be optimized for a desired
25 property. Examples of such properties include, but are not limited to, increased or decreased: thermal stability, chemical stability, hydrophylicity, hydrophobicity, and the like. Methods for the use of computers to model polypeptides and polynucleotides having altered activities are well known in the art and have been reviewed. (Lesyng et al., 1993; Surles et al., 1994; Koehl et al., 1996; Rossi et al., 2001).

30 The invention will be further described by the following non-limiting examples.

Example 1

GeneChip Standard Protocol

Quantitation of total RNA

Total RNA from plant tissue is extracted and quantified.

- 5 1. Quantify total RNA using GeneQuant
 $1\text{OD}_{260}=40 \text{ mg RNA/ml}$; $A_{260}/A_{280}=1.9$ to about 2.1
2. Run gel to check the integrity and purity of the extracted RNA

Synthesis of double-stranded cDNA

- 10 Gibco/BRL SuperScript Choice System for cDNA Synthesis (Cat#1B090-019) was employed to prepare cDNAs. T7-(dT)₂₄ oligonucleotides were prepared and purified by HPLC. (5'-GGCCAGTGAATTGTAATACGACTCACTATAGGGAGGCGG-(dT)₂₄-3' SEQ ID NO:2136).

Step 1. Primer hybridization:

- 15 Incubate at 70°C for 10 minutes
 Quick spin and put on ice briefly

Step 2. Temperature adjustment:

Incubate at 42°C for 2 minutes

Step 3. First strand synthesis:

- 20 DEPC-water- 1 μl
 RNA (10 μg final)-10 μl
 T7=(dT)₂₄ Primer (100 pmol final)-1 μl pmol
 5X 1st strand cDNA buffer-4 μl
 0.1M DTT (10 mM final)- 2 μl
25 10 mM dNTP mix (500 μM final)-1 μl
 Superscript II RT 200 U/ μl - 1 μl
 Total of 20 μl
 Mix well
 Incubate at 42°C for 1 hour

Step 4. Second strand synthesis:

- 30 Place reactions on ice, quick spin
 DEPC-water- 91 μl
 5X 2nd strand cDNA buffer- 30 μl

mM dNTP mix (250 mM final) - 3 μ l

E. coli DNA ligase (10 U/ μ l)-1 μ l

E. coli DNA polymerase 1-10 U/ μ l- 4 μ l

RnaseH 2U/ μ l -1 μ l

5 T4 DNA polymerase 5 U/ μ l-2 μ l

0.5 M EDTA (0.5 M final)--10 μ l

Total 162 μ l

Mix/spin down/incubate 16°C for 2 hours

Step 5. Completing the reaction:

10 Incubate at 16°C for 5 minutes

Purification of double stranded cDNA

1. Centrifuge PLG (Phase Lock Gel, Eppendorf 5 Prime, Inc., PI-188233) at 14,000X, transfer 162 μ l of cDNA to PLG
- 15 2. Add 162 μ l of Phenol:Chloroform:Isoamyl alcohol (pH 8.0), centrifuge 2 minutes
3. Transfer the supernatant to a fresh 1.5 ml tube, add

Glycogen (5 mg/ml)	2
0.5 M NH ₄ OAC (0.75xVol)	120
ETOH (2.5xVol, -20 C)	400
- 20 4. Mix well and centrifuge at 14,000X for 20 minutes
5. Remove supernatant, add 0.5 ml 80% EtOH (-20°C)
6. Centrifuge for 5 minutes, air dry or by speed vac for 5-10 minutes
7. Add 44 μ l DEPC H₂O

Analyze of quantity and size distribution of cDNA

25 Run a gel using 1 μ l of the double-stranded synthesis product

Synthesis of biotinylated cRNA

(use Enzo BioArray High Yield RNA Transcript Labeling Kit Cat#900182)

30	Purified cDNA	22 μ l
	10X Hy buffer	4 μ l
	10X biotin ribonucleotides	4 μ l
	10X DTT	4 μ l
	10X Rnase inhibitor mix	4 μ l

20X T7 RNA polymerase	2 μ l
-----------------------	-----------

Total	40 μ l
-------	------------

Centrifuge 5 seconds, and incubate for 4 hours at 37EC

Gently mix every 30-45 minutes

5

Purification and quantification of cRNA

(use Qiagen Rneasy Mini kit Cat# 74103)

Determine concentration and dilute to 1 μ g/ μ l concentration

10 Fragmentation of cRNA

cRNA (1 μ g/ μ l)	15 μ l
---------------------------	------------

5X Fragmentation Buffer*	6 μ l
--------------------------	-----------

DEPC H ₂ O	9 μ l
-----------------------	-----------

	30 μ l
--	------------

15

*5x Fragmentation Buffer

1M Tris (pH8.1)	4.0 ml
-----------------	--------

MgOAc	0.64 g
-------	--------

KOAC	0.98 g
------	--------

DEPC H ₂ O	
-----------------------	--

Total	20 ml
-------	-------

Filter Sterilize

Array wash and staining

25 Stringent Wash Buffer**

Non-Stringent Wash Buffer***

SAPE Stain****

Antibody Stain*****

30 Wash on fluidics station using the appropriate antibody amplification protocol

**Stringent Buffer: 12X MES 83.3 ml, 5 M NaCl 5.2 ml, 10% Tween 1.0 ml, H₂O 910 ml,

Filter Sterilize

***Non-Stringent Buffer: 20X SSPE 300 ml, 10% Tween 1.0 ml, H₂O 698 ml, Filter Sterilize, Antifoam 1.0.

****SAPE stain: 2X Stain Buffer 600 µl, BSA 48 µl, SAPE 12µl, H₂O 540 µl.

*****Antibody Stain: 2X Stain Buffer 300 µl, H₂O 266.4 µl, BSA 24 ul, Goat IgG 6 µl,
5 Biotinylated Ab 3.6 µl

Image analysis and data mining

1. Two text files are included in the analysis:

- a. One with Absolute analysis: giving the status of each gene, either absent or present in the samples
- 10 b. The other with Comparison analysis: comparing gene expression levels between two samples

Example 2

Analysis of the RPS2 Mediated Interaction in *Arabidopsis*

15 The identification and cloning of resistance genes is extremely important for the treatment of crops. For example, bacterial blight disease caused by *Xanthomonas spp.* infects virtually all crop plants and leads to extensive crop losses worldwide. Therefore, it is of interest to identify diverse and abundant plant resistance genes for use as future crop treatments for pathogen resistance, e.g., to identify particular pathogen resistance (*R*) genes in
20 a plant.

Differential gene expression analysis was used to identify pathogen resistance (*R*) genes in a plant. This method takes advantage of the HR-associated disease resistance. One model plant-pathogen interaction is that of *Arabidopsis thaliana* and *Pseudomonas syringae* pv *tomato*. There are four possible genetic interactions of a *P. syringae* infection of
25 *Arabidopsis* when analyzing HR-associated disease resistance (Table 2). However, there are only two possible outcomes: a compatible outcome occurs when there is disease, and an incompatible outcome occurs when there is no disease. An incompatible outcome, or disease resistance, occurs only when the plant possesses the resistance gene, e.g., *RPS2*, and the pathogen possesses the corresponding *avr* gene, e.g., *avrRpt2*. *RPS2* belongs to the NBS-LRR
30 class of *R* genes, which can confer resistance to a wide variety of phytopathogens. It has been suggested that AvrRpt2 is delivered to the plant via the bacteria's type III secretion system and recognized by a surveillance system involving RPS2 inside the plant cell. The plant response during an incompatible interaction includes a change in ion flux across the plasma membrane,

generation of reactive oxygen species, induction of defense genes, induction of HR, fortification of the cell wall, accumulation of salicylic acid, and anti-microbial compounds.

Table 2

Number	Plant	Pathogen	Outcome	
1	<i>RPS2</i>	no <i>avr</i>	Disease	Compatible
2	<i>RPS2</i>	<i>avrRpt2</i>	No disease	Incompatible
3	<i>rps2</i>	no <i>avr</i>	Disease	Compatible
4	<i>rps2</i>	<i>avrRpt2</i>	Disease	Compatible

5

Methods

Differential Expression

Analysis of differential gene expression is a classic and very powerful tool in experimental biology not only to study large trends in gene regulation but also small differences among similar responses. Historically, methods for analysis only allowed the comparison of a very few genes in each experiment. However, with new methods to identify and quantitate differential mRNA profiles, such as long distance differential display PCR, cDNA microarrays, and gene chips, one can much more quickly and comprehensively identify and analyze differentially expressed genes.

By analyzing and comparing the expression profile of genes in the above 4-way matrix, a number of types of genes can be identified that are involved in the resistance pathway. Resistance genes would be highly expressed or strongly downregulated in outcome number 2 in the four way matrix and less oppositely expressed in outcome numbers 1, 3, and 4. Genes that are highly expressed or strongly downregulated in outcome numbers 1 and 2 and oppositely expressed or not expressed above baseline in outcome numbers 3 and 4 are of interest as being associated with the reaction of a plant having resistance genes to a bacterial infection, regardless of the *avr* genotype of the bacterium. Such a comparison is very useful in identifying strong candidates for different roles in plant/pathogen interactions, as are numerous other kinds of outcomes in the four-way plant/pathogen interaction analysis of gene expression. Such genes include those involved in recognition of pathogen (unrelated to virulence status); genes involved in recognition of pathogen having a virulence or avirulence gene (regardless of the status of the corresponding plant); genes related to the status of the

plant, regardless of the status of the pathogen; and genes that do not change expression during plant-pathogen interaction.

Use of a Gene Chip to Study Gene Regulation in *Arabidopsis* in Response to Exposure to Pathogen

5 Initially isogenic strains of *Arabidopsis thaliana* ecotype Col-0 were used, one having the wild type *RPS2* gene that confers resistance, and one having the *rps2* mutant that confers susceptibility to attack by *Pseudomonas syringae* pathovar *tomato* (Pst). Subsequently, comparisons between ecotypes, mutant *Arabidopsis*, and infection with different pathogens were made. After infection, the RNA was isolated and a probe produced using the Affymetrix
10 GeneChip™ protocol. A gene array representing approximately 8,100 *Arabidopsis thaliana* genes was used to carry out global gene expression profiling in response to exposure to a particular pathogen.

Initially, the analysis involved comparing all four of the interactions to a water control (plants “infected” with water). In the initial analysis, the mRNA levels of approximately 1,600
15 genes were significantly affected (> 2.5-fold change in expression) by exposure to the bacterial pathogen. This suggested a dramatic change in the molecular biology of the cell and a more detailed analysis was performed.

Results

A. Comparison Of Compatible To Incompatible Infections

20 Two different types of interactions between *Arabidopsis* and *Pseudomonas syringae* were analyzed. In one type of experiment, a gene for gene interaction conditioned by the plant resistance (*R*) gene *RPS2* and the bacterial avirulence gene *avrRpt2* at a relatively early stage was analyzed. When the pathogen has an *avr* gene and the plant has the corresponding *R* gene, the plant is resistant to the pathogen and the interaction is called incompatible. When the
25 plant-pathogen system lacks either or both genes, the plant is susceptible to the pathogen and the interaction is called compatible. A hypersensitive response (HR, localized rapid cell death of the plant) is one aspect of resistance.

Isogenic strains of *Arabidopsis thaliana* ecotype Col-0 were used, one having the wild type *RPS2* gene that confers resistance, and one having the mutant *rps2* mutant that confers
30 susceptibility to attack by *Pseudomonas syringae* pathovar *tomato* (Pst) carrying *avrRpt2*. Two strains of *Pseudomonas syringae* were used, one having the *avr* gene *avrRpt2* and the other having no *avr*. The *avr* gene is carried on a plasmid.

A gene array having 8,700 probe sets representing approximately 8,100 *Arabidopsis thaliana* genes was used to carry out global gene expression profiling of each of the infection outcomes. The pairings were as follows:

1. RPS2 WT plant; *P. syringae* (no *avr*)
- 5 2. RPS2 WT plant; *P. syringae/avrRpt2*
3. *rps2*-101C mutant plant; *P. syringae* (no *avr*)
4. *rps2*-101C mutant plant; *P. syringae/avrRpt2*

Additionally, two controls were used:

5. RPS2 WT plant; water control
- 10 6. *Rps2*-101C mutant plant; water control

Data were processed such that genes having a difference in mRNA levels that was greater than 2.5-fold increased or reduced, compared with controls were selected. The fold change for each gene was log-scaled and normalized.

1. Data analysis: identification of expression clusters

15 Data analysis was carried out by comparing expression of each gene in interactions 1-4 (Table 2), plotting that expression level, and identifying the genes of interest, i.e., those that show more than a 2.5X change in expression (about 1,600 genes). Classification of patterns, or expression clusters were as follows:

- a) Genes strongly induced (> 2.5X change in expression level) only in the resistant
20 (incompatible) response;
- b) Genes responding weakly only in the resistance response, but strongly induced in the compatible response;
- c) Genes that show a high level of expression in all outcomes;
- d) Genes that show a high level of repression in all outcomes;
- 25 e) Genes that show a very high level of repression only when the bacterial *avr* is expressed; and
- f) Genes that show a very different level of expression in the presence of the plant resistance compared to the level in the absence of the plant resistance (the mutant *rps2*).

30 Genes that fall within groups 1a and 1b, i.e., those that are differentially expressed only when an incompatible interaction occurs, include genes directly involved in resistance to pathogens. These genes show a peak (either up or down) only during plant-pathogen interaction 2. The differential expression can be of two types: upregulated (increased expression of this gene is potentially important in the incompatible interaction) or

downregulated (decreased expression of this gene is potentially important in the incompatible interaction).

2. Heat shock proteins and transcription factors

All major heat shock proteins (HSPs) were identified to be upregulated only during the incompatible interaction. Heat shock factors (HSFs) are transcription factors which control the transcription of the HSP genes. Eight HSF genes are known in *Arabidopsis*. HSF4 and HSF21 were identified as being upregulated when the plant was infected with *P. syringae*. HSF4 showed strong induction that was restricted to resistance, and HSF4 was the only HSF specifically upregulated during the incompatible interaction. The data suggests that the upregulation of HSPs is downstream of upregulation of HSF4.

To analyze whether the response was a more general one, or specific to a given ecotype, expression of HSF4 was analysed in two different *Arabidopsis* ecotypes, *A. thaliana*, ecotypes Col-0 and Ws. HSF4 was also upregulated in the response of Ws ecotype to infection and, specifically, was upregulated during an incompatible response. HSF21 is thus a preferred protein for resistance applications, and HSF4, a protein which is expressed in all plants, is especially preferred for engineering resistance.

A transgene containing the ACT2 promoter and the HSF4 open reading frame was introduced to *Arabidopsis* and transgenic HSF4 *Arabidopsis* lines generated to overexpress and underexpress HSF4. The expression of HSF4 during pathogen infection may cause lower general resistance to *P. syringae*.

Conditional overexpression lines were also generated using the estradiol-inducible promoter system. Infiltration of 20 :M estradiol into the intercellular space of the leaves of transgenic plants induced expression of HSF4 mRNA for a short time (down by 4 hours). Addition of 20 estradiol to the hydroponic medium yielded sustained HSF4 mRNA accumulation.

B. Genes Involved in *Arabidopsis* Responses to Pathogens

A number of mutations in *Arabidopsis thaliana* that disrupt expression of pathogen-induced genes and cause enhanced disease susceptibility have been identified. Pathogen-induced genes whose expression is altered in these enhanced disease susceptibility mutants are likely to play important roles in conferring disease resistance.

To identify such genes, wild type and various mutant plants were infected with strain *Psm* ES4326 at a dose of 10,000 colony forming units per square centimeter of leaf tissue. Control plants were mock-infected. After thirty hours, tissue samples were collected and used

to prepare RNA. Three sets of experiments were carried out. Each set of experiments included three independent replicate experiments. RNA from replicate experiments was pooled to reduce errors arising from the effects of variations in environmental conditions. Each RNA sample was used to prepare a fluorescently-labelled probe which was applied to an Affymetrix GeneChip™, allowing the expression level of each gene represented on the GeneChip™ to be determined for each sample. The plant genotypes included in each experiment were as follows:

Experiment #1

- 10 Wild-type (ecotype Columbia)
- nahG*
- pad4-1*
- eds5-1*
- eds4*
- 15 *pad2-1*
- npr1-1*
- npr1-3*

Experiment #2

- 20 Wild-type (ecotype Columbia)
- coil*
- ein2*
- pad1*
- FN1-3*
- 25 *eds3*
- eds8*

Experiment #3

- 30 Wild-type (ecotype Columbia)
- pad4-1*
- nahG*
- sid2*
- eds5-3*
- FN1-9*
- 35 *FN3-2*

1. Data analysis

- Expression values that were less than 5 were set to five. This ensures that no values are 0 or negative. Such values interfere with subsequent analysis steps. To obtain a list of pathogen-induced genes, the ratios of infected wild-type to mock infected wild type were calculated for each experiment. Then genes were selected in which expression levels were infected wild-type/mock wild-type > 2.5, and infected wild-type > 50 for at least 2 of 3

experiments. The ratio of 2.5 was chosen because the false positive rate for the GeneChip™ is essentially 0 at this level of stringency, and the absolute value of 50 was chosen to eliminate expression values below the detection limit of the GeneChip™. The result of this analysis was a list of 745 probe sets representing genes that are induced by infection in wild-type plants (note that some genes are represented by more than one probe set, so the number of different genes is somewhat fewer) (see Table 3 below). Hence, the expression of genes comprising SEQ ID NOs:2-6, 8-13, 16, 18, 22-23, 25, 28-29, 31-32, 35-37, 39-43, 45-47, 49-50, 52, 54-55, 57-58, 60-66, 70-72, 74, 76-77, 79, 81, 83, 85, 87-90, 92, 94, 97, 100-107, 111-115, 117-125, 127-135, 138-140, 142-153, 156-158, 160, 162-165, 168-170, 173-181, 183-184, 186-188, 190-198, 200-201, 203-211, 214-215, 218-224, 227-232, 234-249, 251-262, 264, 266-268, 270, 272-275, 277-281, 283, 286-294, 297-298, 302, 304-306, 308-326, 328-339, 341, 344-345, 347, 350-351, 353-358, 361-371, 373-377, 379-386, 388-390, 392, 394-400, 402-406, 408-410, 412-417, 419-427, 429-433, 435-443, 445-452, 454-457, 459-460, 462-464, 466-470, 473-475, 478-479, 481-482, 484-187, 489-494, 496-498, 500-501, 503-506, 508, 510, 512-515, 517-523, 526, 528-529, 531-538, 540, 544-548, 550-558, 560, 563-568, 570, 572-577, 579-580, 582-585, 588-594, 596, 598-600, 602-603, 605-606, 608-612, 614-617, 619-624, 626-630, 632-639, 642, 644, 646-651, 653-657, 659-665, 667-671, 673-678, 681-689, 691-693, 695-713, 715-717, 719, 721-727, 729-733, 736-738, 740, 742, 744, 746, 748-752, 755-756, 758-760, 762-769, 771, 774, 776-781, 783-788, 790-796, 798-799, 802, 804-808, 810-815, 817-831, 833-848, 850-855, 857-869, 871-880, 882-900, 903-907, 909, 911-915, 918-920, 922-925, 927, 929, 931-938, 940, 943-945, 947, and 950-953 is increased after infection of wild-type *Arabidopsis* with *Pseudomonas syringae*.

To identify pathogen-induced genes whose expression is affected by the mutations, genes for which the ratio of infected mutant/infected wild-type was < 0.5 or > 2 for at least one mutant were selected from the list of 745 pathogen-inducible probe sets. The limits of 5 and 2 were chosen because changes of at least 2-fold are likely to be significant for impact on disease resistance, and because the false positive rate for the GeneChip™ at 2-fold is 0.2%. This selection yielded a list of 530 probe sets corresponding to genes, the expression of which is induced by *Pseudomonas* infection in wild-type plants and perturbed in at least one mutant plant (see Tables 4a and 4b below). Thus, the expression of genes comprising SEQ ID NOs:2, 4-6, 11-13, 18, 22-23, 28, 31, 36, 39-43, 45, 47, 49-50, 52, 54-55, 57-58, 60-61, 63-66, 71-72, 74, 77, 81, 83, 85, 87-89, 92, 97, 100-107, 111-112, 114-115, 117-120, 122, 125, 127-128, 134, 138-140, 143-144, 148-151, 153, 156-157, 160, 165, 168-170, 173-174, 176-180, 183,

187-188, 191, 193-194, 197-198, 200, 203-210, 214, 219-224, 227, 230-232, 235-237, 239-240, 243-246, 248-249, 251-254, 256-258, 261, 264, 266-268, 270, 272-275, 277-278, 280, 283, 286-287, 290-293, 297, 302, 305-306, 308-310, 312-316, 321-326, 328-331, 333, 336-339, 341, 345, 351, 353, 355-358, 361-363, 365-366, 368-371, 373, 375, 377, 379-381, 384-385, 388-390, 392, 394-400, 402-406, 410, 412, 415-416, 419-420, 422-425, 429-433, 435-439, 441-443, 445-452, 454, 459-460, 463, 466, 468-470, 473, 481-482, 485-486, 489, 491-494, 497-498, 500-501, 503, 505-506, 508, 510, 513-515, 517, 520-521, 523, 528-529, 531, 533-538, 540, 545-548, 550-551, 553-554, 556-558, 560, 566-567, 575, 580, 582-584, 588-593, 596, 598-600, 602-603, 605-606, 608-610, 612, 614, 616, 620-622, 627-629, 633-634, 636-639, 644, 646, 648-651, 654-657, 659, 661-663, 667, 669, 673-674, 677, 682, 684-687, 689, 691-693, 697, 699, 701, 703-708, 713, 717, 719, 721-727, 730-733, 736, 740, 744, 746, 749-752, 755-756, 758-760, 762-764, 766-769, 774, 776-778, 780-781, 786, 788, 791-796, 799, 802, 804-808, 810-812, 815, 818-821, 823-825, 827-829, 831, 833-836, 838-843, 845, 847-848, 852-853, 855, 858, 860-869, 871-874, 876, 878-880, 884-887, 889, 892-894, 896-900, 904-907, 911-915, 918-920, 922-924, 931, 933, 938, 943-945, 947, and 950-952 is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis*, with *Pseudomonas syringae*.

2. Data interpretation

Genes that encode regulatory proteins such as transcription factors, protein kinases, calcium binding proteins and the like, are likely to play important roles in disease resistance, as they are likely to affect the expression of multiple defense effector genes. The list of 530 probe sets include 81 that correspond to genes encoding regulatory factors. These are likely to be useful for engineering plants to respond more quickly to pathogen attack by activating expression of defense responses (see Table 5 below). Thus, the expression of genes comprising SEQ ID NOs:39, 52, 60, 63, 81, 83, 106, 107, 115, 117, 118, 168, 174, 176, 179, 204, 207, 208, 220, 221, 248, 258, 268, 275, 280, 309, 323, 326, 329, 351, 419, 422, 429, 430, 432, 459, 460, 468, 469, 473, 500, 505, 506, 508, 529, 531, 533, 535, 538, 545, 553, 602, 606, 608, 610, 614, 616, 634, 654, 655, 684, 686, 687, 691, 717, 751, 752, 766, 777, 815, 831, 834, 835, 839, 841, 847, 876, 884, 906, 920, and 924 is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis*, with *Pseudomonas syringae*.

The mutations *nahG*, *pad4-1*, *eds5-1*, *eds4*, *pad2-1*, *npr1-1*, *npr1-3*, *pad1*, *FN1-3*, *eds3*, *eds8*, *sid2*, *eds5-3*, *FN1-3* and *FN3-2* cause enhanced susceptibility to *Pseudomonas syringae*. Consequently, pathogen-inducible genes whose expression is reduced by one of these

mutations are likely to be important for resistance to *Pseudomonas syringae* and possibly other bacterial pathogens. These 333 probe sets are shown in Table 6 (below). Therefore, the expression of genes comprising SEQ ID NOs:12-13, 18, 23, 36, 39-40, 43, 45, 50, 52, 57-58, 60-61, 64, 71-72, 81, 87-89, 97, 100, 102-105, 107, 111-112, 115, 119-120, 122, 125, 127-128, 140, 144, 148-150, 153, 165, 168-169, 176-177, 179, 183, 188, 191, 193-194, 197-198, 203-206, 208-209, 214, 219-222, 227, 230, 232, 237, 244-246, 248-249, 251-253, 258, 261, 264, 266, 268, 273-275, 283, 287, 290, 293, 297, 302, 305-306, 308, 312-315, 321-322, 324, 326, 330, 333, 338, 341, 345, 353, 356-358, 362-363, 366, 369, 371, 375, 377, 380, 384-385, 389, 392, 394-395, 398-399, 402-404, 406, 410, 415, 419, 422, 425, 429-430, 433, 435-439, 443, 445-452, 454, 463, 466, 468-470, 473, 486, 489, 491-492, 494, 498, 500-501, 503, 508, 513-514, 517, 529, 533-538, 548, 550, 553-554, 4556-558, 566, 575, 580, 582-583, 590-591, 593, 600, 602, 609-610, 612, 614, 620-622, 627-629, 637-638, 644, 649, 654-657, 659, 663, 667, 669, 673-674, 677, 684-685, 689, 691-693, 699, 703-705, 708, 719, 721, 724-726, 730-732, 744, 746, 749-750, 752, 755-756, 758, 760, 762-764, 767, 769, 774, 780-781, 786, 788, 791-792, 794-796, 799, 804-808, 810-812, 815, 818-819, 823, 828-829, 833, 840-841, 843, 847, 852-853, 858, 860, 862-865, 867-868, 872-874, 876, 885-887, 889, 892-894, 896-900, 904-905, 907, 911-914, 918-920, 922-924, 931, 933, 938, 947, 950, and 952 is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis* having a mutation that results in enhanced susceptibility to *Pseudomonas* (*nahG*, *pad 4-1*, *eds 5-1*, *eds4*, *pad2-1*, *np4 1-1*, *npr 1-3*, *pad1*, *FN1-3*, *eds3*, *eds8*, *sid2*, *eds5-3*, *FN1-3* and *FN3-2*).

The mutations *coil* and *ein2* block jasmonate and ethylene signaling, respectively. Jasmonate and ethylene-dependent disease resistance responses are known to be important for resistance to the fungal pathogens *Alternaria brassicicola* and *Botrytis cinerea*, and may also be important for resistance to other necrotrophic fungal pathogens. *Alternaria* and *Botrytis* are distantly related, yet plant resistance to these fungi is controlled similarly, suggesting that jasmonate- and ethylene-dependent responses function to limit growth of a wide range of fungal pathogens. Consequently, pathogen-induced genes whose expression is reduced in *coil* and *ein2* mutants are likely to be important for resistance to these necrotrophic fungal pathogens. These 296 probe sets are shown in Table 7 (see below). Hence, the expression of genes comprising SEQ ID NOs:2, 4, 6, 11-13, 18, 22-23, 31, 41-43, 49-50, 54, 57-58, 61, 64-66, 71-72, 74, 77, 85, 87, 89, 92, 97, 101, 103, 106-107, 112, 114, 117-119, 125, 128, 134, 138, 143, 149, 151, 156-157, 165, 169-170, 174, 176-180, 187-188, 191, 193, 206, 208, 219-

220, 222, 224, 231, 236, 239, 243-245, 251-254, 256-257, 267, 272, 287, 290, 292, 297, 302, 312-313, 315-316, 321-322, 324-325, 328, 330, 345, 351, 353, 355-357, 362-363, 366, 368-371, 373, 375, 379, 381, 384, 388-390, 392, 395-400, 405, 410, 415-416, 419, 422, 424, 431-432, 435-436, 438-439, 447, 459-460, 470, 473, 481-482, 489, 491, 493-494, 500-501, 505-506, 513-514, 517, 520-521, 523, 528-529, 531, 535, 537-538, 540, 545-548, 551, 553-554, 557-558, 566, 575, 580, 582, 584, 589, 591, 593, 596, 598-599, 603, 605, 608-609, 612, 628, 633-634, 636-637, 639, 646, 648, 650-651, 656, 661, 663, 667, 674, 685-687, 689, 691, 693, 697, 699, 701, 705, 707, 713, 723-724, 726, 736, 740, 749, 751-752, 756, 758-759, 764, 766-768, 774, 776, 778, 780, 792-796, 799, 802, 806, 810-812, 818, 820-821, 825, 827-829, 833-836, 838-839, 841-843, 848, 855, 860-861, 866, 868-869, 871, 873-874, 876, 878-880, 889, 892, 898-900, 904-905, 907, 915, 918, 922, 924, 933, 943-945, 947, and 951 is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis* having a mutation in a gene whose expression is important for resistance to necrotrophic fungi (a mutation that blocks or interferes with jasmonate and ethylene signaling such as *col1* and *ein2*). Accordingly, these genes are useful to improve the resistance of plants to fungal infection.

The mutations *nahG*, *pad4-1*, *sid2*, *eds5-1*, *eds5-3*, and *eds4* are known to interfere with salicylic acid dependent signaling. Such signaling is known to be important for resistance to the bacterial pathogen *Pseudomonas syringae*, the oomycete pathogen *Peronospora parasitica*, the viral pathogen tobacco mosaic virus, as well as various other plant pathogens. Consequently, pathogen-induced genes whose expression is reduced by one of the mutations that block salicylate signaling are likely to be important for disease resistance, and useful for engineering improved disease resistance. These 288 probesets are shown in Table 8 (see below). Therefore, the expression of genes comprising SEQ ID NOs: 12-13, 18, 23, 36, 39-40, 43, 45, 50, 52, 57-58, 60-61, 64, 71-72, 81, 87-88, 100, 102-105, 107, 111-112, 115, 119-120, 122, 125, 127-128, 140, 148-150, 153, 168-169, 176-177, 188, 191, 193-194, 197-198, 203-206, 209, 219-222, 227, 232, 237, 244-246, 248-249, 251-253, 258, 261, 264, 266, 268, 273-275, 283, 287, 290, 293, 297, 302, 305-306, 308, 312-315, 324, 326, 330, 333, 341, 345, 353, 356, 358, 366, 371, 375, 377, 380, 385, 389, 392, 394, 398, 402-404, 406, 410, 415, 419, 425, 429-430, 433, 435-438, 443, 445-447, 449-452, 454, 463, 466, 468-470, 473, 486, 489, 492, 494, 498, 500-501, 503, 508, 513-514, 517, 533-538, 548, 550, 553-554, 57-558, 566, 575, 582-583, 590-591, 593, 600, 602, 609-610, 612, 620-622, 627-629, 637-638, 644, 649, 654-657, 659, 667, 669, 673, 677, 684, 689, 692-693, 703-705, 719, 721, 724-726, 730-732, 744,

746, 749-750, 752, 755-756, 760, 762-764, 767, 769, 774, 780-781, 786, 788, 791-792, 795-796, 805-808, 810-812, 815, 818-819, 823, 828, 833, 840-841, 843, 852-853, 858, 860, 862-865, 867-868, 872-874, 876, 887, 889, 893-894, 896-898, 900, 905, 907, 911-914, 918-920, 922-923, 931, 933, 938, 947, 950, and 952 which is increased after infection of wild-type *Arabidopsis* and altered after infection of at least one mutant *Arabidopsis* having a mutation in a gene that interferes with salicylic acid dependent signaling (*nahG*, *pad4-1*, *sid2*, *eds5-1*, *eds5-3* and *eds4*). Thus, these genes are particularly useful to improve the resistance of plants to infection by more than one pathogen including bacteria, oomycetes and viruses, such as TMV.

10

Example 3

Further Analysis of the Pathogen Response and Comparison of the Response in Different Ecotypes

Materials and Methods

15 *Arabidopsis* ecotypes (or accessions) (the wild-types of all the *Arabidopsis* ecotypes used here have wild-type alleles of *RPS2* and *RPM1*).

Col, Columbia-0

Ler, Landsberg *erecta*

Ws, Wassilewskija

20 *Arabidopsis* mutants and transgenics

Col *rps2-101C*, a loss-of-function mutant of the resistance gene *RPS2* in Col background.

NahG, transgene for salicylic acid hydroxylase (inactivating salicylic acid). Col background.

25 *ndr1-1*, null mutant allele of *NDRI* (non-race specific disease resistance).

The mutation strongly affects *RPS2*-mediated resistance and partially affects *RPM1*-mediated resistance. Col background.

Bacterial strains

30 Pst, *Pseudomonas syringae* pv. *tomato* DC3000 (virulent strain of *Arabidopsis*)

Psm, *P. syringae* pv. *maculicola* ES4326 (another virulent strain of *Arabidopsis*)

Psp, *P. syringae* pv. *phaseolicola* NPS3121 (very weak pathogen of

Arabidopsis)Avirulence (*avr*) genes of *P. syringae*

avrRpt2: corresponding to the *Arabidopsis* resistance (*R*) gene *RPS2*

avrB: corresponding to the *Arabidopsis* resistance (*R*) gene *RPM1*

5 Experimental ProtocolsA. Gene for gene resistance (6 hours after treatment)

	<u>plant</u>	<u>treatment</u>
	Col WT	H ₂ O
	Col WT	Pst
10	Col WT	Pst/ <i>avrRpt2</i>
	Col <i>rps2-101C</i>	H ₂ O
	Col <i>rps2-101C</i>	Pst
	Col <i>rps2-101C</i>	Pst/ <i>avrRpt2</i>
	Ws WT	H ₂ O
15	Ws WT	Pst
	Ws WT	Pst/ <i>avrRpt2</i>

B. Differences in the response to bacterial pathogens among ecotypes (3, 6, and 9 hours after treatment)

	<u>Plant</u>	<u>treatment</u>
20	Col	H ₂ O
	Col	Pst
	Col	Pst/ <i>avrRpt2</i>
	Ler	H ₂ O
	Ler	Pst
25	Ler	Pst/ <i>avrRpt2</i>
	Ws	H ₂ O
	Ws	Pst
	Ws	Pst/ <i>avrRpt2</i>

Note that overall results for Cvi were very similar to Ler.

30 C. Genetic factors that affect the plant response to incompatible interactions (3, 6, and 9 hours after treatment)

<u>plant</u>	<u>treatment</u>
Col	H ₂ O

	Col	Pst
	Col	Pst/avrRpt2
	Col	Pst/avrB
	Col	Psm
5	Col	Psm/avrRpt2
	Col	Psp (not 9 hours)
	Col	Psp/avrRpt2 (not 9 hours)
	Col NahG	Pst
	Col NahG	Pst/avrRpt2
10	Col NahG	Pst/avrB
	Col ndr1-1	Pst
	Col ndr1-1	Pst/avrRpt2
	Col ndr1-1	Pst/avrB

Results

15 Four hundred sixty-five genes were specifically/preferentially induced in the incompatible interaction (WT and Pst/avrRpt2), and 616 genes were specifically/preferentially repressed in the incompatible interaction. Examples of these genes are provided in Tables 10 and 13. Gene expression patterns in the incompatible interaction in Col and Ws were significantly different, indicating that the genetic diversity among ecotypes can affect gene

20 regulation during the incompatible interaction significantly. In comparison, a relatively small number of genes (314 genes for induction, 167 genes for repression) were affected at this time point during the compatible interactions (but not preferential to the incompatible interactions). A comparison of the results in three genetically different compatible interactions (WT and Pst, rps2 and Pst, rps2 and avrRpt2) revealed that 25 genes were repressed in an avrRpt2-dependent

25 manner (see Table 9). Thus, the expression of genes comprising SEQ ID NOs:1, 15, 19, 20, 24, 26, 27, 34, 38, 51, 56, 59, 67-69, 99, 116, 155, 159, 182, 212, 284, 372, 444, and 789 is downregulated (repressed) in an avrRpt2-dependent manner in *Arabidopsis*. These genes are good candidates to be involved in avrRpt2 virulence functions (in rps2 plants).

Genes that were induced in *rps2* plants after infection irrespective of *avrRpt2* indicate a

30 function of RPS2 other than an interaction with avrRpt2. Thus, global gene expression profiling can identify large and minor trends in gene regulation and is useful in gene discovery.

One general phenomenon when plants are resistant to a pathogen is the early response of pathogen-responsive (induced or repressed) genes compared to plants that are susceptible to

infection. This has been proposed based on observing expression of a very limited number of genes, but it has not been proven as a global trend. To examine the results from early incompatible interactions and late compatible interactions, 4 week old Col-0 plants with well expanded leaves were infected with a high dose ($OD_{600} = 0.02$) or low dose ($OD_{600} = 0.002$) of *P. syringae* and samples collected at 6 or 30 hours, respectively. The two expression patterns were similar. The correlation values between the late compatible and incompatible interaction at either 6 hours, 9 hours or the average of 3-9 hour time points was 0.71, 0.72 and 0.75, respectively.

The majority of genes that did not respond within 9 hours after infection of a virulent strain but that responded in 30 hours (Pst or Psm, for *Pseudomonas syringae* pv. tomato DC3000 and *Pseudomonas syringae* pv. *maculicola* ES4326, respectively; the plant is susceptible to these strains) responded within 6 hours after infection of an avirulent strain (Pst/avrRpt2; Pst carrying the avirulence gene *avrRpt2*; the plant is resistant to this strain). This strongly suggests that early response of the pathogen-responsive genes is crucial for the plant to be resistant.

A comparison of the differences in the expression patterns of the 2 primary ecotypes of *Arabidopsis*' response to infection provides a further way to identify which genes have a more universal role (unchanged expression pattern) and which may be very specific to a particular plant ecotype involved in a very specific gene-for-gene interaction. For example, responses that are common between two ecotypes may be important for resistance. Genes that show the same pattern in both ecotypes may be part of more universal, or commonly-used, mechanisms involved in plant-pathogen interactions. Responses that are different may indicate that the two ecotypes use different combinations of responses to achieve resistance. This implies that a variety of genes can participate in plant-pathogen interactions. Nevertheless, ecotype-specific responses are expected to have counterparts in other plant species.

The differences in resistance response between ecotypes can be used for improving resistance in plants. In responses that are different between ecotypes, using the methods and compounds of the invention, such a response can be added to (induced or repressed) the response seen in the ecotype which does not normally use that response. This will likely give the plant a more robust or a wider range of resistance.

Table shows a comparison of gene expression in 4 ecotypes, i.e., Col-0, Ws-2, Cvi and Ler in response to infection. Table 10A shows the expression data for 9 probe sets corresponding to genes that are specifically induced at 3 hours after incompatible infection of

four different ecotypes of *Arabidopsis* with *P. syringae* pv. tomato DC3000. Table 10B shows expression data for 18 probe sets corresponding to genes that are induced by 6 hours but not at 3 hours after incompatible infection of four different ecotypes of *Arabidopsis* with three different bacterial strains, i.e., *P. syringae* pv. tomato DC3000. Table 10C illustrates the expression data for 6 probe sets corresponding to genes that are activated by *P. syringae* at 6 hours post-infection. Most of the genes are compatible interaction-specific or -preferential.

Four week old plants with fully expanded leaves were infected and samples collected at 3 or 6 hours post-infection ($OD_{600} = 0.02$). Some common patterns were observed. At 3 hours after infection of an avirulent strain, Pst/avrRpt2, the overall qualitative gene expression patterns were very similar for all the ecotypes tested. Common responses to Pst/avrRpt2 could be important for gene-for-gene resistance and so may be useful to identify targets for reverse genetics. Quantitative and qualitative differences in the response were noted, indicating that there are qualitative and/or quantitative differences in the signal transduction mechanisms that regulate the response among the ecotypes. Such signal transduction mechanism differences are attributed to genetic differences among the ecotypes.

In particular, early inducible genes (3 hours) in the incompatible interaction were identified (70 genes are common in all the ecotypes, and 360 genes if selected for induced in at least one ecotype). One group of the early genes (38 genes in Col) were repressed to the control level by 6 hours. These genes did not respond in the compatible interaction at 3 hours and were repressed below the control level in the compatible interaction by 6 hours. This suggests that shutting down these genes in the incompatible interaction by 6 hours could be caused by defense response inhibiting factor(s) delivered by bacteria. Another group of the early genes were expressed even higher at 6 hours in the incompatible interaction. One hundred eighty-eight genes showed significant induction or repression at 3 hours in the compatible interaction in at least one of the ecotypes. Of these, 3 induced genes and 3 repressed genes were induced or repressed in all three ecotypes.

At 3 hours in the incompatible interaction, a major difference among the ecotypes was quantitative; overall expression patterns were very similar, but overall fold change amplitudes were clearly in the order of Ws>Col>Ler. Thus, in this type of analysis it is not appropriate to analyze datasets by comparing the genes from different datasets that are selected by a certain cut-off value (e.g., 2.5-fold difference). This fold change difference was mainly caused by differences in the basal expression of these genes. In fact, a strong negative correlation in each gene was found between the relative basal expression level in Ws (relative to the other

ecotypes; Pearson correlation -0.78) and response in the incompatible interaction (especially at 3 hours) and a moderate positive correlation between the relative basal expression level in Ler and response in the incompatible interaction (Person correlation 0.38) (almost no correlation for the relative basal expression level in Col; Person correlation 0.10). These observations
5 indicate that Ws has the tightest regulation of these incompatible interaction-responsive genes, and Ler has the loosest. Another interesting observation is that the relative susceptibility to a virulent strain (Pst) was in the order of Ws>Col>Ler. Although it is unknown whether these two phenomena are controlled by same gene(s), it is conceivable that leaky expression of early response genes (in Ler) confers relative resistance to a virulent strain. At 6 hours in the
10 incompatible interaction, the gene expression pattern for Col was significantly different from the other ecotypes.

Moreover, different ecotypes may use a different but overlapping set of responses to achieve resistance against the same pathogen. Gene expression profiling can thus reveal ecotype differences. Therefore, it is possible to isolate the genes responsible for these
15 differences in regulatory mechanisms using ecotype differences in gene expression as a phenotype, by a map-based cloning approach.

For example, a majority of the incompatible response-inducible genes have lower basal levels in ecotype Ws and higher basal levels in ecotype Ler. Among the numerous genes, a few genes that display large differences in the basal level in two ecotypes are chosen. The
20 large differences in expression level constitute easy-to-score phenotypic markers. Ws and Ler are crossed to obtain F2 populations. The larger the F2 population is, the better resolution in the map position can be obtained. For each of the F2 plants, expression levels of the chosen phenotypic marker genes are measured and physical markers that distinguish these ecotype genomes are scored. The map position of the responsible gene is determined by analyzing the
25 linkage between the phenotype and the physical markers. If more than a single gene is responsible for the ecotype difference and each of the genes has a quantitative effect on the phenotype, quantitative trait locus (QTL) analysis can be used for mapping. Instead of using F2 populations, the use of recombinant inbred lines (RILs) between the ecotypes of interest may facilitate the analysis, especially using RILs that are already mapped for recombination
30 points. Once the gene(s) responsible for the phenotype is mapped, a combination of increasing the map resolution, sequencing the chromosomal region identified by mapping in both ecotypes, and gene transfer from one ecotype to the other leads to isolation of the gene.

If the phenotype of interest in gene expression depends on bacterial infection, such as expression of ecotype Col-specific inducible genes at 6 hours after infection of Pst/avrRpt2, expression of the corresponding phenotypic marker genes (e.g., genes that show good difference in induction between Col and Ler) can be measured at an appropriate time after
 5 bacterial infection.

Differences in gene expression patterns between two virulent strain backgrounds (Pst and Psm) are relatively small. Gene expression patterns for Pst/avrRpt2 and Pst/avrB were quite similar at 3 hours, but the difference increased at 6 hours. Psp (no avr) shows similar expression pattern to incompatible bacteria although the amplitude of fold difference was
 10 smaller in general. This suggests that Psp, which does not induce the HR in the plant, is still recognized by the plant and induce major part of the defense response seen during the incompatible interaction. It also suggests that plants monitor the effect of the defense response and that if it seems effective (bacteria do not grow like Psp), the plant does not go for a full-blown defense response.

15 Preferred Genes

Preferred early inducible genes were selected as induced > 2.5 fold (except for 2 fold for Psp at 6 hours) in all of the following datasets: Pst/avrRpt2 at 3 hours in Col, Ws, and Ler; Pst/avrRpt2 at 3 hours, Psm/avrRpt2 at 3 hours, Psp at 6 hours, and Pst/avrB at 3 hours, relative to the water control, as well as estradiol-inducible (avrRpm1 at 0, 45, and 120 minutes
 20 and avrRpt2 at 0, 45, and 120 minutes, where the fold change was relative to the appropriate resistance gene mutant carrying the same transgenes. Among these genes, the genes were ranked according to genes that are not induced by SA or BTH and not induced in late time points with Psm. Regulatory genes were given higher rankings (see Table 11). Hence, the expression of genes comprising SEQ ID NOs: 17, 70, 76, 81, 84, 109, 123, 144, 160, 230, 265,
 25 268, 269, 271, 323, 333, 385, 427, 428, 430, 457, 505, 569, 597, 602, 606, 616, 708, 730, 741, 812, 862, and 942 is induced early after infection of different *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121 (at 3 or 6 hours) or is estradiol inducible (at 45 or 120 minutes).

Preferred early repressible genes were selected as repressed > 2.5 fold (except for > 2
 30 fold for Psp at 6 hours) in all of the following datasets: Pst/avrRpt2 at 3 hours, Psm/avrRpt2 at 3 hours, Psp at 6 hours, and Pst/avrB at 3 hours) and Pst/avrRpt2 at 3 hours in Col (the fold change was relative to the appropriate water controls). Among them, the genes were ranked in order of expression (highest to lower levels of expression) (see Table 12). Thus, the

expression for genes comprising SEQ ID NOs:30, 73, 282, 541, 640, 679, 761, 870, 917, and 930 is repressed early after infection of *Arabidopsis* with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121.

Other genes are induced/repressed during incompatible interactions at 3 and/or 6 hours after inoculation of bacteria. Preferred genes in this group were selected as induced/repressed > 2.5 fold in the incompatible interaction compared to water inoculated control and 2 > fold compared to the corresponding compatible interaction at 3 and/or 6 hours after inoculation with Pst/avrRpt2 and Pst/avrB, and Psm/avrRpt2 and Pst/avrRpt2, in all four ecotypes (see Tables 13a and 13b). Hence, the expression of genes comprising SEQ ID NOs:21, 44, 46, 60, 86, 91, 93, 106, 110, 119, 122, 130, 131, 161, 166, 167, 168, 171, 176, 200, 203, 213, 225, 227, 248, 261, 262, 266, 274, 285, 300, 301, 302, 320, 326, 341, 345, 348, 349, 360, 366, 378, 615, 618, 406, 409, 422, 425, 441, 443, 446, 449, 454, 461, 475, 476, 485, 500, 511, 512, 527, 533, 543, 545, 549, 550, 552, 567, 575, 590, 608, 611, 625, 643, 656, 659, 666, 668, 671, 680, 690, 704, 706, 711, 721, 728, 738, 757, 791, 807, 811, 813, 827, 857, 864, 868, 875, 881, 893, 901, 905, 908, 912, 939, 941, 951, and 952 is induced in an incompatible interaction at 3 and/or 6 hours after infection of four *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121, while the expression of genes comprising SEQ ID NOs:7, 33, 82, 136, 141, 154, 185, 189, 199, 202, 434, 471, 483, 499, 516, 530, 578, 586, 631, 658, 694, 714, 718, 734, 770, 772, 816, and 916 is decreased in an incompatible interaction at 3 and/or 6 hours after infection of four *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121.

Garlic T-DNA insertion lines corresponding to these genes are searched by BLAST. Global expression profiling after infection with one of two different pathogens (*P. syringae* and *Alternaria brassicicola*) may be employed as a phenotyping method. Transgenic plants for overexpression, underexpression, and conditional overexpression of selected genes are also prepared.

Example 4

Promoters of Genes Responsive to Pathogen Infection

In many cases the major outcomes of plant-pathogen interactions are largely determined by how plants react in an early stage. Therefore, it is useful to isolate promoters

that rapidly react to pathogen attack for use in expressing proteins that provide tolerance or resistance to pathogen attack.

Genes were selected according to the conditions described below based on the results of a GeneChip™ analysis. These genes were particularly selected for a high level of induction in the *avrRpt2-RPS2* interaction and for a very low mRNA level in the absence of pathogen attack among four *Arabidopsis* ecotypes tested (Col, Ws, Ler, and Cvi). The genes were also analyzed to determine if their expression was similar in other combinations of incompatible interactions (three different bacterial strain backgrounds: *P. syringae* pv. tomato DC3000, *P. syringae* pv. *maculicola* ES4326, and *P. syringae* pv. *phaseolicola* NP3121; three different avirulence genes: *avrRpt2*, *avrB*, and *avrRpm1*; and direct expression of avirulence genes in plants using an estradiol-inducible system). For each gene, the 1.2-kb sequence upstream of the initiation codon is provided in SEQ ID NOs: 1047-1095.

Preferred Highly Inducible Promoters

Promoters were selected that had low basal expression level (i.e., uninduced level) in all the ecotypes (Col, Ler, Ws, and Cvi) and high inducibility in Col. Five such promoters of genes represented by the probe sets in Table 14 were identified: the promoters of germin precursor-like oxalate oxidase gene, extra-large G protein gene, PR-1, EREBP5 gene, and a C2H2-type zinc finger protein gene were chosen. The promoters for the germin-precursor like oxalate oxidase gene and PR-1 gene are relatively slow response promoters (no induction 3 hours after infection), but have high induction by 6 hours. The extralarge G protein gene is an intermediate in terms of response time, but maintains high expression over time. The other two are useful as early transient response promoters (good induction by 3 hours, but shut down by 6 hours) in the incompatible interaction (wild type plant infected with *Pst/avrRpt2*).

Promoter sequences comprising SEQ ID NOs: 1046-1095 and 1047-1055 correspond to genes comprising one of SEQ ID Nos: 17, 21, 80, 81, 109, 156, 174, 176, 221, 227, 296, 302, 303, 306, 333, 340, 360, 500, 505, 524, 575, 601, 602, 614, 628, 687, 733, 782, 811, 835, 862, 900, 905, 912, and 109, 306, 524, 600, 875, 912, 913, 941 and 942, respectively. Promoter-LUC reporter fusions are prepared and tested in a transient expression system using biolistic co-bombardment of *avrRpt2* gene.

Promoters Responsive to Particular Pathogens

Proteins that are useful for protecting plants from pathogen attack may have deleterious effects on plant growth if expressed constitutively. Consequently, it is desirable to have

promoter sequences that control gene expression in such a way that expression is absent or very low in the absence of pathogens, and high in the presence of pathogens.

Wild-type *Arabidopsis* plants (ecotype Columbia) were either mock-infected or infected with the bacterial pathogen *Pseudomonas syringae* pv. *maculiola* strain ES4326 (2 x 10⁴ cfu per square centimeter of leaf). After 30 hours, samples were collected, and RNA was purified. This procedure was repeated three times independently, and the RNAs from corresponding samples were pooled, in order to reduce the impact of variation due to uncontrolled variables. The two pools of RNA representing mock-infected and infected plants were then used for gene expression profiling using an *Arabidopsis* GeneChip®. This entire procedure was repeated three times, yielding three sets of GeneChip® data representing a total of nine independent experiments.

To identify promoter sequences that are likely to be useful for driving expression of transgenes in plants in response to pathogen attack, genes were selected whose expression level was less than 40 in all of the mock-infected samples and whose expression level was greater than 400 in all of the infected samples. The value of 40 was chosen arbitrarily as a low expression level and the value of 400 was chosen arbitrarily as a reasonably high expression level. Thirty-seven genes met these criteria and promoter sequences could be identified for 36 of them. Table 15 indicates the identifying probe set number for these 36 genes, the corresponding *Arabidopsis* gene, the mean expression level of each gene in mock-infected plants, the mean expression level of each gene in infected plants, and the fold induction in expression of each gene after infection. For 11 genes, expression in mock-infected plants was undetectable, so it was not possible to calculate fold induction. Therefore, the expression of genes comprising SEQ ID NOs:104-106, 119, 123, 129, 131, 151-152, 183, 191, 198, 200, 227, 249, 274, 302, 358, 415, 481, 547, 566, 582, 628, 633, 639, 656, 673, 793, 818, 827, 864, 874, 880, and 904-905 is induced in *Pseudomonas syringae* pv. *maculiola*-infected *Arabidopsis*.

It is possible that promoters that strongly activate gene expression in response to infection by a bacterial pathogen might be different from promoters that strongly activate gene expression in response to infection by a fungal pathogen. To test this possibility, a second GeneChip® experiment was conducted, in which wild-type *Arabidopsis* plants (ecotype Columbia) were mock-infected or infected with the fungus *Botrytis cinerea*. Samples were collected at 0, 12, 36, 60, and 84 hours after infection, RNA was purified and used for expression profiling using an *Arabidopsis* GeneChip®. To identify useful promoters, genes

were selected whose expression level was less than 40 in mock-infected samples from all time points and whose expression level was greater than 400 in infected plants at 84 hours after infection. Twenty-three genes met these criteria, and promoter sequences could be identified for 21 of them. These genes are described in Table 16, with their identifying probe set
5 number, the corresponding *Arabidopsis* gene, the mean expression level of each gene in mock-infected plants, and the expression level of each gene in infected plants at various times after infection. Among these 23 genes, 11 genes were previously identified in the search for genes whose expression was strongly induced by *Pseudomonas syringae* infection. These 11 genes correspond to identifying codes 12989, 13015, 13100, 13215, 13565, 14609, 16649, 16914,
10 19284, 19991, and 20356. Hence, the expression of genes comprising SEQ ID NOs:18, 71, 119, 123, 129, 151, 191, 244, 245, 302, 545, 547, 562, 566, 637, 653, 747, 756, 774, 793, 842, 864, and 905 is induced in *Botrytis cinerea*-infected *Arabidopsis*.

The promoter sequences for the 25 genes that were only identified in the *P. syringae* data set are shown in SEQ ID NOs:1001-1025. The promoter sequences for the 10 genes that
15 were only identified in the *B. cinerea* data set are listed in SEQ ID NOs:1026-1035) The promoter sequences of the 11 genes that were identified in both data sets are listed in SEQ ID NOs:1036-1046. The 11 promoter sequences that were identified in both data sets are most likely to be useful for driving expression of transgenes in response to attacks by various pathogens, as these promoters are activated in response to attack by either *Pseudomonas*
20 *syringae* or *Botrytis cinerea*, two very different pathogens. The other promoters may also be useful for driving expression of transgenes that are efficiently expressed in response to infection by certain types of pathogens.

Further, orthologs of the *Arabidopsis* promoters are also useful to drive expression of transgenes. To identify the orthologous promoter, a BLAST search for orthologous genes was
25 conducted. To identify the ortholog, the alignments from the BLAST search are used to determine the range of nucleotides showing homology to the *Arabidopsis* gene. The coding sequences shown at the beginning of each search result that contain regions corresponding to the nucleotides showing homology are likely orthologous genes. Orthologous promoter sequences may be isolated by any method known to the art, e.g., cloning of genomic DNA 5' to the ATG in orthologous genes identified in a computer assisted database search or
30 hybridization of a probe comprising any one of SEQ ID NOs:1001-1046 to genomic plant DNA.

Example 6

Genes the Expression of Which Are Altered by Viral Infection

To identify host genes that are commonly up or down regulated during local RNA or DNA virus infection, gene expression profiling was employed. The host genes may include host factors that are induced by viral infection, e.g., activated host defense genes, suppressed by viral infection, e.g., suppressed host defense genes, genes involved in symptom development, as well as genes regulated by virus inducible promoters. Once the genes are identified, the function of each is then determined. Reverse genetics is then employed to examine the effect of mutations on these genes during virus infection.

Experimental Procedure

Arabidopsis thaliana (Columbia-0 (Col-0)) were grown in a Conviron growth chamber to 4 weeks of age. The growth conditions were 22°C, 12 hour day length and 75% relative humidity. At least four rosette leaves of twenty plants were inoculated with one of five viruses or a mock control (120 plants total). The viruses were turnip vein clearing virus (TVCV), a tobamovirus, an oil seed rape mosaic virus (ORMV), a tobamovirus, tobacco rattle tobavirus (TRV), a tobavirus, cucumber mosaic virus strain Y (CMV-Y), a cucumovirus, and turnip mosaic virus (TuMV), a potyvirus. Each virus was diluted to approximately 0.5 to 1.0 µg/ml in 10 mM potassium phosphate buffer pH 7.2 (or 20 mM Tris-HCl pH 8.0 for the TuMV). The phosphate buffer was used as the mock infection control for the experiments. Inoculated Col-0 leaves were first dusted with carborundum then 10 µl of virus solution or phosphate buffer were pipetted onto the leaf surface. The virus solution or phosphate buffer alone were then rubbed into the leaf surface using a gloved finger, and the leaf surfaces were washed with distilled water at about 10 minutes post inoculation.

Inoculated leaf tissue was removed from each plant at 1, 2, 4 and 5 days post inoculation (dpi), weighed, snap frozen in liquid nitrogen and stored at -80°C. Total RNA was extracted from leaf tissue by the *RNAwiz* method (Ambion, Inc.) and further purified using the *RNeasy* method (Qiagen, Inc.). RNA was diluted to 1 µg/ml and labeled as a probe for Affymetrix GeneChip hybridization according to Affymetrix protocol for synthesizing labeled copy RNA (cRNA) (see Example 1). Labeled cRNA for each virus or mock treatment was hybridized to an Affymetrix GeneChip containing sequences corresponding to 8775 *Arabidopsis* genes. The hybridization data was then analyzed using Affymetrix GeneChip software.

Arabidopsis genes that were induced by at least 2-fold in all virus treatments were identified by importing the data into Microsoft Excel and then subjecting the data to selection criteria. Within each time point, the expression level of a gene exceeded 25 and the fold change was greater than 2 by comparison with the mock-infected treatment. Thus, for genes that were induced by all five viruses, the expression level exceeded 25 and the fold change was greater than 2 for all five viruses. For genes that were repressed by at least 2-fold, the expression level of the gene must exceed 25 in the mock-infected treatment and the fold change must be less than 2 in all of the five virus treatments.

Results

A gene chip from Affymetrix having oligonucleotides corresponding to approximately 8,100 *Arabidopsis* genes was used with labeled cRNA obtained from plant cells infected with a selected viruses at different days post-infection (dpi). For example, for *Arabidopsis*, the RNA may be obtained from *Arabidopsis* infected with potyvirus, tobamovirus, tobnavirus, cucumovirus or geminivirus. After hybridization, laser scanning is employed to detect expression levels and the data obtained is then analyzed. For genes that are induced in response to viral infection, genes that are expressed at levels greater than, for example, 2 fold over control, are selected. Alternatively, for genes that are suppressed in response to viral infection, genes that are expressed at levels lower than control are selected. The advantages of a gene chip in such an analysis include a global gene expression analysis, quantitative results, a highly reproducible system, and a higher sensitivity than Northern blot analyses. Moreover, a gene chip with *Arabidopsis* DNA has a further advantage in that the *Arabidopsis* genome is well characterized.

Data obtained from probe sets which correspond to genes upregulated or downregulated in response to infection by all 5 viruses revealed forty-six genes that were downregulated and 126 that were upregulated in response to viral infection (Tables 17 and 18). Once the induced and/or suppressed genes are identified, the functions of the genes are then characterized by standard methodology.

Therefore, the expression of genes comprising SEQ ID NOs:14, 48, 53, 98, 217, 226, 295, 327, 343, 352, 369, 404, 407, 418, 453, 458, 465, 472, 480, 488, 495, 507, 509, 513, 514, 559, 561, 581, 604, 607, 613, 641, 652, 672, 720, 735, 739, 743, 745, 754, 773, 803, 832, 849, 948, and 949 is downregulated after viral infection, and the expression of genes comprising SEQ ID NOs:3, 51, 54, 60, 61, 66, 75, 76, 78, 88, 95, 96, 101, 106, 108, 123, 126, 128, 129, 131, 137, 145-147, 150, 158, 169, 170, 172, 173, 197, 200, 216, 219, 224, 230, 233, 237, 249,

250, 263, 274, 275, 276, 299, 307, 323, 333, 342, 346, 359, 382, 383, 387, 391, 393, 401, 411, 415, 427, 442, 455, 459, 466, 477, 481, 485, 487, 502, 511, 515, 525, 534, 539, 542, 560, 571, 577, 579, 584, 587, 595, 600, 627, 638, 645, 654, 659, 668, 681, 688, 695, 696, 706, 708, 730, 742, 753, 775, 785, 786, 792, 797, 800, 801, 809, 817, 819, 820, 823, 827, 847, 856, 875, 885, 896, 902, 910, 921, 922, 923, 925, 926, 928, 946, and 952 is upregulated after viral infection.

Rice and other plant orthologs of these *Arabidopsis* sequences were identified as described in Example 14 below. The results are summarized in Tables 22 and 23.

A correlation of the SEQ ID NOs:1-953 and the probe set designations corresponding to genes, the expression of which is altered after infection of *Arabidopsis* with a pathogen is shown in Table 19.

Example 7

Identification of Gene Products that are Modulated upon Infection of a *Chenopodium* Cell with a Virus

Of the many disease resistance mechanisms that can be studied, the HR (hypersensitive resistance) system of *Chenopodium* spp. is attractive because of the broad-spectrum virus resistance it confers. This is shown by the ability of members of the bromo-, como-, cucumo-, ilar-, alfamo-, nepo-, sobemo-, tombus-, tymo-, carla-, clostero-, hordei-, potex-, poty-, tobra- and tobamovirus groups to elicit local lesion HR on *Chenopodium* spp. (CMI/AAB Description of Plant Viruses, 1984; Cooper et al., (1995)). In many instances, the HR completely blocks viral spread. However, certain viruses can break through the hypersensitive response and move from one species of *Chenopodium* to another. The ability of some viruses to infect more than one species of *Chenopodium* provides an opportunity to isolate genes that provide a cell with resistance to viral infection.

The genetic mechanisms of *Chenopodium* spp. HR involve a number of factors. These factors can be studied to further understand the hypersensitive response and the mechanism through which the response acts. There are some similarities between the products of *Chenopodium* spp. genes and gene products involved in common defense signaling pathways in other plants. These similarities allow comparisons to be made between *Chenopodium* and these other plants. One example includes genes that are induced upon viral infection during HR in *C. foetidum* (Visedo et al., (1990)).

Additionally, some circumstantial experimental evidence suggests that *Chenopodium* HR may be somewhat similar to tobacco *N* gene HR (Whitham et al., 1994). Movement defective tobacco mosaic tobamovirus (TMV) replicates within an inoculated cell of a tobacco plant with an *N* gene, but fails to move from cell to cell (Cooper et al., 1996). Hypersensitivity is not induced, thus replication alone is not sufficient to induce HR despite the *N* gene elicitor being mapped to the replicase gene of TMV (Padgett and Beachy, 1993). Therefore, the process of virus movement may trigger hypersensitivity, which implicates intercellular signaling in this type of HR. Support for this position comes from experiments in which cell-to-cell contacts were disrupted in *N* gene tobacco which resulted in the prevention of necrotic lesion formation in infected leaves (Gulyas and Farkas, 1978). Likewise, TMV will not induce HR cell death in NN tobacco protoplasts where plasmodesmata are not intact (Otsuki et al., 1972), although HR does occur in callus cultures where plasmodesmata are intact (Beachy and Murakishi, 1971). By comparison in *C. quinoa*, movement defective brome mosaic bromovirus (BMV) replicates but fails to move from cell to cell. Initial infection is not sufficient to induce HR since local lesions do not form (Schmitz and Rao, 1996). Similarly, in *C. amaranticolor*, cucumber mosaic cucumovirus (CMV) lacking a movement protein replicates within inoculated cells, fails to move and does not elicit cell death (Canto and Palukaitis, 1999). Therefore, like TMV on *N* gene tobacco, the process of viral spread of BMV and CMV in *C. quinoa* and *C. amaranticolor* may induce HR.

20 Methods and Materials

Inoculation of Plants

Leaves of 10-week old *C. amaranticolor* or *C. quinoa* were inoculated with *in vitro* transcripts of TMV-MGfus (Heinlein et al., 1995), TMV virions, tobacco rattle tobravirus (TRV), or they were mock-inoculated. TMV-MGfus encodes GFP (green fluorescent protein) fused to the viral movement protein. Infectious spread can be monitored through the detection of GFP. Using an Olympus stereomicroscope fitted with a U-ULH Olympus lamp, infected *C. amaranticolor* tissue accumulating GFP was excised at 4, 7 and 11 days after inoculation (dai). Leaves inoculated with TRV or TMV were collected at 4 dai, at which point local lesions were forming. Mock-inoculated tissue was collected at the same time. Tissue was frozen in liquid nitrogen and total RNA was purified from it. Three separate sets of plants were inoculated with TMV-MGfus and yielded three independent preparations of RNA.

30 cDNA-AFLP (complementary DNA-amplified fragment length polymorphism)

Poly-A+ RNA was isolated from TMV-MGfus infected *C. amaranticolor* using Qiagen's Oligotex mRNA purification system (Qiagen, Valencia, CA) and cDNA was generated using cDNA synthesis reagents from Life Technologies (Rockville, MD). cDNA was used to generate AFLP fragments with the AFLP reagents from Life Technologies and reactions were performed according to the manufacturer's instructions. cDNA made from one microgram of poly-A+ RNA was digested with EcoRI and MseI and the supplied compatible linkers were ligated to the ends of the digested molecules. A few modifications were introduced. EcoRI-NN primers (GACTGCGTACCAATTCNN; SEQ ID NO:2134), rather than EcoRI-NNN, were used with the 5' fluorescent label NED (Applied Biosystems, Foster City, CA) and MseI-N and MseI-NN [GATGAGTCCTGAGTAAN(N); SEQ ID NO:2135], rather than MseI-NNN, primers were used (Genosys, The Woodlands, TX), to reduce the complexity of the primer sets evaluated. All possible primer combinations (256 + 64) were used for PCR amplification and products were separated on polyacrylamide gels and visualized using a Genomix SC fluorescent scanner (Beckman Coulter, Fullerton, CA). Gene fragments that appeared to be upregulated in infected tissues compared to mock-inoculated tissues were tested to see if they were also upregulated by the same primers from a second preparation of cDNA from RNA from a second set of infected plants. Gene fragments that were upregulated in both RNA preparations were excised from the gel, eluted from the gel in water and reamplified by PCR using the appropriate MseI and EcoRI primers and sequenced with 377 ABI sequencers (Applied Biosystems) using dideoxysequencing methods.

Quantitative RT-PCR

DNase treated total RNA (2 ng per reaction) from the third independent preparation of TMV-MGfus infected *C. amaranticolor*, the first preparation of TRV infected *C. amaranticolor*, or the first preparation of TMV *C. quinoa*, was used with TaqMan One-Step RT-PCR reagents for quantitative analysis in an ABI 7700 (Applied Biosystems). Reactions were performed according to the manufacturer's instructions. Primers and 6-FAM 5' end-labeled probes (6-carboxyfluorescein, Applied Biosystems or Genosys) were designed from the sequences from the *C. amaranticolor* upregulated gene fragments using Primer Express software (Applied Biosystems) and are listed in SEQ ID Nos:954-1000 and 2130-2135. Expression levels were interpolated from standard curves with a correlation coefficient of 0.99 or greater and the quantities were normalized to the expression level of actin in each sample.

Results

The interaction of the elicitor and the R gene product establishes a cascade of reactions and signaling events that is then manifested in a phenotypic HR. In essence, HR is the end result of disease activated signaling events. In order to detect the early expression of genes induced by viral infection, it was necessary to isolate infected tissue before the onset of local lesion formation. Therefore, *C. amaranticolor* was infected with RNA transcripts of TMV-MGfus that express GFP (green fluorescent protein) in infected cells. This allowed the spread of viral infection to be monitored over time. Infection foci comprising over 100 cells could be detected at 4 dai and foci of more than 500 cells could be detected at 7 dai. There was no visible appearances of cell death or chlorotic local lesion formation at the infection foci at 4 and 7 dai. By 11 dai, the infection foci were associated with chlorotic local lesions. Virus infected tissue was excised from leaves at each time point and RNA was purified from the tissue and used for cDNA-AFLP as previously described.

cDNA-AFLP fragments were separated on polyacrylamide sequencing gels and imaged with a fluorescent scanner. Samples derived from mock-inoculated tissue at 7 dai were run next to samples derived from TMV-MGfus infected tissue at 7 dai for comparison. Ninety-eight bands having intensity in the TMV-MGfus lanes that was greater than that of analogous bands in the mock lanes were easily detected. Thirty out of the 98 bands were also upregulated in an independent set of experiments designed to reduce biological variation between experiments. These bands were excised from the gel, reamplified, and sequenced.

The hypothetical protein sequences derived from the reamplified fragments (SEQ ID NOs:1954-1966) translated from all six reading frames were compared to sequences in the GenBank protein sequence database. The results of the BLASTX search (Altschul et al., 1997) are summarized in Table 20a. The results of a BLAST search similar to the one described for Arabidopsis ORFs in Example 6 above is summarized in Table 24. To confirm that the expression levels of DESCA genes were upregulated in infected tissue compared to mock inoculated tissue, the relative amount of DESCA and actin transcript in a third independent set of samples at 4 dai, 7dai, and 11 dai was quantitatively measured (Table 20b).

The expression level of DESCA1 increased the most in the TMV-MGfus infected plants. The expression level of DESCA1 increased 200 times by 4 dai but tapered off drastically by 11 dai. DESCA1 is unrelated to any protein known at this time.

Two sequences, DESCA4 and DESCA10, are both related to pumps found in *Arabidopsis* and yeast (Sanchez-Fernandez et al., 1998; Smart and Fleming, 1996). DESCA4

is expressed highly at 4 dai but the expression drops off over time whereas DESCA10 is only moderately induced and its expression returns to normal by the time of the visible appearance of local lesions in *C. amaranticolor*.

DESCA7 is similar to a salicylate-induced glucosyltransferase gene in tobacco
5 (Horvath and Chua, 1996). DESCA9 is similar to cytochrome P450-like proteins which can produce cytotoxic compounds including phytoalexins that are deployed by a plant to defend against invading microbes. DESCA12 is related to a proanthranilate benzoyltransferase from carnation that plays a direct role in the phytoalexin biosynthesis in carnation (Yang et al., 1998). DESCA11 is similar to the tryptophan biosynthetic enzyme phosphoribosylanthranilate
10 transferase whose gene expression is induced in the presence of ozone in *Arabidopsis* (Conklin and Last, 1995).

DESCA3 is similar to endo-1,4-beta-glucanases that have a role in fruit ripening, abscission, and cell elongation (Lashbrook et al., 1994). DESCA3 is highly expressed in the infected *C. amaranticolor* and remains highly expressed during the appearance of local lesions
15 and necrosis.

Many disease responses are mediated by positive regulators such as transcription factors or kinases that initiate signaling cascades for the activation of defense responses. One gene, DESCA5, is loosely similar to a yeast potential transcriptional regulator. DESCA5 expression is twice as high at the early stages of infection compared to the late stages of
20 infection illustrating an important role played by gene regulation at the early stages of infection. DESCA6 is related to kinases of *Arabidopsis*. Kinases have essential roles in programmed cell death during viral infection (Dunigan and Madlener, 1995). DESCA2 is the most highly expressed of the group suggesting that it is an important regulator at the onset of infection. It is similar to a receptor-like protein kinase in bean that responds to *Fusarium*
25 *solani* attack (Lange et al., 1999).

Some R genes have kinase-like regions that may function in initiating a signal cascade during the onset of HR (Song et al.; 1995, Zhou et al., 1997). Global amino acid sequence alignment (Henikoff and Henikoff, 1992) of DESCA2 with Pto or Xa21, R genes with ser/thr kinase domains, reveals a 37% similarity. DESCA8 has a nucleotide binding site and a
30 leucine-rich repeat that is common for many R genes. (Meyers et al., 1999; Leister et al., 1998).

To link DESCA genes to a multivirus resistance pathway, *C. amaranticolor* was inoculated with TRV (tobacco rattle virus), a virus that is taxonomically distinct from TMV.

Local lesions appeared by 4 dai and RNA was purified from the infected leaves. DESCA gene expression levels in infected tissue were compared to mock inoculated tissue by quantitative RT-PCR and revealed that the same DESCA genes upregulated during a TMV infection are also upregulated during a TRV infection (Table 20b).

5 The gene expression levels in TMV infected *C. quinoa* were measured using the same *C. amaranticolor*-derived primers in quantitative PCR to determine if DESCA genes were up-regulated during HR in another *Chenopodium* species. Most of the DESCA genes were upregulated in *C. quinoa* and were expressed at levels many times higher than in *C. amaranticolor* (Table 3). This may be a result of the infection of *C. quinoa* with the
10 aggressive wild-type virus rather than slower moving TMV-MGfus.

 The experimental procedure presented here can detect any similar gene involved in the aforementioned signaling pathways such as SA signaling. Except for DESCA1, whose expression is increased the most at 200+ fold, many of the fragments have homology to other genes that have been placed in disease resistance pathways in other plants. DESCA12 and
15 DESCA9 are respectively similar to hypersensitivity related gene 201, possibly a proanthranilate benzoyltransferase, and p450 monooxygenases, both which are expressed during the hypersensitive response in tobacco upon infection with *Pseudomonas solanacearum* but are not regulated by SA (Czernic et al., 1996). DESCA7 is similar to a salicylate-induced glucosyltransferase gene in tobacco (Horvath and Chua, 1996). Thus, the disease resistance
20 response in *C. amaranticolor* involves pathways both dependent and independent of SA signaling.

 The surprising discovery of DESCA4, DESCA7, DESCA9, DESCA10, and DESCA12, reveal the underpinnings of an endogenous detoxification system. Briefly, the activation phase involves cytochrome P450 monooxygenases introducing functional groups
25 (e.g. aromatic rings) to potential toxins. The conjugation phase in plants involves the linking of glutathione or glucose to the toxin at which point the conjugated molecule can be recognized by an ATP-binding cassette transporter and pumped into the vacuole, or possibly the neighboring cells, during the elimination phase. The final phase includes either storage or breakdown of such molecules. DESCA9, similar to cytochrome P450, and DESCA12, similar
30 to a gene associated with the production of phytoalexin, may produce potential toxins. In fact, *C. amaranticolor* produces many such compounds that are antiviral to TMV. DESCA7, similar to a glucosyltransferase, may conjugate such toxins to be transported by the ABC-transporters encoded by DESCA4 or DESCA10. In this particular case, the transported

compound could then be deployed by the infected plant cell as an antiviral agent or cytotoxic compound, stored by noninfected cells in anticipation of infection, or eliminated by noninfected cells neighboring infected cells. Since all of these genes are induced by TMV and TRV in *C. amaranticolor*, their induced expressions are a result of a specific or general
5 multiviral or disease resistance pathway.

Possessing the R genes that allow *C. amaranticolor* to initially recognize multiple viruses provides an opportunity to use these genes, and the regulatory elements associated with these genes, to transfer viral resistance to other plants. In addition, possession of genes that produce and transport antiviral and cytotoxic products allows for the transfer of viral resistance
10 through a mechanism involving induced cell death upon viral infection.

Two genes that may be used for early recognition of viral infection are DESCA8 and DESCA2, as these genes may act as signaling components to initiate the resistance cascade. DESCA8 has a nucleotide binding site and a leucine-rich repeat that is common for many R genes and that can be found in other plants (Meyers et al., 1999; Leister et al., 1998).
15 DESCA2 is induced in both *Chenopodium* species and is similar to other R genes, Xa21 and Pto, which have similar ser/thr kinase domains.

Resistance to viral spread may be transferred between *Chenopodium* spp. For example, BMV (brome mosaic virus) induces local lesions in the green variety of *C. hybridum*, however lesion formation does not limit the systemic spread of the virus (Verduin, 1978). The
20 systematic spread of the BMV virus may be restricted in the green variety of *C. hybridum* by transformation with a gene from the purple variety that does limit spread (Komari, 1990). Thus, genes that confer viral resistance may be used for complementation, reverse genetics, overexpression, and gene silencing. Furthermore, as indicated by the functionality of the R genes N and Pto after being transferred into heterologous species, (Whitham et al., 1996;
25 Rommens et al., 1995), the *Chenopodium* genes may function to initiate hypersensitivity in crops, *Arabidopsis* or other useful plants.

Example 8

Other Plant-Pathogen Interactions

The methods set out hereinabove can be used for any type of comparable resistance interaction. For example any of the following plant/pathogen interactions will be produced as compatible and incompatible interactions. The RNA from such an interaction is isolated and subject to a protocol such as one outlined in Example 1, e.g., using a Genechip with a specific plant's genes or microarray, differential display PCR or cDNA-ALFP (Example 7). A four-way analysis is performed and genes which are expressed differently are identified. The plant/pathogen interactions in Table 21 are well known in the art. However, any type of plant/pathogen interaction that involves this type of resistance can be used.

Genes that are upregulated and cause resistance in a wide variety of plants are particularly useful in methods which upregulate or overexpress the gene. One method is to add an exogenous copy, thus providing more of the gene product or allowing for a different induction from that used by the plant. Alternatively, the endogenous gene can be upregulated using a known inducer or using artificial methods such as using an artificial induction signal in the endogenous promoter. Examples of the two methods are provided in Examples 9 and 10.

Accordingly, embodiments of the invention provide the sequences disclosed herein, which sequences can be used in genetic engineering of crops, as probes and markers to study the dynamics of plant/pathogen interactions, and as markers in marker-assisted breeding protocols to identify plants carrying particularly useful combinations of genes associated with pathogen resistance, as well as in plant defense.

Example 9

Transformation of Resistance Genes into Plants

To produce resistant plants, resistance genes such as those identified herein can be introduced into plant cells to generate transgenic plants having enhanced resistance. While HSF4 is any preferred gene for this embodiment of the invention, the invention can be employed with other genes, alone or in combination, whose regulation is strongly responsive to plant/pathogen interactions, such as the genes identified herein. Since some genes are strongly induced and others are strongly repressed in plant/pathogen interactions, and since some genes that are strongly induced in one ecotype can be strongly repressed in another, the invention contemplates use of any of the genes and sequences, or fragments thereof, disclosed

herein, in a construct adapted to cause overexpression, repression, or knock out, of the genes in a transgenic plant.

Transgenic downregulation of genes associated with pathogen resistance can have several useful applications. In one embodiment, transgenic downregulation of genes that are
5 strongly repressed in resistance interactions can enhance resistance. Such transgenic downregulation can employ the genes disclosed herein, or fragments thereof, in an antisense orientation to interfere with accumulation of the products of those genes. Likewise, any other methodology capable of lowering expression of such genes is also included within these embodiments of the invention.

10 Plant transformation can be carried out by conventional means, and can include *Agrobacterium*-mediated transformation, electroporation, particle acceleration, abrasion, and any other useful means leading to expression of a transgene in a plant of interest. Transformed plant cell are then used to regenerate one or more plants in tissue culture. Subsequent generations of transgenic plants can be used directly or bred with other lines to generate plants
15 having enhanced pathogen resistance.

Example 10

Upregulation of Resistance Genes in Crops

Because many or most *Arabidopsis* genes have orthologs in other plants, the genes and
20 sequences disclosed herein are generally useful in constructs to be up-regulated and cause resistance in a wide variety of plants. As examples, the heat shock proteins, and particularly HSF4, are found throughout the plant kingdom. For many such regulatory and responsive genes it is well known that there exist substances that can induce expression. Chemicals such as dexamethasone have been found to induce mammalian HSF proteins. Likewise, a chemical
25 induction of key plant defense genes can be chemically induced. High throughput screening for chemical inducers of the plant HSF4 or other resistance gene is performed. Potentially useful substances are then tested on crop plants and eventually used as a soil additive or sprayed onto plants when needed to induce resistance. Accordingly, embodiments of the invention usefully employ the genes disclosed herein, or fragments thereof, for screening to
30 identify useful chemical inducers and/or repressors of gene responsive to pathogenic infections.

Example 11

Identification of Inducers and Repressors of Resistance Genes

The yeast two-hybrid method and many methods which use its basic idea, provide a technique to identify proteins which interact with a protein of interest. The method relies on the fact that a protein contains domains which can be separated. Thus the protein of interest is fused to the GAL4 DNA binding region of a known protein. The GAL4 (or another) activation signal is fused in a library to produce a library of fused proteins. If one of the proteins from the library interacts with the protein of interest the protein binds and a signal protein is produced, such as luciferase. There are a number of such systems presently, some of which can be used in mammalian cells, allowing for correct processing and folding of certain proteins and others which allow the interaction to occur in the cytoplasm allowing for the identification of other types of proteins.

cDNA from HSF4 and any other protein of interest is cloned in fusion to the yeast GAL4 DNA binding domain on a vector. A library containing cDNA from Arabidopsis is fused to the GAL4 or an activation domain of choice. Expression of luciferase correlates with identification of an interacting protein. This protein is then analyzed as to its action as an inducer or repressor.

Example 12

Determination of the Minimal Promoter Fragment

A promoter sequence as given in SEQ ID Nos: 2137-2661 and 4738-6813, preferably a promoter sequence of one of the genes defined by SEQ ID NOs 536-579 such as SEQ ID Nos: 536; 537; 539-542; 548; 550-553; 555-558; 560; 565-568; 571-576, 578 and 579, or a promoter ortholog thereof is fused to the β -glucuronidase (GUS) gene at the native ATG to obtain a chimeric gene cloned into plasmid DNA. The plasmid DNA is then digested with restriction enzymes to release a fragment comprising the full-length promoter sequence and the GUS gene, which is then used to construct the binary vector. This binary vector is transformed into *Agrobacterium tumefaciens*, which is in turn used to transform *Arabidopsis* plants.

The above plasmid can also be used to form a series of 5' end deletion mutants having increasingly shorter promoter fragments fused to the GUS gene at the native ATG. Various restriction enzymes are used to digest the plasmid DNA to obtain the binary vectors with different lengths of promoter fragments. In particular, a binary vector 1 is

constructed with a 1,900-bp long promoter fragment; a binary vector 2 is constructed with a 1,300-bp long promoter fragment; a binary vector 3 is constructed with a 1000-bp long promoter fragment; a binary vector 4 is constructed with a 800-bp long promoter fragment; a binary vector 5 is constructed with a 700-bp long promoter fragment; a binary vector 6 is constructed with a 600-bp long promoter fragment; and a binary vector 7 is constructed with a 100-bp long promoter fragment. Like the binary vector comprising the full-length promoter fragment, these 5' end deletion mutants are also transformed into *Agrobacterium tumefaciens* and, in turn, *Arabidopsis* plants (for further details of *Arabidopsis* transformation and promoter assay procedures see example 5 above).

The presence of the correct hybrid construct in the transgenic lines is confirmed by PCR amplification.

By using the above protocol it can be determined, which portion of the promoter or the promoter orthologs thereof is required for gene expression.

Minimal promoter fragments having lengths substantially less than the full-length promoter can therefore be operatively linked to coding sequences to form smaller constructs than can be formed using the full-length promoter. As noted earlier, shorter DNA fragments are often more amenable to manipulation than longer fragments. The chimeric gene constructs thus formed can then be transformed into hosts such as crop plants to enable at-will regulation of coding sequences in the hosts.

Example 13

Determination of Promoter Motifs

While a deletion analysis characterizes regions in a promoter that are required overall for its regulation, linker-scanning mutagenesis allows for the identification of short defined motifs whose mutation alters the promoter activity. Accordingly, a set of linker-scanning mutant promoters fused to the coding sequence of the GUS reporter gene are constructed. Each of them contains a 8-10-bp mutation located between defined positions and included in a promoter fragment as given in SEQ ID Nos: 2137-2661 and 4738-6813, preferably a promoter sequence of one of the genes defined by SEQ ID NOs 536-579 such as SEQ ID Nos: 536; 537; 539-542; 548; 550-553; 555-558; 560; 565-568; 571-576, 578 and 579 or the promoter orthologs thereof.

Each construct is transformed into *Arabidopsis* and GUS activity is assayed for 19 to 30 independent transgenic lines. The presence of the correct hybrid construct in transgenic lines is confirmed by PCR amplification of all lines containing the mutant constructs and by random sampling of lines containing the other constructs. Amplified fragments are digested with restriction enzyme (e.g. XbaI) and separated on high resolution agarose gels to distinguish between the different mutant constructs. The effect of each mutation on promoter activity is compared to an equivalent number of transgenic lines containing the unmutated construct. Two repetitions resulting from independent plating of seeds are carried out in every case.

The sequences mutated in the linker-scanning constructs, in particular those that showed marked differences from the control construct, are then examined more closely.

Example 14

Identifying Orthologs

Orthologs were identified through use of BLAST and SCAN software with some additional filters. For the *Arabidopsis* search, a BLAST database was created that was a subset of GenBank ver 123.0 (released April 15, 2001) that contained all of the plant translated regions excluding *Arabidopsis thaliana* sequences. The subset was created with PERL script. A BLAST search with all of the peptide sequences was performed against the GenBank subset. Each query was executed using the "blastall" command with the parameters " -p blastp", "-v 50", "-b 50", "-F F". The BLAST search results were then processed with SCAN (Sequence Comparison Analysis program, version 1.0k, Los Alamos National Laboratories) using default settings and the orthologs were identified following implementation of an E-value cutoff of $\leq 1e-4$. The candidate orthologs were further filtered by comparing words in the description to the text of the annotation fields: product, function and note. The sequence was considered to have the same or similar function if any of the words matched. Words excluded from the filter included: the, like, protein, related, unknown, subunit, hypothetical, and, putative, precursor, clone, homolog, small, beta, class, dna, rna, alpha, gamma, has, not, been, from, to, by, long, type and induced.

For the rice search, amino acid sequences were used that resulted from FGENESH (version 1.C) gene prediction results. The peptide sequences were obtained from gene predictions and formatted into a BLAST database. A BLASTP comparison was then performed against the *Arabidopsis* sequences. The BLASTP results were then filtered through

use of SCAN with the following parameters: "-a 60 60" with an E-value cutoff of $1e-4$. This produced orthologs having 60 or more identities and where 60% of the alignments were made up of identities.

- 5 The following pages compile Tables 3 to 24 referred to in the examples above.

Table 3 Probe Sets corresponding to genes, the expression of which is increased after infection of wild-type *Arabidopsis* with *Pseudomonas syringae*

ProbeSet	Description	Blast Score	EC #	Family
11997_at (AC005967.4_AT)	gb AAD03372.1 (AC005967) unknown protein [Arabidopsis thaliana]	0		
12002_at (AF069442.47_AT)	gb AAC79112.1 (AF069442) hypothetical protein [Arabidopsis thaliana]	0		
12004_at (AL022023.132_AT)	emb CAA17771.1 (AL022023) putative protein [Arabidopsis thaliana]	8E-86		
12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]	1E-168		
12037_at (AC004005.174_AT)	gb AAC23417.1 (AC004005) unknown protein [Arabidopsis thaliana]	0		
12051_at (AL021889.94_AT)	emb CAA17133.1 (AL021889) putative protein [Arabidopsis thaliana]	1E-143		
12062_at (AC006069.147_AT)	gb AAD12706.1 (AC006069) unknown protein [Arabidopsis thaliana]	0		
12068_at (AF118223.24_AT)	gb AAD03449.1 (AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]	1E-162		
12072_at (AL035396.4_AT)	emb CAA23058.1 (AL035396) putative protein [Arabidopsis thaliana]	1E-158		
12079_s_at (A71597.1_S_AT)	emb CAB42594.1 (A71597) unnamed protein product [Arabidopsis thaliana]	5E-64		
12081_at (AC001645.140_AT)	gb AAB63644.1 (AC001645) unknown protein [Arabidopsis thaliana]	1E-117		
12092_at (AC004793.13_AT)	gb AAD21694.1 (AC004793) ESTs gb T20423, gb AA712864, gb H76323 and gb Z25560 come from this gene. [Arabidopsis thaliana]	1E-150		

ProbeSet	Description	Blast Score	EC #	Family
12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]	1E-87		
12136_at (AC007591.60_AT)	gb AAD39663.1 AC007591_2 8 (AC007591) ESTs gb R65145, gb N96612 and gb R90096 come from this gene. [Arabidopsis thaliana]	1E-60		
12150_at (AC004005.151_AT)	gb AAC23415.1 (AC004005) unknown protein [Arabidopsis thaliana]	5E-32		
12187_at (AC005489.31_AT)	gb AAD32893.1 AC005489_3 1 (AC005489) F14N23.31 [Arabidopsis thaliana]	0		
12198_at (AC006954.90_AT)	gb AAD23890.1 AC006954_1 1 (AC006954) unknown protein [Arabidopsis thaliana]	1E-70		
12203_at (AL021710.268_AT)	emb CAA16738.1 (AL021710) hypothetical protein [Arabidopsis thaliana]	7E-55		
12216_at (AC007119.56_AT)	gb AAD23641.1 AC007119_7 (AC007119) unknown protein [Arabidopsis thaliana]	8E-55		
12217_at (AJ223804.1_AT)	gb AAF34796.1 AF228640_1 (AF228640) lipoamide dehydrogenase precursor [Arabidopsis thaliana]	0		
12227_at (AC007576.18_AT)	gb AAD39285.1 AC007576_8 (AC007576) Unknown protein [Arabidopsis thaliana]	1E-102		
12233_at (AJ001807.1_AT)	emb CAA05023.1 (AJ001807) succinyl-CoA- ligase alpha subunit [Arabidopsis thaliana]	0	EC_6.2.1.5	synthetase
12278_at (AJ011674.2_AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]	0		kinase
12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]	0		kinase
12314_at (AC001229.28_AT)	gb AAB60922.1 (AC001229) F5I14.14 [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
12317_at (AC004138.27_AT)	gb AAC32907.1 (AC004138) putative sucrose-proton symporter [Arabidopsis thaliana]	0		
12323_at (AC002333.18_AT)	gb AAB64019.1 (AC002333) putative polygalacturonase [Arabidopsis thaliana]	0		Polygalactur onase
12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]	0		
12341_s_at (AL021637.176_S_A T)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]	0		
12347_at (AC007258.28_AT)	gb AAD39325.1 AC007258_1 4 (AC007258) Putative ATPase [Arabidopsis thaliana]	0	EC_3.6.1.-	ATPase
12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]	0		
12369_at (AC002535.59_AT)	gb AAC62871.1 (AC002535) putative Na ⁺ /Ca ²⁺ antiporter [Arabidopsis thaliana]	0		
12400_at (X98453.1_AT)	emb CAA67092.1 (X98453) peroxidase [Arabidopsis thaliana]	0		peroxidase
12438_at (AL021710.83_AT)	emb CAA16723.1 (AL021710) membrane-bound small GTP-binding - like protein [Arabidopsis thaliana]	1E-122		
12449_s_at (AC002343.179_S_A T)	gb AAB63623.1 (AC002343) cellulose synthase isolog [Arabidopsis thaliana]	0		
12454_at (AC006232.164_AT)	gb AAD15602.1 (AC006232) putative ferredoxin [Arabidopsis thaliana]	5E-85		
12475_at (Y11794.1_AT)	emb CAA72490.1 (Y11794) peroxidase ATP29a [Arabidopsis thaliana]	3E-67		peroxidase
12487_at (AC004411.126_AT)	gb AAC34225.1 (AC004411) putative ABC transporter [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
12497_at (AC006533.51_AT)	gb AAD32284.1 AC006533_8 (AC006533) putative receptor-like protein kinase [Arabidopsis thaliana]	0		
12500_s_at (AF081067.3_S_AT)	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA- amino acid hydrolase [Arabidopsis thaliana]	0		
12521_at (AF049236.28_AT)	gb AAC14413.1 (AF049236) unknown [Arabidopsis thaliana]	0		
12525_at (AC006587.85_AT)	gb AAD21486.1 (AC006587) putative DOF zinc finger protein [Arabidopsis thaliana]	1E-132		
12530_at (Z99707.184_AT)	emb CAB16760.1 (Z99707) hydroxynitrile lyase like protein [Arabidopsis thaliana]	1E-150		LYASE
12535_at (AL035538.156_AT)	emb CAB37540.1 (AL035538) putative protein [Arabidopsis thaliana]	1E-132		
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]	6E-38		methyl- esterase
12571_s_at (AF149413.18_S_AT)	gb AAD40138.1 AF149413_1 9 (AF149413) Arabidopsis thaliana ferrochelatase-I (SW:P42043); Pfam	0		
12574_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]	1E-25		
12584_at (AC004521.233_AT)	gb AAC16096.1 (AC004521) similar to axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana]	0		
12626_at (AC006234.95_AT)	gb AAD20931.1 (AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]	0		kinase
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]	0		
12645_at (AL021712.56_AT)	emb CAA16774.1 (AL021712) fibrillin precursor-like protein [Arabidopsis thaliana]	1E-150		

ProbeSet	Description	Blast Score	EC #	Family
12698_at (AC000106.42_AT)	gb AAB70413.1 (AC000106) Similar to Beta integral membrane protein (gb U43629). EST gb W43122 comes from this gene. [Arabidopsis thaliana]	0		
12712_f_at (Z95774_F_AT)	emb CAB09206.1 (Z95774) R2R3-MYB transcription factor [Arabidopsis thaliana]	6E-21		
12736_f_at (Z97048_F_AT)	emb CAA90748.1 (Z50869) MYB-related protein [Arabidopsis thaliana]	4E-21		
12744_at (AC001645.15_AT)	gb AAB63630.1 (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]	0		
12760_g_at (AC005278.32_G_A T)	gb AAC72120.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb 84105 and gb AI100071 come from this gene. [Arabidopsis thaliana]	0		
12764_f_at (AC004138.69_F_A T)	gb AAC32912.1 (AC004138) putative glutathione S- transferase [Arabidopsis thaliana]	1E-111		
12772_at (AC005278.34_AT)	gb AAC72119.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb H37281, gb T44167, gb T21813, gb N38437, gb Z26470, gb R65072, gb N76373, gb F15470, gb Z35182, gb H76373, gb Z34678 a	0		
12776_at (AL021811.156_AT)	emb CAA16969.1 (AL021811) putative protein [Arabidopsis thaliana]	0		
12797_s_at (AC007138.25_S_A T)	gb AAD22647.1 AC007138_1 (AC007138) S- adenosylmethionine synthase 2 [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
12802_at (AL022373.153_AT)	emb CAA18498.1 (AL022373) DnaJ-like protein [Arabidopsis thaliana]	2E-74		
12851_s_at (ACCSYN1_S_AT)	emb CAA78260.1 (Z12614) 1-aminocyclopropane 1- carboxylate synthase [Arabidopsis thaliana]	3E-29		
12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]	1E-150		
12880_s_at (AIG2_S_AT)	gb AAC49283.1 (U40857) AIG2 [Arabidopsis thaliana]	3E-97		
12883_s_at (APX_S_AT)	emb CAA67425.1 (X98925) stromal ascorbate peroxidase [Arabidopsis thaliana]	1E-161		
12889_s_at (ASAI_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]	0		
12891_at (ATACS6_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]	0		synthase
12892_g_at (ATACS6_G_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]	0		
12904_s_at (ATERF1_S_AT)	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]	1E-126		
12905_s_at (ATERF2_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]	1E-112		
12911_s_at (ATG6PDHE5_S_A T)	emb CAA59011.1 (X84229) glucose-6-phosphate 1- dehydrogenase [Arabidopsis thaliana]	0		
12921_s_at (ATHHMGCOAR_S _AT)	emb CAA33139.1 (X15032) hydroxy methylglutaryl CoA reductase (AA 1-592)	0		
12930_s_at (ATLLS1_S_AT)	gb AAC49679.1 (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]	0		
12951_at (AC005489.5_AT)	gb AAD32867.1 AC005489_5 (AC005489) F14N23.5 [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
12958_at (AC002332.249_AT)	gb AAB80675.1 (AC002332) putative protein kinase [Arabidopsis thaliana]	0		kinase
12965_at (AL021711.118_AT)	emb CAA16752.1 (AL021711) protein kinase- like protein [Arabidopsis thaliana]	0		kinase
12966_s_at (AL023094.197_S_A T)	emb CAA18838.1 (AL023094) bZIP transcription factor ATB2 [Arabidopsis thaliana]	2E-67		
12989_s_at (AC004077.149_S_A T)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]	0		
13003_s_at (AB021936.1_S_AT)	dbj BAA74591.1 (AB021936) nicotianamine synthase [Arabidopsis thaliana]	0		
13005_at (AC004683.61_AT)	gb AAC28763.1 (AC004683) unknown protein [Arabidopsis thaliana]	0		
13014_at (U93215.87_AT)	gb AAB63082.1 (U93215) putative lipase [Arabidopsis thaliana]	0		lipase
13015_s_at (X98673.2_S_AT)	emb CAA67232.1 (X98674) zinc finger protein [Arabidopsis thaliana]	7E-90		
13025_at (AL050400.20_AT)	emb CAB43695.1 (AL050400) putative protein [Arabidopsis thaliana]	0		
13040_at (AC002392.134_AT)	gb AAD12039.1 (AC002392) unknown protein [Arabidopsis thaliana]	0		
13070_at (AC006919.171_AT)	gb AAD24640.1 AC006919_2 0 (AC006919) putative pyruvate kinase [Arabidopsis thaliana]	0		kinase
13094_at (AL035523.163_AT)	emb CAB36745.1 (AL035523) putative protein [Arabidopsis thaliana]	1E-172		
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]	0		mono- oxygenase

ProbeSet	Description	Blast Score	EC #	Family
13110_at (AF074021.34_AT)	gb AAD29776.1 AF074021_8 (AF074021) putative symbiosis-related protein [Arabidopsis thaliana]	1E-65		
13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592,gb T13956,gb T43 869 come from from this gene. [Arabidopsis thaliana]	0		
13119_at (AC007260.23_AT)	gb AAD30579.1 AC007260_1 0 (AC007260) Similar to dTDP-D-glucose 4,6- dehydratase [Arabidopsis thaliana]	0	EC_4.2.1.46	dehydratase
13128_at (AL049607.47_AT)	emb CAB40756.1 (AL049607) protein phosphatase 2C-like protein [Arabidopsis thaliana]	0		
13134_s_at (AC002337.9_S_AT)	gb AAB63818.1 (AC002337) putative galactinol synthase [Arabidopsis thaliana]	0		
13137_at (AC007169.86_AT)	gb AAD26480.1 AC007169_1 2 (AC007169) putative fructokinase [Arabidopsis thaliana]	0		fructokinase
13152_s_at (AC005322.24_S_A T)	gb AAC97998.1 (AC005322) Identical to 1- aminocyclopropane-1- carboxylate oxidase (ACC oxidase) gb X66719 (EAT1). ESTs gb T43073, gb T5714, gb R90435, gb R44023, gb AA597926, gb AI099676, gb AA650810 and gb 29725 come from this gene. [Arabidopsis thaliana]	1E-177		
13154_s_at (AC002333.210_S_A T)	gb AAB64047.1 (AC002333) putative endochitinase [Arabidopsis thaliana]	1E-148		
13157_at (AC002409.35_AT)	gb AAB86449.1 (AC002409) putative cytochrome P450 [Arabidopsis thaliana]	0		
13163_s_at (AC005560.223_S_A T)	gb AAD12692.2 (AC006069) unknown protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]	0		
13177_at (AL049640.42_AT)	emb CAB40989.1 (AL049640) growth factor like protein [Arabidopsis thaliana]	1E-164		
13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	2E-63		
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	2E-63		
13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	2E-63		
13190_s_at (ATTHIREDA_S_AT)	emb CAA80655.1 (Z23108) NADPH thioredoxin reductase [Arabidopsis thaliana]	1E-174		
13211_s_at (BCHI_S_AT)	dbj BAA82816.1 (AB023454) basic endochitinase [Arabidopsis thaliana]	2E-72		
13212_s_at (BGL2_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3- glucanase 2 (BG2) [Arabidopsis thaliana]	0		
13215_s_at (CAFFEROYLCOA METHYLTRANS_S _AT)	gb AAF16576.1 AC012563_2 9 (AC012563) putative S- adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O- methyltransferase [Arabidopsis thaliana]	1E-121		
13217_s_at (CALMODULINLIK E_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]	6E-99		
13219_s_at (CHI4_S_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]	5E-78		
13243_r_at (ELI32_R_AT)	emb CAB37539.1 (AL035538) cinnamyl-alcohol dehydrogenase ELI3-2 [Arabidopsis	0		

ProbeSet	Description	Blast Score	EC #	Family
13244_s_at (ELI32_S_AT)	emb CAB37539.1 (AL035538) cinnamyl-alcohol dehydrogenase ELI3-2 [Arabidopsis]	0		
13246_at (ERECTAL_AT)	gb AAF26067.1 AC012562_2 2 (AC012562) putative protein kinase [Arabidopsis thaliana]	1E-40		kinase
13255_i_at (GAMMAGLUTAM YLTRANSPEPTI_I_ AT)	emb CAA89206.1 (Z49240) gamma-glutamyl transpeptidase [Arabidopsis thaliana]	0	EC_2.3.2.2	glutamyl- trans- peptidase
13259_s_at (GLUTATHIONEPE ROXIDASE1_S_AT)	gb AAD24836.1 AC007071_8 (AC007071) putative glutathione peroxidase [Arabidopsis thaliana]	4E-95		
13261_s_at (GLUTATHIONERE DUCTASE1_S_AT)	gb AAB67841.1 (U37697) glutathione reductase [Arabidopsis thaliana]	0		
13263_s_at (GST1_RC_S_AT)	emb CAA10060.1 (AJ012571) glutathione transferase [Arabidopsis thaliana]	3E-49		
13266_s_at (GST4_S_AT)	emb CAB51026.1 (AJ243812) glutathione synthetase [Arabidopsis thaliana]	0		
13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]	1E-113		
13275_f_at (HSP174_F_AT)	emb CAA35182.1 (X17293) heat shock protein (AA 1 - 156) [Arabidopsis thaliana]	8E-80		
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]	2E-75		
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]	0		
13312_at (AC006223.75_AT)	gb AAD15391.1 (AC006223) putative disease resistance protein [Arabidopsis thaliana]	1E-126		disease

ProbeSet	Description	Blast Score	EC #	Family
13367_at (AC004680.97_AT)	gb AAC31853.1 (AC004680) putative NADH dehydrogenase (ubiquinone oxidoreductase) [Arabidopsis thaliana]	0	EC_1.6.5.3	oxido- reductase
13370_at (AC005322.4_AT)	gb AAC97990.1 (AC005322) Strong similarity to Dsor1 protein kinase gb D13782 from Drosophila melanogaster. [Arabidopsis thaliana]	0		kinase
13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]	1E-169		
13395_at (AL035528.202_AT)	emb CAB36843.1 (AL035528) SAUR-AC-like protein (small auxin up RNA) [Arabidopsis thaliana]	1E-48		
13435_at (AF003102.3_AT)	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]	1E-33		
13437_at (AF096371.8_AT)	gb AAC62791.1 (AF096371) contains similarity to D- isomer specific 2-hydroxyacid dehydrogenases (Pfam: 2- Hacid_DH.hmm, score: 19.11) [Arabidopsis thaliana]	0		
13450_at (AL049657.33_AT)	emb CAB41122.1 (AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana]	0		
13467_at (AL096860.198_AT)	emb CAB51214.1 (AL096860) putative protein [Arabidopsis thaliana]	0		permease
13480_at (AC005223.15_AT)	gb AAD10644.1 (AC005223) 40409 [Arabidopsis thaliana]	1E-169		
13534_at (AF149413.36_AT)	gb AAD40124.1 AF149413_5 (AF149413) contains similarity to soybean early nodulin 93 (N-93) (SW:Q02921) [Arabidopsis thaliana]	2E-38		

ProbeSet	Description	Blast Score	EC #	Family
13536_at (AL021636.47_AT)	emb CAA16575.1 (AL021636) putative protein [Arabidopsis thaliana]	0		
13538_at (AL080254.75_AT)	emb CAB45844.1 (AL080254) calcium-binding protein-like [Arabidopsis thaliana]	1E-105		
13564_at (AC005312.113_AT)	gb AAC78521.1 (AC005312) putative glutathione S- transferase [Arabidopsis thaliana]	1E-127		transferase
13565_at (AL035601.21_AT)	emb CAB38206.1 (AL035601) auxin-responsive GH3-like protein [Arabidopsis thaliana]	0		
13584_at (AC007127.23_AT)	gb AAD25137.1 AC007127_3 (AC007127) putative ubiquitin-like protein [Arabidopsis thaliana]	0		
13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]	0		dehydro- genase
13589_at (AC000132.24_AT)	gb AAB60745.1 (AC000132) ESTs gb ATTS1236,gb T43334,gb N 97019,gb AA395203 come from this gene. [Arabidopsis thaliana]	2E-91		
13604_at (AC000104.20_AT)	gb AAB70431.1 (AC000104) F19P19.10 [Arabidopsis thaliana]	0	EC_2.7.1.-	
13605_at (AL078470.75_AT)	emb CAB43918.1 (AL078470) 26S proteasome subunit 4-like protein [Arabidopsis thaliana]	0		ATPase
13617_at (AC006592.64_AT)	gb AAD22351.1 AC006592_8 (AC006592) putative mitochondrial dicarboxylate carrier protein [Arabidopsis thaliana]	1E-152		
13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ - exchanging protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
13645_at (AC000098.8_AT)	gb AAB71443.1 (AC000098) EST gb ATTS0295 comes from this gene. [Arabidopsis thaliana]	6E-19		
13647_at (AF000657.22_AT)	gb AAB72161.1 (AF000657) unknown protein [Arabidopsis thaliana]	0		
13656_at (AC007138.31_AT)	gb AAD22649.1 AC007138_1 3 (AC007138) predicted protein of unknown function [Arabidopsis thaliana]	0		
13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]	0		
13666_s_at (INDOLE3GPS_S_A T)	gb AAD25838.1 AC006951_1 7 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]	0		
13680_s_at (LOX1_S_AT)	gb AAA17036.1 (U01843) lipoxygenase 1 [Arabidopsis thaliana]	0		
13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]	0		
13688_s_at (MONOPTEROS_S_ AT)	gb AAC60794.1 (AF037229) transcription factor [Arabidopsis thaliana]	0		
13697_at (NI16_AT)	No hits found.			
13705_s_at (AC003671X_S_AT)	gb AAC18810.1 (AC003671) Strong similarity to trehalose- 6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb Z97344. ESTs gb H37594, gb R65023, gb H37578 and gb R64855 come from this gene. [Arabidopsis thaliana]	0		
13706_s_at (AC005724X_S_AT)	gb AAD08939.1 (AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
13716_at (NOVARTIS103_RC_AT)	emb CAA62665.1 (X91259) lectin like protein [Arabidopsis thaliana]	6E-70		
13718_at (NOVARTIS105_RC_AT)	emb CAA96522.1 (Z72152) AMP-binding protein [Brassica napus]	6E-19		
13746_at (NOVARTIS121_RC_AT)	gb AAF18699.1 AC010795_1 4 (AC010795) hypothetical protein [Arabidopsis thaliana]	8E-80		
13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]	2E-27		
13755_at (NOVARTIS15_AT)	emb CAA16797.1 (AL021713) receptor serine/threonine kinase-like protein [Arabidopsis thaliana]	1E-114		
13763_at (NOVARTIS21_AT)	gb AAF24849.1 AC012679_2 0 (AC012679) putative calmodulin-binding protein [Arabidopsis thaliana]	1E-105		
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [Arabidopsis thaliana]	2E-30		
13789_at (AJ132436.2_AT)	emb CAB41008.1 (AJ132436) GA 2-oxidase [Arabidopsis thaliana]	0		oxidase
13803_at (Z97341.376_AT)	emb CAB10444.1 (Z97341) cyanohydrin lyase like protein [Arabidopsis thaliana]	1E-154		
13818_s_at (AC006218.175_S_AT)	gb AAD15433.1 (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]	0		
13825_s_at (AF104919.22_S_AT)	gb AAC72875.1 (AF104919) Arabidopsis thaliana ABC1 protein (GB:AJ001158)	0		
13834_at (AL080237.29_AT)	emb CAB45784.1 (AL080237) cyclic nucleotide gated channel (CNGC4) like protein [Arabidopsis thaliana]	0		
13842_at (AC002396.12_AT)	gb AAC00572.1 (AC002396) similar to zinc metalloproteinases [Arabidopsis thaliana]	0		metallo- proteinase

ProbeSet	Description	Blast Score	EC #	Family
13848_at (AC003981.31_AT)	gb AAC14057.1 (AC003981) F22O13.31 [Arabidopsis thaliana]	0		
13880_s_at (AL049480.183_S_A T)	emb CAB39611.1 (AL049480) possible apospory-associated like protein [Arabidopsis thaliana]	0		
13896_at (AC004473.8_AT)	gb AAC24048.1 (AC004473) Strong similarity to trehalose- 6-phosphate synthase homolog gb 2245136 from A. thaliana chromosome 4 contig gb Z97344. [Arabidopsis thaliana]	0		
13908_s_at (A71590.1_S_AT)	emb CAB42588.1 (A71590) unnamed protein product [Arabidopsis thaliana]	9E-62		
13918_at (AC005388.29_AT)	gb AAC64884.1 (AC005388) Strong similarity to F21B7.33 gi 2809264 from A. thaliana BAC gb AC002560. EST gb N65119 comes from this gene. [Arabidopsis thaliana]	0		
13920_at (AC005990.53_AT)	gb AAC98026.1 (AC005990) EST gb AA597511 comes from this gene. [Arabidopsis thaliana]	1E-131		
13944_at (U89959.24_AT)	gb AAC24380.1 (U89959) Unknown protein [Arabidopsis thaliana]	0		
13949_s_at (Z97343.352_S_AT)	emb CAB10528.1 (Z97343) thioesterase like protein [Arabidopsis thaliana]	1E-167		
13963_at (AL021711.26_AT)	emb CAA16746.1 (AL021711) putative protein [Arabidopsis thaliana]	1E-137		
13964_at (AL021889.3_AT)	emb CAA17126.2 (AL021889) N-acetylmithine deacetylase-like protein, fragment [Arabidopsis thaliana]	0		
13966_at (AL022023.172_AT)	emb CAA17775.1 (AL022023) putative protein [Arabidopsis thaliana]	1E-173		

ProbeSet	Description	Blast Score	EC #	Family
13999_at (AF071527.56_AT)	gb AAD11584.1 AAD11584 (AF071527) hypothetical protein [Arabidopsis thaliana]	1E-173		
14015_s_at (A71588.1_S_AT)	emb CAB42612.1 (A71639) unnamed protein product [Arabidopsis thaliana]	1E-63		
14016_s_at (A71596.1_S_AT)	emb CAB42592.1 (A71596) unnamed protein product [Arabidopsis thaliana]	3E-58		
14025_s_at (AC007293.3_S_AT)	gb AAD12260.1 (AF098632) subtilisin-like protease [Arabidopsis thaliana]	0		
14026_at (AC000106.5_AT)	gb AAB70397.1 (AC000106) Similar to probable Mg- dependent ATPase (pir S56671). ESTs gb T46782,gb AA04798 come from this gene. [Arabidopsis thaliana]	0		
14030_at (AC005970.225_AT)	gb AAC95171.1 (AC005970) putative protein kinase [Arabidopsis thaliana]	0		kinase
14032_at (AL035601.11_AT)	emb CAB38204.1 (AL035601) cytochrome P450-like protein [Arabidopsis thaliana]	0		
14041_at (AC003970.28_AT)	gb AAC33208.1 (AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi 1143445 [Arabidopsis thaliana]	0		dehydro- genase
14052_at (AC004122.24_AT)	gb AAC34333.1 (AC004122) Highly Similar to branched- chain amino acid aminotransferase [Arabidopsis thaliana]	1E-174		
14068_s_at (AC006922.197_S_A T)	gb AAD31580.1 AC006922_1 2 (AC006922) putative farnesylated protein [Arabidopsis thaliana]	1E-132		
14070_at (AL049658.217_AT)	emb CAB41143.1 (AL049658) putative peptide transporter [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
14083_at (AC005662.56_AT)	gb AAC78535.1 (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]	1E-155		
14089_at (AC006223.65_AT)	gb AAD15390.1 (AC006223) putative hydrolase [Arabidopsis thaliana]	1E-135		
14100_at (AF002109.108_AT)	gb AAB95282.1 (AF002109) putative peroxisomal membrane carrier protein [Arabidopsis thaliana]	1E-166		
14110_i_at (AL035528.279_I_A T)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]	0		disease
14116_at (AF077407.30_AT)	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]	0		
14122_at (AF058826.23_AT)	gb AAC13608.1 (AF058826) similar to eukaryotic protein kinase domains (Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]	0		kinase
14139_at (NOVARTIS30_AT)	gb AAD09343.1 (AF026538) ABA-responsive protein [Hordeum vulgare]	7E-36		
14141_at (NOVARTIS31_AT)				
14148_at (NOVARTIS38_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]	4E-53		
14170_at (NOVARTIS51_AT)	gb AAF29406.1 AC022354_5 (AC022354) unknown protein [Arabidopsis thaliana]	9E-26		
14197_at (NOVARTIS71_AT)				
14214_at (NOVARTIS83_AT)	gb AAF24849.1 AC012679_2 0 (AC012679) putative calmodulin-binding protein [Arabidopsis thaliana]	2E-92		
14223_at (NOVARTIS9_AT)	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
14240_s_at (NR1_S_AT)	gb AAF08556.1 AC012193_5 (AC012193) nitrate reductase 1 (NR1) [Arabidopsis thaliana]	1E-148		
14242_s_at (NRA_S_AT)	gb AAF19225.1 AC007505_1 (AC007505) nitrate reductase [Arabidopsis thaliana]	0		
14248_at (PAD3_AT)	gb AAD31062.1 AC007357_1 1 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.	0		
14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]	0		
14254_s_at (PAL1- MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis	1E-134		
14256_f_at (PAL1- INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]	7E-77		
14257_s_at (PAL2- MRNA_S_AT)	gb AAC18871.1 (L33678) phenylalanine ammonia lyase [Arabidopsis thaliana]	0		
14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]	1E-110		
14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]	0		
14408_at (AC002291.14_AT)	gb AAC00635.1 (AC002291) Unknown protein [Arabidopsis thaliana]	0		
14448_at (AC002387.243_AT)	gb AAB82641.1 (AC002387) putative auxin-regulated protein [Arabidopsis thaliana]	2E-94		

ProbeSet	Description	Blast Score	EC #	Family
14450_at (AC002986.49_AT)	gb AAC17046.1 (AC002986) EST gb N65759 comes from this gene. [Arabidopsis thaliana]	4E-78		
14459_at (AC006200.69_AT)	gb AAD14519.1 (AC006200) unknown protein [Arabidopsis thaliana]	0		kinase
14460_at (AC006201.21_AT)	gb AAD20117.1 (AC006201) unknown protein [Arabidopsis thaliana]	0		
14461_at (AC006202.73_AT)	gb AAD29832.1 AC006202_1 0 (AC006202) putative carbonic anhydrase [Arabidopsis thaliana]	1E-134		
14468_at (AC007576.62_AT)	gb AAD39306.1 AC007576_2 9 (AC007576) Unknown protein [Arabidopsis thaliana]	2E-89		
14475_at (AL021811.121_AT)	emb CAA16965.1 (AL021811) putative protein [Arabidopsis thaliana]	0		
14487_at (Z97341.343_AT)	emb CAB46039.1 (Z97341) HSP like protein [Arabidopsis thaliana]	1E-160		
14498_at (AC004261.51_AT)	gb AAD11996.1 (AC004261) unknown protein [Arabidopsis thaliana]	2E-43		
14584_at (AC007658.25_AT)	gb AAD32844.1 AC007658_3 (AC007658) unknown protein [Arabidopsis thaliana]	2E-74		
14591_at (AL035440.107_AT)	emb CAB36521.1 (AL035440) putative protein [Arabidopsis thaliana]	1E-178		
14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]	0		
14614_at (AC004165.66_AT)	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]	0		glucosy- ltransferase
14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]	1E-94		
14638_s_at (PRXCB_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]	0		
14640_s_at (PUTATIVEMLOHI _S_AT)	gb AAC28997.1 (AC004697) similar to Mlo proteins from H. vulgare [Arabidopsis thaliana]	0		
14643_s_at (RAR047_S_AT)	gb AAD20078.1 (AC006836) putative steroid sulfotransferase [Arabidopsis thaliana]	1E-162		
14660_s_at (THIOREDOXL_S_ AT)	gb AAB86519.1 (AC002329) putative thioredoxin reductase [Arabidopsis thaliana]	2E-34		
14663_s_at (TREHALASEPREC USOR_RC_S_AT)	gb AAB63620.1 (AC002343) trehalase precursor isolog [Arabidopsis thaliana]	0		
14667_s_at (TRPB_S_AT)	gb AAA32878.1 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]	0		
14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]	1E-158		
14673_s_at (TSB2_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta- subunit [Arabidopsis thaliana] thaliana]	0		
14675_s_at (VSP_S_AT)	dbj BAA22096.1 (D85191) vegetative storage protein [Arabidopsis thaliana]	1E-146		
14682_i_at (WT1012A_RC_I_A T)				
14686_s_at (WT1073_S_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]	1E-116		

ProbeSet	Description	Blast Score	EC #	Family
14696_at (WT740_RC_AT)	gb AAD23643.1 AC007119_9 (AC007119) unknown protein [Arabidopsis thaliana]	5E-45		
14697_g_at (WT740_RC_G_AT)	gb AAD23643.1 AC007119_9 (AC007119) unknown protein [Arabidopsis thaliana]	5E-45		
14705_i_at (WT77_RC_I_AT)	emb CAB69849.1 (AL137189) anthranilate N- benzoyltransferase-like protein [Arabidopsis thaliana]	1E-38		
14706_r_at (WT77_RC_R_AT)	emb CAB69849.1 (AL137189) anthranilate N- benzoyltransferase-like protein [Arabidopsis thaliana]	1E-38		
14711_s_at (ZFPL_S_AT)	gb AAD25930.1 AF085279_3 (AF085279) hypothetical Cys- 3-His zinc finger protein [Arabidopsis thaliana]	3E-37		
14735_s_at (AF008124_S_AT)	gb AAB71832.1 (AF008125) multidrug resistance- associated protein homolog [Arabidopsis thaliana]	0		
14750_s_at (AF096370.12_S_AT)	gb AAC62777.1 (AF096370) contains similarity to NAM (no apical meristem) -like proteins [Arabidopsis thaliana]	1E-175		
14763_at (X86958.1_AT)	emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]	1E-25		kinase
14779_at (AC004680.71_AT)	gb AAC31851.1 (AC004680) hypothetical protein [Arabidopsis thaliana]	0		
14780_at (AC004683.103_AT)	gb AAC28770.1 (AC004683) DREB-like AP2 domain transcription factor [Arabidopsis thaliana]	1E-126		
14786_at (AC005397.115_AT)	gb AAC62908.1 (AC005397) putative desiccation related protein [Arabidopsis thaliana]	2E-90		
14793_at (AC006202.10_AT)	emb CAB67652.1 (AL132966) putative protein [Arabidopsis thaliana]	2E-79		

ProbeSet	Description	Blast Score	EC #	Family
14838_s_at (M96073.6_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]	0		
14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]	1E-103		
14884_at (AL031032.95_AT)	emb CAA19873.1 (AL031032) putative protein [Arabidopsis thaliana]	1E-149		
14895_s_at (Z97344.138_S_AT)	emb CAB10562.1 (Z97344) acetylornithine deacetylase [Arabidopsis thaliana]	4E-68		
14900_at (AC000348.12_AT)	gb AAB61488.1 (AC000348) T7N9.12 [Arabidopsis thaliana]	0		
14923_at (AC006283.158_AT)	gb AAD20693.1 (AC006283) unknown protein [Arabidopsis thaliana]	0		
14924_at (AC006283.46_AT)	gb AAD20686.1 (AC006283) hypothetical protein [Arabidopsis thaliana]	7E-85		
14928_at (AC006569.88_AT)	gb AAD21756.1 (AC006569) unknown protein [Arabidopsis thaliana]	0		
14959_at (AC007202.26_AT)	gb AAD30230.1 AC007202_1 2 (AC007202) T8K14.13 [Arabidopsis thaliana]	0		
14972_at (AC005499.38_AT)	gb AAC67344.1 (AC005499) unknown protein [Arabidopsis thaliana]	1E-123		
14978_at (AC002333.49_AT)	gb AAB64024.1 (AC002333) putative glucosyltransferase [Arabidopsis thaliana]	0		glucosyl- transferase
15032_at (AC002294.8_AT)	gb AAB71471.1 (AC002294) Unknown protein [Arabidopsis thaliana]	1E-115		
15042_at (AL021961.3_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]	1E-167		

ProbeSet	Description	Blast Score	EC #	Family
15052_at (AC002332.103_AT)	gb AAB80656.1 (AC002332) putative calcium-binding EF- hand protein [Arabidopsis thaliana]	1E-120		
15073_at (AC007069.93_AT)	gb AAD21785.1 (AC007069) putative purple acid phosphatase [Arabidopsis thaliana]	0		
15085_s_at (AL031018.274_S_A T)	emb CAA19817.1 (AL031018) putative protein [Arabidopsis thaliana]	0		
15088_s_at (AC002311.37_S_A T)	gb AAB72158.1 (AF000657) unknown protein [Arabidopsis thaliana]	9E-48		
15091_at (AC004683.97_AT)	gb AAC28768.1 (AC004683) unknown protein [Arabidopsis thaliana]	1E-101		
15098_s_at (ATU26945_S_AT)	emb CAA21463.1 (AL031986) senescence- associated protein sen1 [Arabidopsis thaliana]	1E-103		
15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]	6E-81		
15123_s_at (ATU40857_S_AT)	gb AAC49283.1 (U40857) AIG2 [Arabidopsis thaliana]	3E-97		
15124_s_at (ATU59508_S_AT)	gb AAB40615.1 (U59508) osmotic stress-induced proline dehydrogenase [Arabidopsis thaliana]	0		
15125_f_at (D85190_F_AT)	dbj BAA22095.1 (D85190) vegetative storage protein [Arabidopsis thaliana]	1E-142		
15129_s_at (AF030386_S_AT)	gb AAB86938.1 (AF030386) NOI protein [Arabidopsis thaliana]	1E-30		
15132_s_at (AF121878_S_AT)	gb AAD30449.1 AF121878_1 (AF121878) cytidine deaminase [Arabidopsis thaliana]	1E-169		
15137_s_at (ATU57320_S_AT)	gb AAB47973.1 (U57320) blue copper-binding protein II [Arabidopsis thaliana]	5E-70		

ProbeSet	Description	Blast Score	EC #	Family
15140_s_at (ATU93845_S_AT)	gb AAB52420.1 (U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence	0		
15141_s_at (D85191_S_AT)	dbj BAA22096.1 (D85191) vegetative storage protein [Arabidopsis thaliana]	1E-146		
15154_s_at (ATHMTGDAS_S_AT)	emb CAB51206.1 (AL096860) glutamine- dependent asparagine synthetase [Arabidopsis thaliana]	0		
15161_s_at (ATU90522_S_AT)	gb AAB53975.1 (U90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]	0		
15162_s_at (U01880_S_AT)	gb AAA20642.1 (U01880) pre-hevein-like protein [Arabidopsis thaliana]	1E-113		
15188_s_at (AF081202_S_AT)	gb AAC31606.1 (AF081202) villin 2 [Arabidopsis thaliana]	0		
15192_s_at (ATHERD1_S_AT)	dbj BAA04506.1 (D17582) ERD1 protein [Arabidopsis thaliana]	0		
15196_s_at (ATU43412_S_AT)	gb AAC49573.1 (U43412) 3'- phosphoadenosine 5'- phosphosulfate reductase [Arabidopsis thaliana]	0		
15197_s_at (ATU52851_S_AT)	gb AAB09723.1 (U52851) arginine decarboxylase [Arabidopsis thaliana]	0		
15199_s_at (AB005804_S_AT)	dbj BAA28624.1 (AB005804) aldehyde oxidase [Arabidopsis thaliana]	0		
15211_s_at (ATH243813_S_AT)	emb CAB51027.1 (AJ243813) glutathione synthetase [Arabidopsis thaliana]	0		
15216_s_at (ATU75191_S_AT)	gb AAB51576.1 (U75198) germin-like protein [Arabidopsis thaliana]	8E-97		

ProbeSet	Description	Blast Score	EC #	Family
15342_at (AC006593.101_AT)	gb AAD20671.1 (AC006593) unknown protein [Arabidopsis thaliana]	0		
15379_at (AC002335.182_AT)	gb AAB64323.1 (AC002335) unknown protein [Arabidopsis thaliana]	7E-75		
15389_at (AC004786.100_AT)	gb AAC32433.1 (AC004786) unknown protein [Arabidopsis thaliana]	2E-37		
15406_at (AC006931.179_AT)	gb AAD21731.1 (AC006931) unknown protein [Arabidopsis thaliana]	2E-98		
15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]	2E-51		
15463_at (AL031326.226_AT)				
15479_at (AL049483.205_AT)	emb CAB39671.1 (AL049483) putative protein [Arabidopsis thaliana]	4E-68		
15483_s_at (AC005819.20_S_A T)	gb AAC69922.1 (AC005819) putative cytochrome b5 [Arabidopsis thaliana]	4E-58		
15485_at (AC006233.109_AT)	gb AAD41998.1 AC006233_1 0 (AC006233) unknown protein [Arabidopsis thaliana]	1E-169		
15496_at (AC006282.167_AT)	gb AAD20156.1 (AC006282) putative glucosyl transferase [Arabidopsis thaliana]	0		transferase
15518_at (AC005322.28_AT)	gb AAC97999.1 (AC005322) ESTs gb H36249, gb AA59732 and gb AA651219 come from this gene. [Arabidopsis thaliana]	1E-125		
15522_i_at (AL078637.213_I_A T)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]	8E-48		
15523_s_at (AL078637.213_S_A T)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]	8E-48		
15524_at (AC005508.25_AT)	gb AAD14499.1 (AC005508) 44123 [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
15526_at (AC004122.16_AT)	gb AAC34332.1 (AC004122) Unknown protein [Arabidopsis thaliana]	0		
15531_i_at (AL078637.191_I_A T)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]	0		
15532_r_at (AL078637.191_R_A T)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]	0		
15540_at (AC006585.205_AT)	gb AAD18030.1 (AF118129) Tsi1-interacting protein TSIP1 [Nicotiana tabacum]	1E-33		
15543_at (AF096371.10_AT)	gb AAC62794.1 (AF096371) T2L5.6 gene product [Arabidopsis thaliana]	1E-108		
15544_at (AL021633.110_AT)	emb CAA16532.1 (AL021633) predicted protein [Arabidopsis thaliana]	1E-147		
15547_at (AC005970.122_AT)	gb AAC95168.1 (AC005970) unknown protein [Arabidopsis thaliana]	1E-110		
15551_at (AL035440.289_AT)	emb CAB36537.1 (AL035440) putative dihydrolipoamide succinyltransferase [Arabidopsis thaliana]	0	EC_2.3.1.61	succinyl- transferase
15580_s_at (AF057043_S_AT)	gb AAC13497.1 (AF057043) acyl-CoA oxidase [Arabidopsis thaliana]	0		
15582_s_at (ATH131392_S_AT)	emb CAA10364.1 (AJ131392) alternative oxidase [Arabidopsis thaliana]	0		
15594_s_at (ATU56635_S_AT)	gb AAB01222.1 (U56635) glutamate dehydrogenase 2 [Arabidopsis thaliana]	0		
15613_s_at (ATHHOMEOA_S_ AT)	emb CAA79670.1 (Z19602) HAT4 [Arabidopsis thaliana]	1E-144		
15614_s_at (ATHMER15B_S_A T)	emb CAB52471.1 (AL109796) xyloglucan endo- 1, 4-beta-D-glucanase precursor [Arabidopsis thaliana]	1E-162		

ProbeSet	Description	Blast Score	EC #	Family
15617_s_at (ATHSAR1_S_AT)	gb AAA56991.1 (M90418) formerly called HAT24; synaptobrevin-related protein [Arabidopsis thaliana]	1E-112		
15622_s_at (ATU43945_S_AT)	gb AAB40594.1 (U43945) strictosidine synthase [Arabidopsis thaliana]	0		
15625_s_at (ATU74610_S_AT)	gb AAB17995.1 (U74610) glyoxalase II [Arabidopsis thaliana]	1E-141		
15629_s_at (AB003280_S_AT)	dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]	0		
15632_s_at (AB012570_S_AT)	dbj BAA37112.1 (AB012570) ATHP3 [Arabidopsis thaliana]	7E-77		
15641_s_at (AF117063_S_AT)	gb AAD10829.1 (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]	0		
15646_s_at (ATHSAT1G_S_AT)	gb AAC37474.1 (L42212) serine acetyltransferase [Arabidopsis thaliana]	0		
15665_s_at (AF022658_S_AT)	gb AAB80922.1 (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]	3E-94		
15669_s_at (AF047834_S_AT)	gb AAF24813.1 AC007592_6 (AC007592) F12K11.9 [Arabidopsis thaliana]	0		
15670_s_at (AF061638_S_AT)	gb AAC64005.1 (AF061638) branched-chain alpha-keto acid decarboxylase E1 beta subunit [Arabidopsis thaliana]	0		
15672_s_at (AF082299_S_AT)				
15674_s_at (AF091844_S_AT)	gb AAC61769.1 (AF091844) aminoalcoholphosphotransferase [Arabidopsis thaliana]	0		
15680_s_at (ATHATPK19B_S_AT)	dbj BAA07661.1 (D42061) ribosomal-protein S6 kinase homolog [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
15778_at (X98676.2_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]	8E-87		
15779_g_at (X98676.2_G_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]	8E-87		
15792_at (AC002341.106_AT)	gb AAB67625.1 (AC002341) hypothetical protein [Arabidopsis thaliana]	1E-174		
15798_at (AC002521.173_AT)	gb AAC05351.1 (AC002521) putative receptor-like protein kinase [Arabidopsis thaliana]	0		
15815_s_at (Z97342.366_S_AT)	emb CAB10487.1 (Z97342) hypothetical protein [Arabidopsis thaliana]	1E-175		
15839_at (AC005662.203_AT)	gb AAC78548.1 (AC005662) unknown protein [Arabidopsis thaliana]	8E-22		
15859_at (AC006587.164_AT)	gb AAD21491.1 (AC006587) unknown protein [Arabidopsis thaliana]	4E-17		
15866_s_at (AC007133.59_S_A T)	gb AAC79625.1 (AC005770) unknown protein [Arabidopsis thaliana]	5E-27		
15874_at (AL022223.106_AT)	emb CAA18223.1 (AL022223) putative protein [Arabidopsis thaliana]	1E-133		
15886_at (AL078637.204_AT)	emb CAB45070.1 (AL078637) putative protein [Arabidopsis thaliana]	1E-126		phoshorylas e
15900_at (AC005311.74_AT)				
15919_at (AC007060.42_AT)	gb AAD25764.1 AC007060_2 2 (AC007060) EST gb AA721821 comes from this gene. [Arabidopsis thaliana]	0		
15921_s_at (AC007067.1_S_AT)	gb AAD39561.1 AC007067_1 (AC007067) T10O24.1 [Arabidopsis thaliana]	1E-24		
15924_at (AC007138.61_AT)	gb AAD22658.1 AC007138_2 2 (AC007138) predicted protein of unknown function [Arabidopsis thaliana]	8E-94		

ProbeSet	Description	Blast Score	EC #	Family
15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]	0		
15978_at (X68592.6_AT)	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]	0		translocase
15982_s_at (AC006260.78_S_A T)	emb CAA66863.1 (X98190) peroxidase ATP2a [Arabidopsis thaliana]	0		
16001_at (AF035385.2_AT)	gb AAC39468.1 (AF035385) unknown [Arabidopsis thaliana]	4E-72		
16003_s_at (AL021749.64_S_AT)	emb CAA16877.1 (AL021749) ADP, ATP carrier-like protein [Arabidopsis thaliana]	0		
16021_s_at (AL022224.182_S_A T)	emb CAA18251.1 (AL022224) endomembrane- associated protein [Arabidopsis thaliana]	3E-63		
16031_at (X94248.1_AT)	emb CAA63932.1 (X94248) ferritin [Arabidopsis thaliana]	1E-136		
16043_at (AC005489.17_AT)	gb AAD32879.1 AC005489_1 7 (AC005489) F14N23.17 [Arabidopsis thaliana]	0		
16053_i_at (Y14251.4_I_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]	1E-110		transferase
16054_s_at (Y14251.4_S_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]	1E-110		
16058_s_at (ATU94495_S_AT)	gb AAD24836.1 AC007071_8 (AC007071) putative glutathione peroxidase [Arabidopsis thaliana]	5E-95		
16059_s_at (D88206_S_AT)	dbj BAA24694.1 (D88206) protein kinase [Arabidopsis thaliana]	0		
16063_s_at (AB008103_S_AT)	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]	1E-126		

ProbeSet	Description	Blast Score	EC #	Family
16073_f_at (AF062908_F_AT)	gb AAC83630.1 (AF062908) putative transcription factor [Arabidopsis thaliana]	1E-122		
16080_f_at (AF118822_F_AT)	gb AAD20612.1 (AF118822) senescence-associated protein [Arabidopsis thaliana]	3E-26		
16083_s_at (AF153283_S_AT)	gb AAD34615.1 AF153283_1 (AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]	1E-116		
16087_s_at (ATHATPK6A_S_A T)	dbj BAA07656.1 (D42056) ribosomal-protein S6 kinase homolog [Arabidopsis thaliana]	0		
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]	0		
16092_s_at (ATHKAT1_S_AT)	gb AAA32824.1 (M86990) potassium channel protein [Arabidopsis thaliana]	0		
16103_s_at (ATU60445_S_AT)	gb AAD51782.1 AF145299_1 (AF145299) 14-3-3 protein GF14 nu [Arabidopsis thaliana]	1E-148		
16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]	1E-113		
16108_s_at (D78604_S_AT)	gb AAD03379.1 (AC005967) putative cytochrome P450 [Arabidopsis thaliana]	0		
16130_s_at (AF078683_S_AT)	gb AAC68664.1 (AF078683) RING-H2 finger protein RHA1a [Arabidopsis thaliana]	3E-96		
16133_s_at (AF089810_S_AT)	gb AAF26045.1 AC015986_8 (AC015986) ARG1 protein (Altered Response to Gravity) [Arabidopsis thaliana]	0		
16134_s_at (AF132016_S_AT)	gb AAD33584.1 AF132016_1 (AF132016) RING-H2 zinc finger protein ATL6 [Arabidopsis thaliana]	0		
16159_s_at (ATU37697_S_AT)	gb AAB67841.1 (U37697) glutathione reductase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
16161_s_at (ATU39072_S_AT)	gb AAA91165.1 (U39072) AtGRP2b [Arabidopsis thaliana]	8E-57		
16173_s_at (D78607_S_AT)	dbj BAA28539.1 (D78607) cytochrome P450 monooxygenase [Arabidopsis thaliana]	0		
16203_at (AC007519.53_AT)	gb AAD46036.1 AC007519_2 1 (AC007519) Contains similarity to gb M74161 inositol polyphosphate 5- phosphatase from Homo sapiens and contains a PF 00783 inositol polyphosphate phosphatase catalytic domain. [Arabidopsis thaliana]	0		
16230_at (AL049655.78_AT)	emb CAB41089.1 (AL049655) putative protein [Arabidopsis thaliana]	0		
16232_s_at (AL080252.77_S_AT)	emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana]	1E-119		
16233_at (AL080254.83_AT)	emb CAB45846.1 (AL080254) putative protein [Arabidopsis thaliana]	0		
16236_g_at (X92657.3_G_AT)	emb CAA63346.1 (X92657) cationic amino acid transporter [Arabidopsis thaliana]	1E-37		
16272_at (AC006304.136_AT)	gb AAD20108.1 (AC006304) hypothetical protein [Arabidopsis thaliana]	0		
16288_at (AF024504.17_AT)	gb AAB80790.2 (AF024504) similar to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]	1E-143		hydroxylase
16298_at (AL021890.71_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]	1E-68		
16299_at (AL024486.185_AT)	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]	1E-170		

ProbeSet	Description	Blast Score	EC #	Family
16301_s_at (AL031018.105_S_AT)	emb CAA19807.1 (AL031018) hypothetical protein [Arabidopsis thaliana]	1E-149		
16306_at (AL049751.112_AT)	emb CAB41935.1 (AL049751) putative protein [Arabidopsis thaliana]	0		
16329_s_at (AF013294.17_S_AT)	emb CAA10659.1 (AJ132387) Ca ²⁺ -ATPase [Arabidopsis thaliana] [Arabidopsis thaliana]	0		
16335_at (AL079347.105_AT)	emb CAB45450.1 (AL079347) xanthine dehydrogenase-like protein [Arabidopsis thaliana]	0		dehydro- genase
16340_at (AC004255.15_AT)	gb AAC13905.1 (AC004255) T1F9.15 [Arabidopsis thaliana]	0		
16357_at (AF149413.38_AT)	gb AAD40144.1 AF149413_2 5 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]	0		kinase
16363_at (AC004255.14_AT)	gb AAC13904.1 (AC004255) T1F9.14 [Arabidopsis thaliana]	0		
16383_at (AC006300.64_AT)	gb AAD20719.1 (AC006300) putative disease resistance protein [Arabidopsis thaliana]	0		disease
16391_at (AL050351.194_AT)	emb CAB43642.1 (AL050351) receptor protein kinase-like protein [Arabidopsis thaliana]	0		
16398_s_at (AL022603.3_S_AT)	emb CAA20204.1 (AL031187) serine/threonine kinase-like protein [Arabidopsis thaliana]	0		
16405_at (AC005850.9_AT)	gb AAD25549.1 AC005850_6 (AC005850) Putative serine/threonine kinase [Arabidopsis thaliana]	0		kinase

ProbeSet	Description	Blast Score	EC #	Family
16409_at (AC004393.2_AT)	gb AAC18783.1 (AC004393) Strong similarity to receptor kinase gb M80238 from A.	0		kinase
16440_s_at (AF002109.137_S_A T)	gb AAB95285.1 (AF002109) putative nematode-resistance protein [Arabidopsis thaliana]	0		
16457_s_at (AC005397.17_S_A T)	gb AAD23036.1 AC006526_2 (AC006526) unknown protein [Arabidopsis thaliana]	3E-29		
16461_i_at (AC004683.79_I_AT)	gb AAC28766.1 (AC004683) peroxidase [Arabidopsis thaliana]	0		peroxidase
16462_s_at (AC004683.79_S_A T)	gb AAC28766.1 (AC004683) peroxidase [Arabidopsis thaliana]	0		
16465_at (Y08892.1_AT)	emb CAA70105.1 (Y08892) Hsc70-G8 protein [Arabidopsis thaliana]	4E-46		
16470_s_at (AF068299.4_S_AT)	gb AAD14544.1 (AF068299) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]	0		
16483_at (X68053_AT)	emb CAA48189.1 (X68053) transcription factor [Arabidopsis thaliana]	0		
16496_s_at (AF030386.1_S_AT)	gb AAB86938.1 (AF030386) NOI protein [Arabidopsis thaliana]	1E-30		
16510_at (AL034567.198_AT)	emb CAA22575.1 (AL034567) putative protein [Arabidopsis thaliana]	1E-168		
16522_at (X77500.2_AT)	emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]	0		
16524_at (AC006577.38_AT)	gb AAD25783.1 AC006577_1 9 (AC006577) Strong similarity to gb S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF 00171 Aldehyde dehydrogenase family. ESTs gb T46213, gb T42164, gb T43682, gb N96380, gb T42973, gb Z34663, gb Z4	0		dehydro- genase

ProbeSet	Description	Blast Score	EC #	Family
16526_at (Z49227.1_AT)	emb CAA89201.2 (Z49227) adenine nucleotide translocase [Arabidopsis thaliana]	0		translocase
16538_s_at (AB010259_S_AT)	dbj BAA28347.1 (AB010259) DRH1 [Arabidopsis thaliana]	0		
16541_s_at (AB023423_S_AT)	dbj BAA75015.1 (AB023423) sulfate transporter [Arabidopsis thaliana]	0		
16545_s_at (AF037229_S_AT)	gb AAC60794.1 (AF037229) transcription factor [Arabidopsis thaliana]	0		
16553_f_at (AF078821_F_AT)	gb AAC68670.1 (AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]	2E-93		
16568_s_at (ATHATCDPK_S_AT)	gb AAB03246.1 (U31835) calmodulin-domain protein kinase CDPK isoform 6 [Arabidopsis thaliana]	0		
16570_s_at (ATHCDPKA_S_AT)	gb AAF27092.1 AC011809_1 (AC011809) calcium- dependent protein kinase 1 [Arabidopsis thaliana]	0		
16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3- glucanase 2 (BG2) [Arabidopsis thaliana]	0		
16589_s_at (ATU26937_S_AT)	gb AAD24605.1 AC005825_1 2 (AC005825) putative MYB family transcription factor [Arabidopsis thaliana]	1E-143		
16594_s_at (ATU39783_S_AT)	gb AAB82307.1 (U39783) amino acid transport protein [Arabidopsis thaliana]	0		
16603_s_at (ATU81293_S_AT)	gb AAB58497.1 (U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase [Arabidopsis thaliana]	0		
16609_s_at (AB008104_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]	1E-112		

ProbeSet	Description	Blast Score	EC #	Family
16611_s_at (AB008782_S_AT)	dbj BAA23424.1 (AB008782) sulfate transporter [Arabidopsis thaliana]	0		
16635_s_at (AF126057_S_AT)	emb CAB43670.1 (AL050352) putative protein [Arabidopsis thaliana]	0		
16638_s_at (AF139098_S_AT)	gb AAD37511.1 AF139098_1 (AF139098) putative zinc finger protein [Arabidopsis thaliana]	1E-103		
16646_s_at (ATHDHS1_S_AT)	gb AAA32784.1 (M74819) 3- deoxy-D-arabino- heptulosonate y-phosphate synthase [Arabidopsis thaliana]	0		
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_2 9 (AC012563) putative S- adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O- methyltransferase [Arabidopsis thaliana]	1E-121		
16701_at (AC005312.61_AT)	gb AAC78514.1 (AC005312) putative phloem-specific lectin [Arabidopsis thaliana]	1E-170		
16721_at (AC006533.58_AT)	gb AAD32285.1 AC006533_9 (AC006533) putative poly(ADP-ribose) glycohydrolase [Arabidopsis thaliana]	0		kinase
16747_at (AL021713.3_AT)	emb CAA16788.1 (AL021713) DNA binding- like protein [Arabidopsis thaliana]	0		
16753_at (AL031032.110_AT)	emb CAA19874.1 (AL031032) putative protein [Arabidopsis thaliana]	0		
16781_at (AC002392.100_AT)	gb AAD12030.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]	0		kinase
16810_at (AC002339.46_AT)	gb AAC02763.1 (AC002339) putative polygalacturonase [Arabidopsis thaliana]	0		Polygalactur onase

ProbeSet	Description	Blast Score	EC #	Family
16817_s_at (AL096882.91_S_AT)	emb CAB51412.1 (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]	0		
16859_at (AL035523.135_AT)	emb CAB36742.1 (AL035523) alpha-amylase- like protein [Arabidopsis thaliana]	0		
16864_i_at (AF037367.4_I_AT)	emb CAB66108.1 (AL133248) endo- polygalacturonase [Arabidopsis thaliana]	0		polygalac- turonase
16865_s_at (AF037367.4_S_AT)	emb CAB66108.1 (AL133248) endo- polygalacturonase [Arabidopsis thaliana]	0		
16888_s_at (AC004684.174_S_A T)	gb AAC23647.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]	1E-170		
16902_at (AC007119.67_AT)	gb AAD23643.1 AC007119_9 (AC007119) unknown protein [Arabidopsis thaliana]	6E-91		
16903_g_at (AC007119.67_G_A T)	gb AAD23643.1 AC007119_9 (AC007119) unknown protein [Arabidopsis thaliana]	6E-91		
16908_at (AC002396.22_AT)	gb AAC00577.1 (AC002396) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]	0		
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]	1E-143		
16916_s_at (X77199.8_S_AT)	emb CAA54420.1 (X77199) heat shock cognate 70-2 [Arabidopsis thaliana]	3E-52		
16927_s_at (AF035384.2_S_AT)	gb AAC39467.1 (AF035384) endo-xyloglucan transferase [Arabidopsis thaliana]	2E-65		
16940_g_at (AC002334.110_G_ AT)	gb AAC04922.1 (AC002334) putative synaptobrevin [Arabidopsis thaliana]	1E-123		

ProbeSet	Description	Blast Score	EC #	Family
16951_i_at (AC005662.30_I_AT)	gb AAC78532.1 (AC005662) calmodulin-like protein [Arabidopsis thaliana]	1E-88		
16952_s_at (AC005662.30_S_AT)	gb AAC78532.1 (AC005662) calmodulin-like protein [Arabidopsis thaliana]	1E-88		
16955_at (AL031326.215_AT)	emb CAA20468.1 (AL031326) putative protein [Arabidopsis thaliana]	4E-87		
16968_at (AL021961.93_AT)	emb CAA17559.1 (AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]	0		
16970_s_at (Y18291.5_S_AT)	emb CAA77109.1 (Y18291) uncoupling protein [Arabidopsis thaliana]	1E-175		
16972_at (AC004261.89_AT)	gb AAA87347.1 (M88307) calmodulin [Brassica juncea]	5E-81		
16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	4E-64		
16989_at (AL030978.46_AT)	emb CAA19720.1 (AL030978) GH3 like protein [Arabidopsis thaliana]	0		
16995_at (AC002391.188_AT)	gb AAB87114.1 (AC002391) unknown protein [Arabidopsis thaliana]	0		
17007_at (AC005896.26_AT)	gb AAC98046.1 (AC005896) putative adenylate kinase [Arabidopsis thaliana]	1E-155		kinase
17008_at (AC006585.212_AT)	gb AAD23027.1 AC006585_2 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]	0		transaminase
17009_at (AL021633.163_AT)	emb CAA16537.1 (AL021633) putative protein [Arabidopsis thaliana]	0		
17039_s_at (D78602_S_AT)	dbj BAA28534.1 (D78602) cytochrome P450 monooxygenase [Arabidopsis thaliana]	0		
17041_s_at (D89631_S_AT)	gb AAC14417.1 (AF049236) unknown [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
17051_s_at (AF098947_S_AT)	gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]	0		
17066_s_at (ATHLIPOXY_S_AT)	gb AAA17036.1 (U01843) lipoxygenase 1 [Arabidopsis thaliana]	0		
17073_s_at (ATT54391_S_AT)	gb AAD20078.1 (AC006836) putative steroid sulfotransferase [Arabidopsis thaliana]	1E-162		
17075_s_at (ATU09961_S_AT)	gb AAA19628.1 (U09961) nitrilase [Arabidopsis thaliana]	0		
17083_s_at (ATU18770_S_AT)	gb AAD25838.1 AC006951_1 7 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]	0		
17104_s_at (D88541_S_AT)	dbj BAA13640.1 (D88541) phosphoserine aminotransferase [Arabidopsis thaliana]	0		
17111_s_at (ATHACSC_S_AT)	emb CAA78260.1 (Z12614) 1-aminocyclopropane 1- carboxylate synthase [Arabidopsis thaliana]	0		
17119_s_at (AF132212_S_AT)	gb AAD38925.1 AF132212_1 (AF132212) OPDA-reductase homolog [Arabidopsis thaliana]	0		
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]	1E-94		
17180_at (AF007270.30_AT)	gb AAB61058.1 (AF007270) contains similarity to GATA- type zinc fingers (PS:PS00344) [Arabidopsis thaliana]	0		
17187_at (AF128396.2_AT)	gb AAD17371.1 (AF128396) similar to arginases (Pfam: PF00491, Score=353.2, E=1.4e-119, N=1) [Arabidopsis thaliana]	0		arginase

ProbeSet	Description	Blast Score	EC #	Family
17300_at (X66017.2_AT)	emb CAA46815.1 (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]	0		reductase
17303_s_at (AC004683.25_S_A T)	gb AAC67339.2 (AC005499) putative WRKY-type DNA binding protein [Arabidopsis thaliana]	0		
17323_at (U95973.69_AT)	gb AAB65477.1 (U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]	0		kinase
17338_at (AC002535.97_AT)	gb AAC62855.1 (AC002535) putative pectinesterase [Arabidopsis thaliana]	0		pectin- esterase
17341_at (AL021713.89_AT)	emb CAA16797.1 (AL021713) receptor serine/threonine kinase-like protein [Arabidopsis thaliana]	0		
17352_at (AC007127.33_AT)	gb AAD25140.1 AC007127_6 (AC007127) putative protein kinase [Arabidopsis thaliana]	0		kinase
17356_s_at (Z97338.190_S_AT)	emb CAB10307.1 (Z97338) UTP-glucose glucosyltransferase [Arabidopsis thaliana]	0		
17371_at (AF076243.44_AT)	gb AAD29762.1 AF076243_9 (AF076243) putative receptor- like protein kinase [Arabidopsis thaliana]	0		
17376_at (AL021890.218_AT)	emb CAA17164.1 (AL021890) putative protein [Arabidopsis thaliana]	1E-119		
17379_at (AF085279.9_AT)	gb AAF18728.1 AC018721_3 (AC018721) putative CCCH- type zinc finger protein [Arabidopsis thaliana]	0		
17380_at (AL021961.39_AT)	emb CAA17554.1 (AL021961) putative protein [Arabidopsis thaliana]	0		
17398_at (AC002535.143_AT)	gb AAC62863.1 (AC002535) putative protein disulfide- isomerase [Arabidopsis thaliana]	0		isomerase

ProbeSet	Description	Blast Score	EC #	Family
17413_s_at (AJ006961.4_S_AT)	emb CAA67551.1 (X99097) peroxidase [Arabidopsis thaliana]	2E-84		
17451_at (AC002343.47_AT)	gb AAB63613.1 (AC002343) unknown protein [Arabidopsis thaliana]	0		
17452_g_at (AC002343.47_G_AT)	gb AAB63613.1 (AC002343) unknown protein [Arabidopsis thaliana]	0		
17458_at (AC006260.91_AT)	gb AAD18148.1 (AC006260) unknown protein [Arabidopsis thaliana]	1E-138		
17464_at (AC000132.72_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]	0		kinase
17482_s_at (Z97343.441_S_AT)	emb CAB10533.1 (Z97343) GTP-binding RAB1C like protein [Arabidopsis thaliana]	1E-112		
17484_at (X79052.2_AT)	emb CAA55654.1 (X79052) SRG1 [Arabidopsis thaliana]	0		
17485_s_at (Z97340.345_S_AT)	emb CAB10405.1 (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana]	1E-169		
17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]	1E-158		
17490_s_at (M90416.2_S_AT)	gb AAF01532.1 AC009325_2 (AC009325) homeobox- leucine zipper protein HAT5 (HD-ZIP protein 5) (HD-ZIP protein ATHB-1) [Arabidopsis thaliana]	4E-52		
17500_s_at (ATHCALLGA_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]	6E-99		
17511_s_at (AF067605_S_AT)	gb AAB71482.1 (AC002294) similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
17514_s_at (AF076277_S_AT)	gb AAD03545.1 (AF076278) ethylene response factor 1 [Arabidopsis thaliana]	1E-104		
17516_s_at (AF072536_S_AT)	gb AAC24592.1 (AF072536) H-protein promoter binding factor-1 [Arabidopsis thaliana]	0		
17522_s_at (D78606_S_AT)	dbj BAA28538.1 (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]	0		
17533_s_at (ATU43488_S_AT)	gb AAB18367.1 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]	1E-171		
17544_s_at (ATU40856_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]	1E-150		
17548_s_at (AF118823_S_AT)	gb AAD20613.1 (AF118823) senescence-associated protein [Arabidopsis thaliana]	2E-26		
17578_at (AF093604_AT)	gb AAF00071.1 AF093604_1 (AF093604) apyrase [Arabidopsis thaliana]	0		
17585_s_at (AF134487_S_AT)	emb CAA06460.1 (AJ005261) cytidine deaminase [Arabidopsis thaliana]	1E-168		
17595_s_at (AF166352_S_AT)	gb AAC28764.1 (AC004683) putative beta-alanine-pyruvate aminotransferase [Arabidopsis thaliana]	0		
17636_at (AF077409.7_AT)	gb AAC28219.1 (AF077409) contains similarity to C3HC4- type zinc fingers (Pfam: zf- C3HC4.hmm, score: 32.94) [Arabidopsis thaliana]	1E-138		
17648_at (AL021684.43_AT)	emb CAA16674.1 (AL021684) predicted protein [Arabidopsis thaliana]	0		
17653_at (AL035679.144_AT)	emb CAB38823.1 (AL035679) putative protein [Arabidopsis thaliana]	0		
17702_at (AC005700.212_AT)	gb AAC69951.1 (AC005700) Mutator-like transposase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
17719_at (AC006592.17_AT)	gb AAD22346.1 AC006592_3 (AC006592) hypothetical protein [Arabidopsis thaliana]	0		
17744_s_at (AC004684.168_S_A T)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]	1E-170		
17752_at (AC003974.37_AT)	gb AAC04483.1 (AC003974) putative protein kinase [Arabidopsis thaliana]	0		kinase
17758_at (AF076243.41_AT)	gb AAD29761.1 AF076243_8 (AF076243) putative receptor- like protein kinase [Arabidopsis thaliana]	0		
17775_at (AC004392.2_AT)	gb AAC28500.1 (AC004392) Similar to glucose-6- phosphate/phosphate- translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]	0		
17781_at (AL049746.177_AT)	emb CAB41861.1 (AL049746) ABC transporter- like protein [Arabidopsis thaliana]	0		
17840_s_at (AC002333.223_S_A T)	gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]	1E-161		
17854_at (Z99707.366_AT)	emb CAB16762.1 (Z99707) caltractin-like protein [Arabidopsis thaliana]	1E-91		
17860_at (AL078467.4_AT)	emb CAB43873.1 (AL078467) putative protein [Arabidopsis thaliana]	1E-177		
17876_at (AJ007587.2_AT)	emb CAA07574.1 (AJ007587) monooxygenase [Arabidopsis thaliana]	0		mono- oxygenase
17877_g_at (AJ007587.2_G_AT)	emb CAA07574.1 (AJ007587) monooxygenase [Arabidopsis thaliana]	0		
17881_at (AC002391.54_AT)	gb AAB87100.1 (AC002391) putative WRKY-type DNA- binding protein [Arabidopsis thaliana]	1E-133		

ProbeSet	Description	Blast Score	EC #	Family
17882_at (AL035523.49_AT)	emb CAB36734.1 (AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT- like [Arabidopsis thaliana]	1E-24		
17893_at (AC004401.135_AT)	gb AAC17827.1 (AC004401) similar to late embryogenesis abundant proteins [Arabidopsis thaliana]	2E-43		
17894_at (AC005724.44_AT)	gb AAD08938.1 (AC005724) unknown protein [Arabidopsis thaliana]	1E-147		
17899_at (Z97339.197_AT)	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]	5E-55		
17900_s_at (AC000106.13_S_A T)	gb AAB70401.1 (AC000106) Similar to Glycine SRC2 (gb AB000130). ESTs gb H76869,gb T21700,gb ATT S5089 come from this gene. [Arabidopsis thaliana]	2E-97		
17907_s_at (AC004684.165_S_A T)	gb AAC23645.1 (AC004684) unknown protein [Arabidopsis thaliana]	4E-24		
17930_s_at (AJ006960.4_S_AT)	emb CAA07352.1 (AJ006960) peroxidase [Arabidopsis thaliana]	1E-111		
17945_at (Z97341.411_AT)	emb CAB10448.1 (Z97341) limonene cyclase like protein [Arabidopsis thaliana]	0		
17955_at (AL021768.242_AT)	emb CAA16940.1 (AL021768) small GTP- binding protein-like [Arabidopsis thaliana]	1E-110		
17956_i_at (AC005967.32_I_AT)	gb AAD03381.1 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]	0	EC_3.4.11.1	amino- peptidase
17963_at (AL049730.88_AT)	emb CAB41717.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]	6E-46		
17967_at (AL096859.32_AT)	emb CAB51172.1 (AL096859) protein kinase 6- like protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
18010_s_at (AJ001264_S_AT)	emb CAA77109.1 (Y18291) uncoupling protein [Arabidopsis thaliana]	1E-175		
18012_s_at (AJ002295_S_AT)	emb CAB59428.1 (AJ002295) inositol-1,4,5- trisphosphate 5-Phosphatase [Arabidopsis thaliana]	0		
18045_at (AJ011976_AT)	emb CAA71798.1 (Y10845) O-acetylserine(thiol) lyase [Brassica juncea]	1E-148		
18054_at (AJ238846_AT)	emb CAB54517.1 (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]	1E-150		
18109_s_at (AC002391.206_S_A T)	gb AAB87118.1 (AC002391) putative metal ion transporter (NRAMP) [Arabidopsis thaliana]	0		
18121_s_at (AC002337.21_S_A T)	gb AAB63819.1 (AC002337) MYB transcription factor (Atmyb2) [Arabidopsis thaliana]	1E-167		
18122_at (AC002338.110_AT)	gb AAC16938.1 (AC002338) putative protein kinase [Arabidopsis thaliana]	0		kinase
18140_at (Z97341.319_AT)	emb CAB10440.1 (Z97341) growth regulator like protein [Arabidopsis thaliana]	0		
18148_at (AC004669.25_AT)	gb AAC20719.1 (AC004669) putative dioxygenase [Arabidopsis thaliana]	0		
18176_at (AL035540.31_AT)	emb CAB37503.1 (AL035540) protein kinase like protein [Arabidopsis thaliana]	0		kinase
18194_i_at (AL096859.227_I_A T)	emb CAB51196.1 (AL096859) glucuronosyl transferase-like protein [Arabidopsis thaliana]	0		glucosyl- transferase
18213_at (AL022140.126_AT)	emb CAA18110.1 (AL022140) putative protein [Arabidopsis thaliana]	1E-174		
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_2 2 (AC012375) T22C5.18 [Arabidopsis thaliana]	1E-119		

ProbeSet	Description	Blast Score	EC #	Family
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_2 2 (AC012375) T22C5.18 [Arabidopsis thaliana]	1E-119		
18224_s_at (AL021890.57_S_AT)	emb CAA17150.1 (AL021890) putative protein [Arabidopsis thaliana]	4E-81		
18226_s_at (AC002343.142_S_AT)	emb CAB51645.1 (AL109619) putative protein [Arabidopsis thaliana]	0		
18228_at (X91259.1_AT)	emb CAA62665.1 (X91259) lectin like protein [Arabidopsis thaliana]	1E-142		
18234_at (AC000348.3_AT)	gb AAB61479.1 (AC000348) T7N9.3 [Arabidopsis thaliana]	1E-154		
18236_s_at (AC004683.69_S_AT)	gb AAC28764.1 (AC004683) putative beta-alanine-pyruvate aminotransferase [Arabidopsis thaliana]	0		
18241_at (AC006580.71_AT)	gb AAD21720.1 (AC006931) putative RNA-binding protein [Arabidopsis thaliana]	0		
18242_g_at (AC006580.71_G_AT)	gb AAD21720.1 (AC006931) putative RNA-binding protein [Arabidopsis thaliana]	0		
18255_at (AC005770.25_AT)	gb AAC79625.1 (AC005770) unknown protein [Arabidopsis thaliana]	0		
18258_s_at (AC006439.222_S_AT)	gb AAD15515.1 (AC006439) unknown protein [Arabidopsis thaliana]	4E-58		
18263_at (AC005724.36_AT)	gb AAD08937.1 (AC005724) unknown protein [Arabidopsis thaliana]	1E-139		
18266_at (AC004684.33_AT)	gb AAC23628.1 (AC004684) unknown protein [Arabidopsis thaliana]	0		
18267_at (AC006223.23_AT)	gb AAD15384.1 (AC006223) unknown protein [Arabidopsis thaliana]	2E-38		
18268_s_at (AC006418.38_S_AT)	gb AAD20161.1 (AC006418) putative ubiquitin [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
18280_at (AC007369.2_AT)	gb AAD30591.1 AC007369_1 (AC007369) Unknown protein [Arabidopsis thaliana]	1E-135		
18284_at (AL021961.67_AT)	emb CAA17557.1 (AL021961) putative protein [Arabidopsis thaliana]	6E-97		
18287_at (AC007661.142_AT)	gb AAD32777.1 AC007661_1 4 (AC007661) unknown protein [Arabidopsis thaliana]	0		
18299_s_at (M23872.2_S_AT)	gb AAA32878.1 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]	0		
18314_i_at (AL078579.83_I_AT)	emb CAB43971.1 (AL078579) putative beta- glucosidase [Arabidopsis thaliana]	0		
18348_at (AL022603.104_AT)	emb CAA18711.1 (AL022603) putative protein [Arabidopsis thaliana]	1E-160		
18456_s_at (AC004697.159_S_A T)	gb AAC28997.1 (AC004697) similar to Mlo proteins from H. vulgare [Arabidopsis thaliana]	0		
18508_s_at (AC006532.89_S_A T)	gb AAA33709.1 (L16797) glutamate decarboxylase [Petunia x hybrida]	0		
18544_at (AC007060.14_AT)	gb AAD25749.1 AC007060_7 (AC007060) Strong similarity to F19I3.8 gi 3033381 putative UDP-galactose-4-epimerase from Arabidopsis thaliana BAC gb AC004238 and is a member of PF 01370 the NAD dependent epimerase/dehydratase family. EST gb AA597338 comes fro	0	EC_5.1.3.2	epimerase
18582_s_at (AC003671.36_S_A T)	gb AAC18810.1 (AC003671) Strong similarity to trehalose- 6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb Z97344. ESTs gb H37594, gb R65023, gb H37578 and gb R64855 come from this gene. [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
18587_s_at (AC007166.53_S_AT)	gb AAF18667.1 AC007166_9 (AC007166) unknown protein [Arabidopsis thaliana]	0		
18590_at (AJ222713.4_AT)	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]	1E-151		
18591_at (X74756.2_AT)	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana]	2E-99		
18596_at (AC005698.13_AT)	gb AAD43614.1 AC005698_1 3 (AC005698) T3P18.13 [Arabidopsis thaliana]	0		
18597_at (AL080282.74_AT)	emb CAB45881.1 (AL080282) berberine bridge enzyme-like protein [Arabidopsis thaliana]	0		
18601_s_at (AC002387.279_S_AT)	gb AAF18602.1 AC002387_1 (AC002387) putative microtubule-associated protein [Arabidopsis thaliana]	8E-45		
18604_at (AF069298.31_AT)	gb AAC19273.1 (AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3- acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]	3E-82		
18622_g_at (AJ005902.2_G_AT)	emb CAA06759.1 (AJ005902) vag2 [Arabidopsis thaliana]	3E-47		
18625_at (AC005278.22_AT)	gb AAC72125.1 (AC005278) ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana]	0		
18631_at (AC002510.112_AT)	gb AAB84346.1 (AC002510) unknown protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
18636_at (AC006577.22_AT)	gb AAD25775.1 AC006577_1 (AC006577) Belongs to the PF00657 Lipase/Acylhydrolase with GDSE-motif family. ESTs gb T75865, gb R30449, gb AI239373, gb F19931 and gb F19930 come from this gene. [Arabidopsis thaliana]	0		
18650_s_at (AF013294.25_S_AT)	gb AAB62867.1 (AF013294) AT0Z11 gene product [Arabidopsis thaliana]	3E-41		
18662_s_at (AC002343.20_S_AT)	gb AAB63608.1 (AC002343) unknown protein [Arabidopsis thaliana]	0		
18668_at (AJ249794_AT)	emb CAB56692.1 (AJ249794) lipoxygenase [Arabidopsis thaliana]	0		
18681_at (L23573_AT)	gb AAD02548.1 (AF049922) PGP169-12 [Petunia x hybrida]	8E-94		
18686_s_at (U18126_S_AT)	gb AAA57314.1 (U18126) inner mitochondrial membrane protein [Arabidopsis thaliana]	2E-78		
18698_s_at (X17528_S_AT)	emb CAA35570.1 (X17528) citrate synthetase [Arabidopsis thaliana]	0		
18720_s_at (X92419_S_AT)	emb CAB52583.1 (X92420) SNAP25AB protein [Arabidopsis thaliana]	1E-157		
18735_s_at (Z29490_S_AT)	emb CAA82626.1 (Z29490) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]	0		
18753_s_at (AF118222.28_S_AT)	gb AAD03425.1 (AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85, N=1) [Arabidopsis thaliana]	0		
18782_at (AC003040.90_AT)	gb AAC23760.1 (AC003040) putative protein kinase [Arabidopsis thaliana]	0		kinase

ProbeSet	Description	Blast Score	EC #	Family
18803_at (AC005315.94_AT)	gb AAC33232.1 (AC005315) putative SCARECROW gene regulator [Arabidopsis thaliana]	0		
18885_at (AC006921.147_AT)	gb AAD21443.1 (AC006921) unknown protein [Arabidopsis thaliana]	1E-126		
18888_at (AC007591.68_AT)	gb AAD39666.1 AC007591_3 1 (AC007591) Is a member of the PF 00903 glyoxalase family. ESTs gb T44721, gb T21844 and gb AA395404 come from this gene. [Arabidopsis thaliana]	1E-101		
18899_s_at (X13434.1_S_AT)	emb CAA79494.1 (Z19050) nitrate reductase [Arabidopsis thaliana]	0		
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]	0		protease
18909_s_at (AF055848.2_S_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]	0		
18928_at (AC002333.181_AT)	gb AAB64044.1 (AC002333) putative endochitinase [Arabidopsis thaliana]	1E-157		endo- chitinase
18930_at (AC005990.57_AT)	gb AAC98028.1 (AC005990) Similar to gb L19255 carbonic anhydrase from Nicotiana tabacum and a member of the prokaryotic-type carbonic anhydrase family PF 00484. EST gb Z235745 comes from this gene. [Arabidopsis thaliana]	1E-149		anhydrase
18933_at (AC007020.48_AT)	gb AAD25665.1 AC007020_7 (AC007020) putative ferritin [Arabidopsis thaliana]	1E-129		
18936_at (AJ003119.4_AT)	emb CAA05875.1 (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]	0	EC_3.1.3.16	phosphatase
18949_at (Z54136.1_AT)	emb CAA90809.1 (Z54136) MYB-related protein [Arabidopsis thaliana]	1E-145		

ProbeSet	Description	Blast Score	EC #	Family
18953_at (AF077955.1_AT)	gb AAC69851.1 (AF077955) branched-chain alpha keto- acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]	0		dehydro- genase
18963_at (AC004561.99_AT)	gb AAC95194.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-127		transferase
18966_at (AC004561.106_AT)	gb AAC95196.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-128		transferase
18980_at (U78721.20_AT)	gb AAC69126.1 (U78721) putative protein phosphatase 2C [Arabidopsis thaliana]	0	EC_3.1.3.16	phosphatase
19019_i_at (X82623.2_I_AT)	emb CAA57943.1 (X82623) SRG2At [Arabidopsis thaliana]	7E-33		
19060_at (AC003671.34_AT)	gb AAC18809.1 (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana]	0		
19092_at (AL078606.188_AT)	emb CAB44327.1 (AL078606) protein kinase- like protein [Arabidopsis thaliana]	0		kinase
19110_s_at (X86947.2_S_AT)	emb CAA60510.1 (X86947) Protein Kinase catalytic domain (fragment) [Arabidopsis thaliana]	4E-27		
19132_s_at (AL022603.298_S_A T)	emb CAA18722.1 (AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]	0		
19137_at (X74755.2_AT)	emb CAA52771.1 (X74755) ATAF1 [Arabidopsis thaliana]	1E-138		
19140_at (AC005170.24_AT)	gb AAC63657.1 (AC005170) unknown protein [Arabidopsis thaliana]	9E-83		

ProbeSet	Description	Blast Score	EC #	Family
19161_at (AL078579.9_AT)	emb CAB43966.1 (AL078579) putative acyl-CoA binding protein [Arabidopsis thaliana]	0		
19171_at (AC002335.160_AT)	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]	7E-40		
19178_at (Y18227.2_AT)	dbj BAA86999.1 (AB035137) blue copper binding protein [Arabidopsis thaliana]	2E-57		
19181_s_at (AF053065.2_S_AT)	gb AAC39464.1 (AF053065) late embryogenesis abundant protein homolog [Arabidopsis thaliana]	3E-34		
19182_at (AL031804.245_AT)	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]	0		
19207_at (AC006069.117_AT)	gb AAD12704.1 (AC006069) unknown protein [Arabidopsis thaliana]	1E-104		
19230_at (AC003113.15_AT)	gb AAB96860.1 (AC003113) F25O1.15 [Arabidopsis thaliana]	1E-134		
19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]	0		
19257_s_at (AC000104.57_S_AT)	emb CAA44318.1 (X62461) H1flk [Arabidopsis thaliana] [Arabidopsis thaliana]	0		
19284_at (AC003028.196_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]	0		
19288_at (AC005824.130_AT)	gb AAC73031.1 (AC005824) putative cytochrome P450 [Arabidopsis thaliana]	0		
19325_at (AL022604.42_AT)	emb CAA18731.1 (AL022604) putative protein [Arabidopsis thaliana]	0		
19364_at (AL022023.142_AT)	emb CAA17779.1 (AL022023) putative protein [Arabidopsis thaliana]	1E-126		

ProbeSet	Description	Blast Score	EC #	Family
19376_at (AF024504.11_AT)	gb AAB80784.2 (AF024504) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]	0		peptidase
19383_at (AC006200.203_AT)	gb AAD14534.1 (AC006200) unknown protein [Arabidopsis thaliana]	1E-101		
19395_at (AF007270.32_AT)	gb AAB61059.1 (AF007270) contains similarity to DNA polymerase III, alpha chain (SP:P47277) [Arabidopsis thaliana]	1E-179		polymerase
19405_at (AJ223803.1_AT)	emb CAA11553.1 (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit [Arabidopsis thaliana]	0	EC_2.3.1.61	succinyl- transferase
19407_at (AC004697.81_AT)	gb AAC28981.1 (AC004697) putative adenylate kinase [Arabidopsis thaliana]	1E-142	EC_2.7.4.3	kinase
19409_at (AC007357.56_AT)	gb AAD31077.1 AC007357_2 6 (AC007357) EST gb T21221 comes from this gene. [Arabidopsis thaliana]	2E-17		
19411_at (AC007661.104_AT)	gb AAD32774.1 AC007661_1 1 (AC007661) unknown protein [Arabidopsis thaliana]	1E-110		
19421_at (X70990.4_AT)	emb CAA50317.1 (X70990) sucrose synthase [Arabidopsis thaliana]	0		synthase
19432_s_at (AL035680.11_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta- subunit [Arabidopsis thaliana]	0		
19451_at (AC004392.6_AT)	gb AAC28502.1 (AC004392) Similar to F4I1.26 putative beta-glucosidase gi 3128187 from A. thaliana BAC gb AC004521. ESTs gb N97083, gb F19868 and gb F15482 come from this gene. [Arabidopsis thaliana]	0		glucosidase
19460_s_at (AC000132.66_S_A T)	gb AAB60749.1 (AC000132) Identical to A. thaliana HEMA2 (gb U27118). [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
19462_s_at (AF001168.2_S_AT)	emb CAB75467.1 (AL138659) serine/threonine-specific kinase lecRK1 precursor, lectin	0		
19464_at (AC005560.51_AT)	gb AAC67338.1 (AC005560) putative MAP kinase [Arabidopsis thaliana]	0	EC_2.7.1.37	kinase
19465_at (AL021768.96_AT)	emb CAA16929.1 (AL021768) resistance protein RPP5-like [Arabidopsis thaliana]	0		
19531_at (AL021960.91_AT)	emb CAA17531.1 (AL021960) amino acid transport protein AAT1 [Arabidopsis thaliana]	0		
19546_at (AC005398.172_AT)	gb AAC69380.1 (AC005398) putative endoxyloglucan glycosyltransferase [Arabidopsis thaliana]	0		transferase
19555_at (AF058919.48_AT)	gb AAC13630.1 (AF058919) F6N23.8 gene product [Arabidopsis thaliana]	0		
19591_at (AJ010735.4_AT)	emb CAA09330.1 (AJ010735) gr1-protein [Arabidopsis thaliana]	0	EC_3.5.-.-	amido-hydrolase
19614_at (AC003970.32_AT)	gb AAC33210.1 (AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi 1143445 [Arabidopsis thaliana]	0		dehydro-genase
19623_at (AF000657.40_AT)	gb AAB72175.1 (AF000657) cytochrome C [Arabidopsis thaliana]	2E-63		
19624_at (AL049481.196_AT)	emb CAB39628.1 (AL049481) cytochrome c [Arabidopsis thaliana]	4E-63		
19625_s_at (AC002311.26_S_A T)	gb AAC00610.1 (AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]	0		
19635_at (AL049746.38_AT)	emb CAB41856.1 (AL049746) ABC-type transport-like protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
19639_at (AL080252.22_AT)	emb CAB45788.1 (AL080252) putative protein [Arabidopsis thaliana]	0		
19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-118		transferase
19641_at (AC004561.66_AT)	gb AAC95189.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-128		transferase
19645_at (AC004561.70_AT)	gb AAC95190.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-130		transferase
19646_s_at (AC005819.55_S_A T)	gb AAC69925.1 (AC005819) homeodomain transcription factor (ATHB-7) [Arabidopsis thaliana]	9E-57		
19655_at (Y14199.1_AT)	emb CAA74591.1 (Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]	0		kinase
19667_at (AL021710.5_AT)	emb CAA16716.1 (AL021710) glycolate oxidase - like protein [Arabidopsis thaliana]	0	EC_1.1.2.3	dehydro- genase
19672_at (AC005687.19_AT)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]	1E-105		
19673_g_at (AC005687.19_G_A T)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]	1E-105		
19700_s_at (AL031326.154_S_A T)	emb CAA20463.1 (AL031326) putative protein [Arabidopsis thaliana]	8E-85		
19701_s_at (AC005724.67_S_A T)	gb AAD08939.1 (AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]	0		
19704_i_at (AJ005927.2_I_AT)	emb CAA06769.1 (AJ005927) squalene epoxidase homologue [Arabidopsis thaliana]	0		epoxidase

ProbeSet	Description	Blast Score	EC #	Family
19707_s_at (Z95768.3_S_AT)	emb CAB09200.1 (Z95768) R2R3-MYB transcription factor [Arabidopsis thaliana]	4E-21		
19741_at (AL049171.72_AT)	emb CAB38956.1 (AL049171) pyrophosphate- dependent phosphofructo-1- kinase [Arabidopsis thaliana]	0		kinase
19755_at (AC006593.64_AT)	gb AAD20668.1 (AC006593) ethylene reponse factor-like AP2 domain transcription factor [Arabidopsis thaliana]	8E-97		
19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]	0		
19818_i_at (AL021749.33_I_AT)	emb CAA16876.2 (AL021749) hypothetical protein [Arabidopsis thaliana]	0		
19819_s_at (AL021749.33_S_AT)	emb CAA16876.2 (AL021749) hypothetical protein [Arabidopsis thaliana]	0		
19844_at (AJ007588.2_AT)	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]	0		mono- oxygenase
19845_g_at (AJ007588.2_G_AT)	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]	0		
19848_s_at (AC004261.94_S_A T)	dbj BAA08282.1 (D45848) calmodulin-related protein [Arabidopsis thaliana]	0		
19851_at (U23794.3_AT)	gb AAB60293.1 (U23794) ILR1 [Arabidopsis thaliana]	0	EC_3.5.-.-	amido- hydrolase
19878_at (AL080252.102_AT)	emb CAB45799.1 (AL080252) nodulin-like protein [Arabidopsis thaliana]	0		
19879_s_at (Z97338.342_S_AT)	emb CAB10321.1 (Z97338) UFD1 like protein [Arabidopsis thaliana]	0		
19881_at (AC004077.49_AT)	gb AAC26705.1 (AC004077) putative trans- prenyltransferase [Arabidopsis thaliana]	1E-154		synthetase

ProbeSet	Description	Blast Score	EC #	Family
19892_at (AC005770.30_AT)	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]	2E-36		protease
19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]	0		dehydro- genase
19895_s_at (U77347.4_S_AT)	gb AAC49679.1 (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]	0		
19916_at (AC006577.34_AT)	gb AAD25781.1 AC006577_1 7 (AC006577) EST gb R64848 comes from this gene. [Arabidopsis thaliana]	0		
19944_at (AC002130.4_AT)	gb AAB95233.1 (AC002130) FIN21.4 [Arabidopsis thaliana]	1E-128		
19946_at (AC004482.14_AT)	gb AAF18611.1 AC005170_1 (AC005170) similar to senescence-associated protein [Arabidopsis thaliana]	4E-92		
19956_at (AC006282.11_AT)	gb AAD20139.1 (AC006282) unknown protein [Arabidopsis thaliana]	1E-123		
19960_at (AL035527.360_AT)	emb CAB36823.1 (AL035527) putative protein [Arabidopsis thaliana]	1E-128		
19970_s_at (AC003674.10_S_A T)	gb AAB97120.1 (AC003674) unknown protein [Arabidopsis thaliana]	1E-154		
19982_at (AC002986.28_AT)	gb AAC17040.1 (AC002986) Similarity to A. thaliana gene product F21M12.20, gb AC000132. EST gb Z25651 comes from this gene. [Arabidopsis thaliana]	0		
19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]	1E-112		
20017_at (AC004521.66_AT)	gb AAC16079.1 (AC004521) unknown protein [Arabidopsis thaliana]	1E-101		

ProbeSet	Description	Blast Score	EC #	Family
20023_at (AC006577.46_AT)	gb AAD25787.1 AC006577_2 3 (AC006577) Similar to gi 1653162 (p)ppGpp 3- pyrophosphohydrolase from Synechocystis sp genome gb D90911. EST gb W43807 comes from this gene. [Arabidopsis thaliana]	0	EC_2.7.6.5	pyro- phospho- kinase
20030_at (AL078637.51_AT)	emb CAB45058.1 (AL078637) putative protein [Arabidopsis thaliana]	1E-168		
20051_at (AC000106.38_AT)	gb AAB70412.1 (AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb Z49209). ESTs gb T44436,gb 42252 come from this gene. [Arabidopsis thaliana]	1E-166		
20053_at (AC002292.27_AT)	gb AAB71973.1 (AC002292) Unknown protein [Arabidopsis thaliana]	0		
20096_at (AC004238.31_AT)	gb AAC12821.1 (AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]	0		
20098_at (AC004697.123_AT)	gb AAC28986.1 (AC004697) similar to latex allergen from Hevea brasiliensis [Arabidopsis thaliana]	0		
20133_i_at (AC007178.71_I_AT)	gb AAD28682.1 AC007178_2 (AC007178) hypothetical protein [Arabidopsis thaliana]	0		
20134_s_at (AC007178.71_S_A T)	gb AAD28682.1 AC007178_2 (AC007178) hypothetical protein [Arabidopsis thaliana]	0		
20142_at (AL035521.155_AT)	emb CAB36716.1 (AL035521) extra-large G- protein-like [Arabidopsis thaliana]	0		
20144_at (AL079350.68_AT)	emb CAB45516.1 (AL079350) receptor kinase- like protein [Arabidopsis thaliana]	0		kinase
20165_at (AC002311.16_AT)	gb AAC00605.1 (AC002311) Unknown protein [Arabidopsis thaliana]	6E-75		

ProbeSet	Description	Blast Score	EC #	Family
20179_at (AL035538.229_AT)	emb CAB37546.1 (AL035538) putative protei [Arabidopsis thaliana]	2E-63		
20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]	2E-57		
20194_at (AC007584.48_AT)	gb AAD32907.1 AC007584_5 (AC007584) unknown protein [Arabidopsis thaliana]	0		
20200_at (AL050400.67_AT)	emb CAB43700.1 (AL050400) hypothetical protein [Arabidopsis thaliana]	4E-95		
20215_s_at (AF117125.2_S_AT)	gb AAD29957.1 (AF117125) endoplasmic reticulum-type calcium-transporting ATPase 4 [Arabidopsis thaliana]	0		
20223_at (AL022347.145_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]	0		kinase
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]	0	EC_3.2.1.26	hydrolase
20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]	0		
20245_s_at (AC005309.97_S_A T)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]	0		
20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]	0		
20247_at (AC004392.4_AT)	gb AAC28501.1 (AC004392) Similar to beta-glucosidase BGQ60 precursor gb L41869 from Hordeum vulgare. [Arabidopsis thaliana]	0	EC_3.2.1.21	glucosidase
20258_at (AF130252.1_AT)	gb AAD28759.1 AF130252_1 (AF130252) calcium dependent protein kinase CP4 [Arabidopsis thaliana]	0		kinase

ProbeSet	Description	Blast Score	EC #	Family
20262_at (AC002294.26_AT)	gb AAB71480.1 (AC002294) Similar to transcription factor gb Z46606 1658307 and others [Arabidopsis thaliana]	0		
20263_at (AB004798.1_AT)	dbj BAA20519.1 (AB004798) ascorbate oxidase [Arabidopsis thaliana]	0		oxidase
20269_at (AC002387.237_AT)	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]	0		pectin- esterase
20271_at (Z99707.27_AT)	emb CAB16771.1 (Z99707) cytochrome P450-like protein [Arabidopsis thaliana]	0		
20285_s_at (AC003674.18_S_A T)	gb AAB97121.1 (AC003674) putative protein kinase [Arabidopsis thaliana]	0		
20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]	1E-166		chitinase
20288_g_at (Y14590.5_G_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]	1E-166		
20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]	0		
20297_at (AC007153.27_AT)	gb AAD30627.1 AC007153_1 9 (AC007153) Similar to indole-3-acetate beta- glucosyltransferase [Arabidopsis thaliana]	0		glucosyl- transferase
20323_at (AC004561.62_AT)	gb AAC95188.1 (AC004561) putative small heat shock protein [Arabidopsis thaliana]	1E-67		
20346_at (AL031135.156_AT)	emb CAA20030.1 (AL031135) protein kinase - like protein [Arabidopsis thaliana]	0		
20348_at (AC005967.35_AT)	gb AAD03382.1 (AC005967) putative limonene cyclase [Arabidopsis thaliana]	0		cyclase
20356_at (AC004561.74_AT)	gb AAC95191.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-128		transferase

ProbeSet	Description	Blast Score	EC #	Family
20365_s_at (AC005850.19_S_A T)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]	0		
20370_at (AC004561.263_AT)	gb AAC95219.1 (AC004561) putative tropinone reductase [Arabidopsis thaliana]	1E-151		reductase
20382_s_at (AC002338.35_S_A T)	gb AAC16930.1 (AC002338) putative WRKY-type DNA binding protein [Arabidopsis thaliana]	0		
20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]	0		chitinase
20421_at (US1294.2_AT)	emb CAB10242.1 (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]	8E-98		
20422_g_at (U81294.2_G_AT)	emb CAB10242.1 (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]	8E-98		
20432_at (U43486.2_AT)	gb AAB18365.1 (U43486) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]	1E-174		trans- glycosylase
20433_at (AC006232.147_AT)	gb AAD15611.1 (AC006232) putative beta-1,3-glucanase [Arabidopsis thaliana]	0		glucanase
20450_at (AJ005930.2_AT)	emb CAA06772.1 (AJ005930) squalene epoxidase homologue [Arabidopsis thaliana]	0		epoxidase
20461_at (AL049480.157_AT)	emb CAB39609.1 (AL049480) pumilio-like protein [Arabidopsis thaliana]	0		
20462_at (U82399.2_AT)	gb AAB40725.1 (U82399) putative protein kinase PK1 [Arabidopsis thaliana]	3E-38		kinase
20479_i_at (AF069495.2_I_AT)	emb CAB38908.1 (AL035708) cytochrome P450-like protein [Arabidopsis thaliana]	0		
20480_s_at (AF069495.2_S_AT)	emb CAB38908.1 (AL035708) cytochrome P450-like protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
20485_at (AC007660.131_AT)	gb AAD32811.1 AC007660_1 2 (AC007660) putative two- component response regulator protein [Arabidopsis thaliana]	1E-80		
20491_at (AC004561.146_AT)	gb AAC95203.1 (AC004561) putative tropinone reductase [Arabidopsis thaliana]	1E-153	EC_1.1.1.10 0	reductase
20511_at (AC007290.24_AT)	gb AAD26884.1 AC007290_3 (AC007290) putative nucleotide-binding protein [Arabidopsis thaliana]	0		
20517_at (Y17722.7_AT)	emb CAB50690.1 (Y17722) telomere repeat-binding protein TRP1 [Arabidopsis thaliana]	0		
20529_at (Z97341.125_AT)	emb CAB10426.1 (Z97341) cysteine proteinase inhibitor like protein [Arabidopsis thaliana]	7E-35		
20551_at (AC006081.211_AT)	gb AAD24395.1 AC006081_7 (AC006081) unknown protein [Arabidopsis thaliana]	0		
20572_s_at (AC005560.229_S_A T)	gb AAD12710.1 (AC006069) unknown protein [Arabidopsis thaliana]	1E-114		
20577_at (AL078464.72_AT)	emb CAB43841.1 (AL078464) putative protein [Arabidopsis thaliana]	0		
20584_at (AC004450.75_AT)	gb AAC64305.1 (AC004450) putative clathrin binding protein (epsin) [Arabidopsis thaliana]	2E-92		
20586_i_at (AC005824.195_I_A T)	gb AAC73042.1 (AC005824) unknown protein [Arabidopsis thaliana]	2E-67		
20587_s_at (AC005824.195_S_A T)	gb AAC73042.1 (AC005824) unknown protein [Arabidopsis thaliana]	2E-67		
20589_at (AF081066.3_AT)	gb AAC31939.1 (AF081066) IAA-amino acid hydrolase homolog ILL3 [Arabidopsis thaliana]	0		hydrolase
20591_at (AL080252.115_AT)	emb CAB45800.1 (AL080252) nodulin-like protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
20646_at (AC002291.20_AT)	gb AAC00619.1 (AC002291) Unknown protein [Arabidopsis thaliana]	0		
20656_at (AL035396.46_AT)	emb CAA23064.1 (AL035396) putative protein [Arabidopsis thaliana]	0		
20658_s_at (AL050400.70_S_AT)	emb CAB43701.1 (AL050400) beta-carotene hydroxylase [Arabidopsis thaliana]	1E-165		
20669_s_at (AC002388.6_S_AT)	gb AAD32838.1 AC007659_2 0 (AC007659) unknown protein [Arabidopsis thaliana]	0		
20685_at (AL049751.46_AT)	emb CAB41928.1 (AL049751) short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana]	1E-139	EC_1.1.1.-	dehydro- genase
20686_at (Y14424.2_AT)	emb CAA74766.1 (Y14424) hypothetical protein [Arabidopsis thaliana]	0		
20689_s_at (AC002335.19_S_A T)	gb AAB64310.1 (AC002335) putative calcium binding protein [Arabidopsis thaliana]	6E-95		
20715_at (AF079183.1_AT)	gb AAC69857.1 (AF079183) RING-H2 finger protein RHG1a [Arabidopsis thaliana]	4E-99		

Table 4a Probe Sets in addition to those in Table 4b corresponding to genes, the expression of which is induced by *Pseudomonas* infection in wild-type *Arabidopsis* plants and perturbed in at least one mutant plant

ProbeSet	Description	Blast Score
13716_at (NOVARTIS103_RC_AT)	emb CAA62665.1 (X91259) lectin like protein [<i>Arabidopsis thaliana</i>]	6E-70
13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [<i>Arabidopsis thaliana</i>]	2E-27
13755_at (NOVARTIS15_AT)	emb CAA16797.1 (AL021713) receptor serine/threonine kinase-like protein [<i>Arabidopsis thaliana</i>]	1E-114
13763_at (NOVARTIS21_AT)	gb AAF24849.1 AC012679_20 (AC012679) putative calmodulin-binding protein [<i>Arabidopsis thaliana</i>]	1E-105
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [<i>Arabidopsis thaliana</i>]	2E-30
14139_at (NOVARTIS30_AT)	gb AAD09343.1 (AF026538) ABA-responsive protein [<i>Hordeum vulgare</i>]	7E-36
14148_at (NOVARTIS38_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [<i>Arabidopsis thaliana</i>]	4E-53
14170_at (NOVARTIS51_AT)	gb AAF29406.1 AC022354_5 (AC022354) unknown protein [<i>Arabidopsis thaliana</i>]	9E-26
14197_at (NOVARTIS71_AT)	No hits found.	
14214_at (NOVARTIS83_AT)	gb AAF24849.1 AC012679_20 (AC012679) putative calmodulin-binding protein [<i>Arabidopsis thaliana</i>]	2E-92
14223_at (NOVARTIS9_AT)	emb CAA19683.1 (AL024486) putative protein [<i>Arabidopsis thaliana</i>]	0

Table 4b Probe Sets as referred to in Table 3 corresponding to genes, the expression of which is induced by *Pseudomonas* infection in wild-type *Arabidopsis* plants and perturbed in at least one mutant plant

11997_at (AC005967.4_AT)	12004_at (AL022023.132_AT)
12007_at (Z99708.249_AT)	12037_at (AC004005.174_AT)
12072_at (AL035396.4_AT)	12079_s_at (A71597.1_S_AT)
12081_at (AC001645.140_AT)	12115_at (AL033545.26_AT)
12136_at (AC007591.60_AT)	12150_at (AC004005.151_AT)
12198_at (AC006954.90_AT)	12216_at (AC007119.56_AT)
12233_at (AJ001807.1_AT)	12307_at (AC002392.162_AT)

12314_at (AC001229.28_AT)	12317_at (AC004138.27_AT)
12323_at (AC002333.18_AT)	12332_s_at (AB023448.2_S_AT)
12341_s_at (AL021637.176_S_AT)	12349_s_at (X84728.6_S_AT)
12369_at (AC002535.59_AT)	12400_at (X98453.1_AT)
12438_at (AL021710.83_AT)	12449_s_at (AC002343.179_S_AT)
12454_at (AC006232.164_AT)	12475_at (Y11794.1_AT)
12487_at (AC004411.126_AT)	12497_at (AC006533.51_AT)
12500_s_at (AF081067.3_S_AT)	12525_at (AC006587.85_AT)
12530_at (Z99707.184_AT)	12535_at (AL035538.156_AT)
12538_at (AF033205.2_AT)	12574_at (X82624.2_AT)
12584_at (AC004521.233_AT)	12626_at (AC006234.95_AT)
12645_at (AL021712.56_AT)	12712_f_at (Z95774_F_AT)
12736_f_at (Z97048_F_AT)	12744_at (AC001645.15_AT)
12760_g_at (AC005278.32_G_AT)	12764_f_at (AC004138.69_F_AT)
12772_at (AC005278.34_AT)	12797_s_at (AC007138.25_S_AT)
12851_s_at (ACCSYN1_S_AT)	12879_s_at (AIG1_S_AT)
12880_s_at (AIG2_S_AT)	12883_s_at (APX_S_AT)
12889_s_at (ASA1_S_AT)	12891_at (ATACS6_AT)
12892_g_at (ATACS6_G_AT)	12904_s_at (ATERF1_S_AT)
12905_s_at (ATERF2_S_AT)	12911_s_at (ATG6PDHE5_S_AT)
12921_s_at (ATHHMGCOAR_S_AT)	12951_at (AC005489.5_AT)
12958_at (AC002332.249_AT)	12965_at (AL021711.118_AT)
12966_s_at (AL023094.197_S_AT)	12989_s_at (AC004077.149_S_AT)
13003_s_at (AB021936.1_S_AT)	13014_at (U93215.87_AT)
13040_at (AC002392.134_AT)	13070_at (AC006919.171_AT)
13094_at (AL035523.163_AT)	13134_s_at (AC002337.9_S_AT)
13152_s_at (AC005322.24_S_AT)	13154_s_at (AC002333.210_S_AT)
13157_at (AC002409.35_AT)	13176_at (AL031394.56_AT)
13177_at (AL049640.42_AT)	13190_s_at (ATTHIREDA_S_AT)
13211_s_at (BCHI_S_AT)	13212_s_at (BGL2_S_AT)
13215_s_at (cafferoylcoamethyltrans_S_AT)	13219_s_at (CHI4_S_AT)
13243_r_at (ELI32_R_AT)	13244_s_at (ELI32_S_AT)
13255_i_at (gammaglutamyltranspepti_I_AT)	13266_s_at (GST4_S_AT)
13273_s_at (HSF4_S_AT)	13275_f_at (HSP174_F_AT)
13277_i_at (HSP176A_I_AT)	13285_s_at (HSP83_S_AT)
13312_at (AC006223.75_AT)	13370_at (AC005322.4_AT)
13381_at (AC006580.8_AT)	13395_at (AL035528.202_AT)
13435_at (AF003102.3_AT)	13437_at (AF096371.8_AT)

13467_at (AL096860.198_AT)	13536_at (AL021636.47_AT)
13538_at (AL080254.75_AT)	13565_at (AL035601.21_AT)
13588_at (AL021961.24_AT)	13589_at (AC000132.24_AT)
13617_at (AC006592.64_AT)	13627_at (AL035394.196_AT)
13645_at (AC000098.8_AT)	13656_at (AC007138.31_AT)
13659_at (AL022347.46_AT)	13666_s_at (INDOLE3GPS_S_AT)
13680_s_at (LOX1_S_AT)	13685_s_at (MLOLIKE2_S_AT)
13688_s_at (MONOPTEROS_S_AT)	13697_at (NI16_AT)
13705_s_at (AC003671X_S_AT)	13789_at (AJ132436.2_AT)
13803_at (Z97341.376_AT)	13818_s_at (AC006218.175_S_AT)
13842_at (AC002396.12_AT)	13848_at (AC003981.31_AT)
13880_s_at (AL049480.183_S_AT)	13908_s_at (A71590.1_S_AT)
13918_at (AC005388.29_AT)	13920_at (AC005990.53_AT)
13949_s_at (Z97343.352_S_AT)	13963_at (AL021711.26_AT)
13999_at (AF071527.56_AT)	14015_s_at (A71588.1_S_AT)
14016_s_at (A71596.1_S_AT)	14025_s_at (AC007293.3_S_AT)
14030_at (AC005970.225_AT)	14032_at (AL035601.11_AT)
14041_at (AC003970.28_AT)	14052_at (AC004122.24_AT)
14068_s_at (AC006922.197_S_AT)	14070_at (AL049658.217_AT)
14089_at (AC006223.65_AT)	14100_at (AF002109.108_AT)
14110_i_at (AL035528.279_I_AT)	14240_s_at (NR1_S_AT)
14242_s_at (NRA_S_AT)	14248_at (PAD3_AT)
14249_i_at (PAD4_I_AT)	14254_s_at (PAL1-MRNA_S_AT)
14256_f_at (PAL1-INTRON_F_AT)	14320_at (AC005956.54_AT)
14408_at (AC002291.14_AT)	14448_at (AC002387.243_AT)
14450_at (AC002986.49_AT)	14461_at (AC006202.73_AT)
14468_at (AC007576.62_AT)	14475_at (AL021811.121_AT)
14487_at (Z97341.343_AT)	14584_at (AC007658.25_AT)
14609_at (AC002340.147_AT)	14620_s_at (PAT1_S_AT)
14635_s_at (PR.1_S_AT)	14638_s_at (PRXCB_S_AT)
14640_s_at (putativemloHI_S_AT)	14643_s_at (RAR047_S_AT)
14663_s_at (trehalaseprecursor_RC_S_AT)	14667_s_at (TRPB_S_AT)
14672_s_at (TSA1_S_AT)	14673_s_at (TSB2_S_AT)
14675_s_at (VSP_S_AT)	14705_i_at (WT77_RC_I_AT)
14706_r_at (WT77_RC_R_AT)	14711_s_at (ZFPL_S_AT)
14735_s_at (AF008124_S_AT)	14750_s_at (AF096370.12_S_AT)
14763_at (X86958.1_AT)	14779_at (AC004680.71_AT)
14780_at (AC004683.103_AT)	14786_at (AC005397.115_AT)

14793_at (AC006202.10_AT)	14882_at (AL022605.63_AT)
14900_at (AC000348.12_AT)	14923_at (AC006283.158_AT)
14924_at (AC006283.46_AT)	14928_at (AC006569.88_AT)
14959_at (AC007202.26_AT)	14978_at (AC002333.49_AT)
15052_at (AC002332.103_AT)	15073_at (AC007069.93_AT)
15088_s_at (AC002311.37_S_AT)	15091_at (AC004683.97_AT)
15098_s_at (ATU26945_S_AT)	15116_f_at (AF121356_F_AT)
15123_s_at (ATU40857_S_AT)	15124_s_at (ATU59508_S_AT)
15125_f_at (D85190_F_AT)	15132_s_at (AF121878_S_AT)
15137_s_at (ATU57320_S_AT)	15141_s_at (D85191_S_AT)
15154_s_at (ATHMTGDAS_S_AT)	15161_s_at (ATU90522_S_AT)
15162_s_at (U01880_S_AT)	15188_s_at (AF081202_S_AT)
15196_s_at (ATU43412_S_AT)	15199_s_at (AB005804_S_AT)
15211_s_at (ATH243813_S_AT)	15216_s_at (ATU75191_S_AT)
15342_at (AC006593.101_AT)	15406_at (AC006931.179_AT)
15431_at (AL030978.64_AT)	15479_at (AL049483.205_AT)
15483_s_at (AC005819.20_S_AT)	15485_at (AC006233.109_AT)
15496_at (AC006282.167_AT)	15518_at (AC005322.28_AT)
15522_i_at (AL078637.213_I_AT)	15523_s_at (AL078637.213_S_AT)
15524_at (AC005508.25_AT)	15526_at (AC004122.16_AT)
15531_i_at (AL078637.191_I_AT)	15532_r_at (AL078637.191_R_AT)
15540_at (AC006585.205_AT)	15543_at (AF096371.10_AT)
15544_at (AL021633.110_AT)	15547_at (AC005970.122_AT)
15551_at (AL035440.289_AT)	15594_s_at (ATU56635_S_AT)
15613_s_at (ATHHOMEOA_S_AT)	15622_s_at (ATU43945_S_AT)
15625_s_at (ATU74610_S_AT)	15632_s_at (AB012570_S_AT)
15641_s_at (AF117063_S_AT)	15665_s_at (AF022658_S_AT)
15669_s_at (AF047834_S_AT)	15670_s_at (AF061638_S_AT)
15672_s_at (AF082299_S_AT)	15778_at (X98676.2_AT)
15779_g_at (X98676.2_G_AT)	15792_at (AC002341.106_AT)
15798_at (AC002521.173_AT)	15815_s_at (Z97342.366_S_AT)
15839_at (AC005662.203_AT)	15859_at (AC006587.164_AT)
15866_s_at (AC007133.59_S_AT)	15874_at (AL022223.106_AT)
15886_at (AL078637.204_AT)	15919_at (AC007060.42_AT)
15921_s_at (AC007067.1_S_AT)	15924_at (AC007138.61_AT)
15970_s_at (X71794.2_S_AT)	15978_at (X68592.6_AT)
15982_s_at (AC006260.78_S_AT)	16001_at (AF035385.2_AT)
16003_s_at (AL021749.64_S_AT)	16021_s_at (AL022224.182_S_AT)

16031_at (X94248.1_AT)	16043_at (AC005489.17_AT)
16053_i_at (Y14251.4_I_AT)	16063_s_at (AB008103_S_AT)
16073_f_at (AF062908_F_AT)	16083_s_at (AF153283_S_AT)
16091_s_at (ATHHSP83_S_AT)	16103_s_at (ATU60445_S_AT)
16105_s_at (ATU68017_S_AT)	16108_s_at (D78604_S_AT)
16130_s_at (AF078683_S_AT)	16173_s_at (D78607_S_AT)
16203_at (AC007519.53_AT)	16232_s_at (AL080252.77_S_AT)
16233_at (AL080254.83_AT)	16272_at (AC006304.136_AT)
16298_at (AL021890.71_AT)	16299_at (AL024486.185_AT)
16301_s_at (AL031018.105_S_AT)	16306_at (AL049751.112_AT)
16335_at (AL079347.105_AT)	16340_at (AC004255.15_AT)
16357_at (AF149413.38_AT)	16363_at (AC004255.14_AT)
16383_at (AC006300.64_AT)	16398_s_at (AL022603.3_S_AT)
16405_at (AC005850.9_AT)	16409_at (AC004393.2_AT)
16440_s_at (AF002109.137_S_AT)	16461_i_at (AC004683.79_I_AT)
16462_s_at (AC004683.79_S_AT)	16465_at (Y08892.1_AT)
16470_s_at (AF068299.4_S_AT)	16510_at (AL034567.198_AT)
16522_at (X77500.2_AT)	16526_at (Z49227.1_AT)
16541_s_at (AB023423_S_AT)	16545_s_at (AF037229_S_AT)
16553_f_at (AF078821_F_AT)	16570_s_at (ATHCDPKA_S_AT)
16578_s_at (ATHRPRP1B_S_AT)	16589_s_at (ATU26937_S_AT)
16594_s_at (ATU39783_S_AT)	16603_s_at (ATU81293_S_AT)
16609_s_at (AB008104_S_AT)	16611_s_at (AB008782_S_AT)
16638_s_at (AF139098_S_AT)	16646_s_at (ATHDHS1_S_AT)
16649_s_at (ATHORF_S_AT)	16701_at (AC005312.61_AT)
16721_at (AC006533.58_AT)	16747_at (AL021713.3_AT)
16781_at (AC002392.100_AT)	16810_at (AC002339.46_AT)
16859_at (AL035523.135_AT)	16864_i_at (AF037367.4_I_AT)
16865_s_at (AF037367.4_S_AT)	16888_s_at (AC004684.174_S_AT)
16914_s_at (AL049500.57_S_AT)	16916_s_at (X77199.8_S_AT)
16968_at (AL021961.93_AT)	16989_at (AL030978.46_AT)
16995_at (AC002391.188_AT)	17007_at (AC005896.26_AT)
17008_at (AC006585.212_AT)	17039_s_at (D78602_S_AT)
17041_s_at (D89631_S_AT)	17051_s_at (AF098947_S_AT)
17066_s_at (ATHLIPOXY_S_AT)	17073_s_at (ATT54391_S_AT)
17075_s_at (ATU09961_S_AT)	17104_s_at (D88541_S_AT)
17111_s_at (ATHACSC_S_AT)	17119_s_at (AF132212_S_AT)
17128_s_at (ATHRPRP1A_S_AT)	17180_at (AF007270.30_AT)

17187_at (AF128396.2_AT)	17300_at (X66017.2_AT)
17303_s_at (AC004683.25_S_AT)	17323_at (U95973.69_AT)
17338_at (AC002535.97_AT)	17341_at (AL021713.89_AT)
17356_s_at (Z97338.190_S_AT)	17371_at (AF076243.44_AT)
17379_at (AF085279.9_AT)	17413_s_at (AJ006961.4_S_AT)
17451_at (AC002343.47_AT)	17452_g_at (AC002343.47_G_AT)
17484_at (X79052.2_AT)	17485_s_at (Z97340.345_S_AT)
17487_s_at (U18993.2_S_AT)	17511_s_at (AF067605_S_AT)
17514_s_at (AF076277_S_AT)	17522_s_at (D78606_S_AT)
17533_s_at (ATU43488_S_AT)	17544_s_at (ATU40856_S_AT)
17548_s_at (AF118823_S_AT)	17585_s_at (AF134487_S_AT)
17595_s_at (AF166352_S_AT)	17648_at (AL021684.43_AT)
17653_at (AL035679.144_AT)	17702_at (AC005700.212_AT)
17719_at (AC006592.17_AT)	17752_at (AC003974.37_AT)
17758_at (AF076243.41_AT)	17775_at (AC004392.2_AT)
17781_at (AL049746.177_AT)	17840_s_at (AC002333.223_S_AT)
17860_at (AL078467.4_AT)	17876_at (AJ007587.2_AT)
17877_g_at (AJ007587.2_G_AT)	17893_at (AC004401.135_AT)
17899_at (Z97339.197_AT)	17930_s_at (AJ006960.4_S_AT)
17945_at (Z97341.411_AT)	17963_at (AL049730.88_AT)
18012_s_at (AJ002295_S_AT)	18054_at (AJ238846_AT)
18109_s_at (AC002391.206_S_AT)	18121_s_at (AC002337.21_S_AT)
18122_at (AC002338.110_AT)	18148_at (AC004669.25_AT)
18176_at (AL035540.31_AT)	18194_i_at (AL096859.227_I_AT)
18213_at (AL022140.126_AT)	18224_s_at (AL021890.57_S_AT)
18228_at (X91259.1_AT)	18236_s_at (AC004683.69_S_AT)
18242_g_at (AC006580.71_G_AT)	18255_at (AC005770.25_AT)
18258_s_at (AC006439.222_S_AT)	18263_at (AC005724.36_AT)
18266_at (AC004684.33_AT)	18267_at (AC006223.23_AT)
18299_s_at (M23872.2_S_AT)	18456_s_at (AC004697.159_S_AT)
18508_s_at (AC006532.89_S_AT)	18544_at (AC007060.14_AT)
18582_s_at (AC003671.36_S_AT)	18587_s_at (AC007166.53_S_AT)
18590_at (AJ222713.4_AT)	18591_at (X74756.2_AT)
18596_at (AC005698.13_AT)	18597_at (AL080282.74_AT)
18604_at (AF069298.31_AT)	18622_g_at (AJ005902.2_G_AT)
18625_at (AC005278.22_AT)	18631_at (AC002510.112_AT)
18636_at (AC006577.22_AT)	18668_at (AJ249794_AT)
18686_s_at (U18126_S_AT)	18698_s_at (X17528_S_AT)

18735_s_at (Z29490_S_AT)	18753_s_at (AF118222.28_S_AT)
18782_at (AC003040.90_AT)	18803_at (AC005315.94_AT)
18885_at (AC006921.147_AT)	18888_at (AC007591.68_AT)
18899_s_at (X13434.1_S_AT)	18908_i_at (AF055848.2_I_AT)
18909_s_at (AF055848.2_S_AT)	18928_at (AC002333.181_AT)
18930_at (AC005990.57_AT)	18933_at (AC007020.48_AT)
18949_at (Z54136.1_AT)	18953_at (AF077955.1_AT)
18963_at (AC004561.99_AT)	18966_at (AC004561.106_AT)
19019_i_at (X82623.2_I_AT)	19060_at (AC003671.34_AT)
19092_at (AL078606.188_AT)	19110_s_at (X86947.2_S_AT)
19137_at (X74755.2_AT)	19140_at (AC005170.24_AT)
19181_s_at (AF053065.2_S_AT)	19207_at (AC006069.117_AT)
19247_at (AF071527.44_AT)	19257_s_at (AC000104.57_S_AT)
19284_at (AC003028.196_AT)	19288_at (AC005824.130_AT)
19325_at (AL022604.42_AT)	19364_at (AL022023.142_AT)
19383_at (AC006200.203_AT)	19395_at (AF007270.32_AT)
19405_at (AJ223803.1_AT)	19407_at (AC004697.81_AT)
19409_at (AC007357.56_AT)	19411_at (AC007661.104_AT)
19421_at (X70990.4_AT)	19432_s_at (AL035680.11_S_AT)
19451_at (AC004392.6_AT)	19460_s_at (AC000132.66_S_AT)
19465_at (AL021768.96_AT)	19546_at (AC005398.172_AT)
19555_at (AF058919.48_AT)	19591_at (AJ010735.4_AT)
19614_at (AC003970.32_AT)	19624_at (AL049481.196_AT)
19625_s_at (AC002311.26_S_AT)	19635_at (AL049746.38_AT)
19640_at (AC004561.78_AT)	19641_at (AC004561.66_AT)
19645_at (AC004561.70_AT)	19655_at (Y14199.1_AT)
19667_at (AL021710.5_AT)	19672_at (AC005687.19_AT)
19673_g_at (AC005687.19_G_AT)	19700_s_at (AL031326.154_S_AT)
19704_i_at (AJ005927.2_I_AT)	19707_s_at (Z95768.3_S_AT)
19741_at (AL049171.72_AT)	19755_at (AC006593.64_AT)
19762_at (AL035527.204_AT)	19818_i_at (AL021749.33_I_AT)
19844_at (AJ007588.2_AT)	19848_s_at (AC004261.94_S_AT)
19851_at (U23794.3_AT)	19881_at (AC004077.49_AT)
19892_at (AC005770.30_AT)	19895_s_at (U77347.4_S_AT)
19944_at (AC002130.4_AT)	19956_at (AC006282.11_AT)
19960_at (AL035527.360_AT)	19970_s_at (AC003674.10_S_AT)
19982_at (AC002986.28_AT)	19991_at (AC007017.124_AT)
20017_at (AC004521.66_AT)	20023_at (AC006577.46_AT)

20030_at (AL078637.51_AT)	20051_at (AC000106.38_AT)
20053_at (AC002292.27_AT)	20096_at (AC004238.31_AT)
20098_at (AC004697.123_AT)	20133_i_at (AC007178.71_I_AT)
20134_s_at (AC007178.71_S_AT)	20144_at (AL079350.68_AT)
20179_at (AL035538.229_AT)	20189_at (AC005489.2_AT)
20194_at (AC007584.48_AT)	20223_at (AL022347.145_AT)
20238_at (X74514.2_AT)	20239_g_at (X74514.2_G_AT)
20245_s_at (AC005309.97_S_AT)	20247_at (AC004392.4_AT)
20263_at (AB004798.1_AT)	20269_at (AC002387.237_AT)
20271_at (Z99707.27_AT)	20287_at (Y14590.5_AT)
20288_g_at (Y14590.5_G_AT)	20291_s_at (M92353.4_S_AT)
20297_at (AC007153.27_AT)	20323_at (AC004561.62_AT)
20348_at (AC005967.35_AT)	20356_at (AC004561.74_AT)
20365_s_at (AC005850.19_S_AT)	20370_at (AC004561.263_AT)
20420_at (AL024486.131_AT)	20421_at (U81294.2_AT)
20422_g_at (U81294.2_G_AT)	20432_at (U43486.2_AT)
20433_at (AC006232.147_AT)	20450_at (AJ005930.2_AT)
20461_at (AL049480.157_AT)	20462_at (U82399.2_AT)
20479_i_at (AF069495.2_I_AT)	20480_s_at (AF069495.2_S_AT)
20485_at (AC007660.131_AT)	20529_at (Z97341.125_AT)
20572_s_at (AC005560.229_S_AT)	20589_at (AF081066.3_AT)
20646_at (AC002291.20_AT)	20656_at (AL035396.46_AT)
20658_s_at (AL050400.70_S_AT)	20669_s_at (AC002388.6_S_AT)
20685_at (AL049751.46_AT)	20686_at (Y14424.2_AT)
20689_s_at (AC002335.19_S_AT)	

Table 5 Probe Sets as referred to in Tables 4a and 4b corresponding to genes encoding regulatory proteins, the expression of which is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis*, with *Pseudomonas syringae*

ProbeSet	Regulatory factor
12497_at (AC006533.51_AT)	putative receptor-like protein kinase
16409_at (AC004393.2_AT)	putative receptor-like kinase
12307_at (AC002392.162_AT)	putative receptor-like protein kinase
13659_at (AL022347.46_AT)	serine/threonine kinase-like protein
17341_at (AL021713.89_AT)	receptor serine/threonine kinase-like protein
12958_at (AC002332.249_AT)	putative protein kinase
17758_at (AF076243.41_AT)	putative receptor-like protein kinase
16570_s_at (ATHCDPKA_S_AT)	CDPK1 calcium dependent protein kinase 1
19092_at (AL078606.188_AT)	protein kinase-like protein
17371_at (AF076243.44_AT)	putative receptor-like protein kinase
20223_at (AL022347.145_AT)	putative ser/thr protein kinase
19655_at (Y14199.1_AT)	MAP3K delta-1 protein kinase
14030_at (AC005970.225_AT)	putative protein kinase
20462_at (U82399.2_AT)	putative protein kinase PK1
16781_at (AC002392.100_AT)	putative receptor-like protein kinase
14763_at (X86958.1_AT)	protein kinase catalytic domain (fragment)
17752_at (AC003974.37_AT)	putative protein kinase
13755_at (NOVARTIS15_AT)	putative ser/thr kinase
13370_at (AC005322.4_AT)	similar to Dsor1 protein kinase
20144_at (AL079350.68_AT)	receptor kinase-like protein
16357_at (AF149413.38_AT)	putative protein kinase
18176_at (AL035540.31_AT)	putative protein kinase
15798_at (AC002521.173_AT)	putative receptor-like protein kinase
12965_at (AL021711.118_AT)	protein kinase-like protein
16398_s_at (AL022603.3_S_AT)	putative ser/thr protein kinase
18122_at (AC002338.110_AT)	putative protein kinase
17323_at (U95973.69_AT)	putative ser/thr protein kinase
18782_at (AC003040.90_AT)	putative protein kinase
16405_at (AC005850.9_AT)	putative serine/threonine protein kinase

ProbeSet	Regulatory factor
14110_i_at (AL035528.279_I_AT)	putative R protein. Like Hcr9-9A, Lycopersicon pimpinellifolium F18A5_290 chr.4
14214_at (NOVARTIS83_AT)	putative calmodulin-binding protein (duplicate)
13763_at (NOVARTIS21_AT)	putative calmodulin-binding protein (duplicate)
12438_at (AL021710.83_AT)	membrane-bound small GTP-binding - like protein
19848_s_at (AC004261.94_S_AT)	calmodulin-related protein
16103_s_at (ATU60445_S_AT)	GRF7 general regulatory factor encoding 14-3-3 protein
14249_i_at (PAD4_I_AT)	PAD4 phytoalexin deficient 4
19465_at (AL021768.96_AT)	RPP5-like NBS-LRR resistance protein
14640_s_at (putativemloHI_S_AT)	Mlo-like (duplicate)
18456_s_at (AC004697.159_S_AT)	Mlo-like (duplicate)
14320_at (AC005956.54_AT)	putative RING zinc finger protein
18054_at (AJ238846_AT)	SGP1 monomeric G-protein
16130_s_at (AF078683_S_AT)	RHA1a RING-H2 finger protein
20485_at (AC007660.131_AT)	putative two-component response regulator protein
15052_at (AC002332.103_AT)	putative calcium-binding EF-hand protein
15632_s_at (AB012570_S_AT)	ATHP3 two-compoent phosphorelay mediator with a single HPt domain
16553_f_at (AF078821_F_AT)	RHA1b RING-H2 finger protein
13685_s_at (MLOLIKE2_S_AT)	Mlo-like 2 (duplicate)
20365_s_at (AC005850.19_S_AT)	Mlo-like 2 (duplicate)
13312_at (AC006223.75_AT)	putative disease resistance protein
17180_at (AF007270.30_AT)	similar to GATA-type zinc fingers
15779_g_at (X98676.2_G_AT)	zinc finger protein (duplicate)
15778_at (X98676.2_AT)	zinc finger protein (duplicate)
14711_s_at (ZFPL_S_AT)	hypothetical Cys-3-His zinc finger protein
17379_at (AF085279.9_AT)	putative CCCH-type zinc finger protein
12525_at (AC006587.85_AT)	putative DOF zinc finger protein
16589_s_at (ATU26937_S_AT)	AtMYB7 transcription factor
12712_f_at (Z95774_F_AT)	AtMYB51 R2R3 myb transcription factor
13273_s_at (HSF4_S_AT)	HSF4 heat shock transcription factor 4 (duplicate)
16105_s_at (ATU68017_S_AT)	HSF4 heat shock transcription factor 4 (duplicate)
18803_at (AC005315.94_AT)	putative SCARECROW homeobox gene regulator

ProbeSet	Regulatory factor
12905_s_at (ATERF2_S_AT)	EREBP2 ethylene responsive element binding factor 2 (duplicate)
16609_s_at (AB008104_S_AT)	EREBP2 ethylene responsive element binding factor 2 (duplicate)
19755_at (AC006593.64_AT)	ethylene reponse factor-like AP2 domain transcription factor
17514_s_at (AF076277_S_AT)	ERF1 ethylene response factor 1 transcription factor
18121_s_at (AC002337.21_S_AT)	AtMYB2 MYB transcription factor
13688_s_at (monopteros_S_AT)	transcription factor
12904_s_at (ATERF1_S_AT)	EREBP1 ethylene responsive element binding factor 1 (duplicate)
16063_s_at (AB008103_S_AT)	EREBP1 ethylene responsive element binding factor 1 (duplicate)
16638_s_at (AF139098_S_AT)	putative zinc finger protein
16545_s_at (AF037229_S_AT)	transcription factor
13435_at (AF003102.3_AT)	RAP2.9 AP2 domain containing putative transcription factor
15665_s_at (AF022658_S_AT)	putative c2h2 zinc finger transcription factor
19673_g_at (AC005687.19_G_AT)	RAP2.6 AP2 domain containing putative transcription factor (duplicate)
19672_at (AC005687.19_AT)	RAP2.6 AP2 domain containing putative transcription factor (duplicate)
14780_at (AC004683.103_AT)	DREB-like AP2 domain transcription factor
17303_s_at (AC004683.25_S_AT)	WRKY33 transcription factor
18949_at (Z54136.1_AT)	MYB-related protein
19707_s_at (Z95768.3_S_AT)	AtMYB44 transcription factor
16073_f_at (AF062908_F_AT)	putative transcription factor
12966_s_at (AL023094.197_S_AT)	ATB2 bZIP transcription factor
12736_f_at (Z97048_F_AT)	AtMYB13 transcription factor

Table 6 Probe Sets as referred to in Tables 4a and 4b corresponding to genes, the expression of which is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis* having a mutation that results in enhanced susceptibility to *Pseudomonas*

12079_s_at (A71597.1_S_AT)	12081_at (AC001645.140_AT)
12115_at (AL033545.26_AT)	12150_at (AC004005.151_AT)
12233_at (AJ001807.1_AT)	12307_at (AC002392.162_AT)
12314_at (AC001229.28_AT)	12332_s_at (AB023448.2_S_AT)
12341_s_at (AL021637.176_S_AT)	12400_at (X98453.1_AT)
12438_at (AL021710.83_AT)	12475_at (Y11794.1_AT)
12487_at (AC004411.126_AT)	12497_at (AC006533.51_AT)
12500_s_at (AF081067.3_S_AT)	12530_at (Z99707.184_AT)
12574_at (X82624.2_AT)	12584_at (AC004521.233_AT)
12712_f_at (Z95774_F_AT)	12760_g_at (AC005278.32_G_AT)
12764_f_at (AC004138.69_F_AT)	12772_at (AC005278.34_AT)
12851_s_at (ACCSYN1_S_AT)	12879_s_at (AIG1_S_AT)
12883_s_at (APX_S_AT)	12889_s_at (ASA1_S_AT)
12891_at (ATACS6_AT)	12892_g_at (ATACS6_G_AT)
12905_s_at (ATERF2_S_AT)	12911_s_at (ATG6PDHE5_S_AT)
12921_s_at (ATHHMGCOAR_S_AT)	12958_at (AC002332.249_AT)
12989_s_at (AC004077.149_S_AT)	13003_s_at (AB021936.1_S_AT)
13014_at (U93215.87_AT)	13040_at (AC002392.134_AT)
13070_at (AC006919.171_AT)	13094_at (AL035523.163_AT)
13157_at (AC002409.35_AT)	13177_at (AL049640.42_AT)
13190_s_at (ATTHIREDA_S_AT)	13211_s_at (BCHI_S_AT)
13212_s_at (BGL2_S_AT)	13219_s_at (CHI4_S_AT)
13266_s_at (GST4_S_AT)	13273_s_at (HSF4_S_AT)
13275_f_at (HSP174_F_AT)	13370_at (AC005322.4_AT)
13381_at (AC006580.8_AT)	13435_at (AF003102.3_AT)
13467_at (AL096860.198_AT)	13538_at (AL080254.75_AT)
13565_at (AL035601.21_AT)	13588_at (AL021961.24_AT)
13589_at (AC000132.24_AT)	13617_at (AC006592.64_AT)
13627_at (AL035394.196_AT)	13656_at (AC007138.31_AT)
13659_at (AL022347.46_AT)	13666_s_at (INDOLE3GPS_S_AT)
13680_s_at (LOX1_S_AT)	13688_s_at (MONOPTEROS_S_AT)
13697_at (NI16_AT)	13716_at (NOVARTIS103_RC_AT)
13751_at (NOVARTIS127_AT)	13755_at (NOVARTIS15_AT)
13763_at (NOVARTIS21_AT)	13764_at (NOVARTIS22_AT)

13818_s_at (AC006218.175_S_AT)	13842_at (AC002396.12_AT)
13880_s_at (AL049480.183_S_AT)	13920_at (AC005990.53_AT)
14015_s_at (A71588.1_S_AT)	14016_s_at (A71596.1_S_AT)
14025_s_at (AC007293.3_S_AT)	14030_at (AC005970.225_AT)
14032_at (AL035601.11_AT)	14041_at (AC003970.28_AT)
14052_at (AC004122.24_AT)	14068_s_at (AC006922.197_S_AT)
14110_i_at (AL035528.279_I_AT)	14139_at (NOVARTIS30_AT)
14148_at (NOVARTIS38_AT)	14170_at (NOVARTIS51_AT)
14214_at (NOVARTIS83_AT)	14242_s_at (NRA_S_AT)
14248_at (PAD3_AT)	14249_i_at (PAD4_I_AT)
14408_at (AC002291.14_AT)	14450_at (AC002986.49_AT)
14461_at (AC006202.73_AT)	14487_at (Z97341.343_AT)
14584_at (AC007658.25_AT)	14609_at (AC002340.147_AT)
14620_s_at (PAT1_S_AT)	14635_s_at (PR.1_S_AT)
14638_s_at (PRXCB_S_AT)	14663_s_at (trehalaseprecursor_RC_S_AT)
14667_s_at (TRPB_S_AT)	14672_s_at (TSA1_S_AT)
14673_s_at (TSB2_S_AT)	14705_i_at (WT77_RC_I_AT)
14706_r_at (WT77_RC_R_AT)	14735_s_at (AF008124_S_AT)
14763_at (X86958.1_AT)	14786_at (AC005397.115_AT)
14882_at (AL022605.63_AT)	14924_at (AC006283.46_AT)
14959_at (AC007202.26_AT)	14978_at (AC002333.49_AT)
15073_at (AC007069.93_AT)	15091_at (AC004683.97_AT)
15098_s_at (ATU26945_S_AT)	15116_f_at (AF121356_F_AT)
15124_s_at (ATU59508_S_AT)	15125_f_at (D85190_F_AT)
15137_s_at (ATU57320_S_AT)	15154_s_at (ATHMTGDAS_S_AT)
15162_s_at (U01880_S_AT)	15196_s_at (ATU43412_S_AT)
15199_s_at (AB005804_S_AT)	15216_s_at (ATU75191_S_AT)
15406_at (AC006931.179_AT)	15431_at (AL030978.64_AT)
15483_s_at (AC005819.20_S_AT)	15496_at (AC006282.167_AT)
15518_at (AC005322.28_AT)	15522_i_at (AL078637.213_I_AT)
15526_at (AC004122.16_AT)	15531_i_at (AL078637.191_I_AT)
15540_at (AC006585.205_AT)	15543_at (AF096371.10_AT)
15544_at (AL021633.110_AT)	15551_at (AL035440.289_AT)
15594_s_at (ATU56635_S_AT)	15622_s_at (ATU43945_S_AT)
15632_s_at (AB012570_S_AT)	15665_s_at (AF022658_S_AT)
15672_s_at (AF082299_S_AT)	15778_at (X98676.2_AT)
15779_g_at (X98676.2_G_AT)	15815_s_at (Z97342.366_S_AT)
15839_at (AC005662.203_AT)	15859_at (AC006587.164_AT)

15866_s_at (AC007133.59_S_AT)	15874_at (AL022223.106_AT)
15886_at (AL078637.204_AT)	15924_at (AC007138.61_AT)
15970_s_at (X71794.2_S_AT)	15978_at (X68592.6_AT)
15982_s_at (AC006260.78_S_AT)	16001_at (AF035385.2_AT)
16003_s_at (AL021749.64_S_AT)	16021_s_at (AL022224.182_S_AT)
16031_at (X94248.1_AT)	16043_at (AC005489.17_AT)
16053_i_at (Y14251.4_I_AT)	16083_s_at (AF153283_S_AT)
16091_s_at (ATHHSP83_S_AT)	16103_s_at (ATU60445_S_AT)
16105_s_at (ATU68017_S_AT)	16108_s_at (D78604_S_AT)
16130_s_at (AF078683_S_AT)	16233_at (AL080254.83_AT)
16272_at (AC006304.136_AT)	16298_at (AL021890.71_AT)
16299_at (AL024486.185_AT)	16306_at (AL049751.112_AT)
16340_at (AC004255.15_AT)	16357_at (AF149413.38_AT)
16363_at (AC004255.14_AT)	16383_at (AC006300.64_AT)
16409_at (AC004393.2_AT)	16461_i_at (AC004683.79_I_AT)
16462_s_at (AC004683.79_S_AT)	16470_s_at (AF068299.4_S_AT)
16545_s_at (AF037229_S_AT)	16570_s_at (ATHCDPKA_S_AT)
16578_s_at (ATHRPRP1B_S_AT)	16589_s_at (ATU26937_S_AT)
16594_s_at (ATU39783_S_AT)	16603_s_at (ATU81293_S_AT)
16609_s_at (AB008104_S_AT)	16701_at (AC005312.61_AT)
16721_at (AC006533.58_AT)	16781_at (AC002392.100_AT)
16810_at (AC002339.46_AT)	16859_at (AL035523.135_AT)
16864_i_at (AF037367.4_I_AT)	16865_s_at (AF037367.4_S_AT)
16914_s_at (AL049500.57_S_AT)	16968_at (AL021961.93_AT)
16989_at (AL030978.46_AT)	16995_at (AC002391.188_AT)
17007_at (AC005896.26_AT)	17051_s_at (AF098947_S_AT)
17066_s_at (ATHLIPOXY_S_AT)	17075_s_at (ATU09961_S_AT)
17128_s_at (ATHRPRP1A_S_AT)	17180_at (AF007270.30_AT)
17338_at (AC002535.97_AT)	17341_at (AL021713.89_AT)
17356_s_at (Z97338.190_S_AT)	17371_at (AF076243.44_AT)
17413_s_at (AJ006961.4_S_AT)	17451_at (AC002343.47_AT)
17452_g_at (AC002343.47_G_AT)	17484_at (X79052.2_AT)
17485_s_at (Z97340.345_S_AT)	17487_s_at (U18993.2_S_AT)
17533_s_at (ATU43488_S_AT)	17544_s_at (ATU40856_S_AT)
17585_s_at (AF134487_S_AT)	17653_at (AL035679.144_AT)
17752_at (AC003974.37_AT)	17758_at (AF076243.41_AT)
17775_at (AC004392.2_AT)	17781_at (AL049746.177_AT)
17840_s_at (AC002333.223_S_AT)	17877_g_at (AJ007587.2_G_AT)

17893_at (AC004401.135_AT)	17899_at (Z97339.197_AT)
17930_s_at (AJ006960.4_S_AT)	17945_at (Z97341.411_AT)
17963_at (AL049730.88_AT)	18054_at (AJ238846_AT)
18109_s_at (AC002391.206_S_AT)	18148_at (AC004669.25_AT)
18176_at (AL035540.31_AT)	18194_i_at (AL096859.227_I_AT)
18213_at (AL022140.126_AT)	18228_at (X91259.1_AT)
18242_g_at (AC006580.71_G_AT)	18255_at (AC005770.25_AT)
18258_s_at (AC006439.222_S_AT)	18267_at (AC006223.23_AT)
18508_s_at (AC006532.89_S_AT)	18544_at (AC007060.14_AT)
18590_at (AJ222713.4_AT)	18591_at (X74756.2_AT)
18596_at (AC005698.13_AT)	18604_at (AF069298.31_AT)
18622_g_at (AJ005902.2_G_AT)	18625_at (AC005278.22_AT)
18686_s_at (U18126_S_AT)	18698_s_at (X17528_S_AT)
18735_s_at (Z29490_S_AT)	18753_s_at (AF118222.28_S_AT)
18803_at (AC005315.94_AT)	18885_at (AC006921.147_AT)
18888_at (AC007591.68_AT)	18899_s_at (X13434.1_S_AT)
18909_s_at (AF055848.2_S_AT)	18928_at (AC002333.181_AT)
18930_at (AC005990.57_AT)	18933_at (AC007020.48_AT)
18953_at (AF077955.1_AT)	18966_at (AC004561.106_AT)
19019_i_at (X82623.2_I_AT)	19137_at (X74755.2_AT)
19140_at (AC005170.24_AT)	19181_s_at (AF053065.2_S_AT)
19207_at (AC006069.117_AT)	19247_at (AF071527.44_AT)
19257_s_at (AC000104.57_S_AT)	19288_at (AC005824.130_AT)
19325_at (AL022604.42_AT)	19364_at (AL022023.142_AT)
19383_at (AC006200.203_AT)	19405_at (AJ223803.1_AT)
19407_at (AC004697.81_AT)	19409_at (AC007357.56_AT)
19411_at (AC007661.104_AT)	19421_at (X70990.4_AT)
19432_s_at (AL035680.11_S_AT)	19451_at (AC004392.6_AT)
19460_s_at (AC000132.66_S_AT)	19465_at (AL021768.96_AT)
19546_at (AC005398.172_AT)	19555_at (AF058919.48_AT)
19624_at (AL049481.196_AT)	19641_at (AC004561.66_AT)
19645_at (AC004561.70_AT)	19667_at (AL021710.5_AT)
19741_at (AL049171.72_AT)	19755_at (AC006593.64_AT)
19818_i_at (AL021749.33_I_AT)	19848_s_at (AC004261.94_S_AT)
19881_at (AC004077.49_AT)	19892_at (AC005770.30_AT)
19944_at (AC002130.4_AT)	19956_at (AC006282.11_AT)
19970_s_at (AC003674.10_S_AT)	19982_at (AC002986.28_AT)
19991_at (AC007017.124_AT)	20017_at (AC004521.66_AT)

20030_at (AL078637.51_AT)	20051_at (AC000106.38_AT)
20098_at (AC004697.123_AT)	20133_i_at (AC007178.71_I_AT)
20134_s_at (AC007178.71_S_AT)	20144_at (AL079350.68_AT)
20238_at (X74514.2_AT)	20239_g_at (X74514.2_G_AT)
20245_s_at (AC005309.97_S_AT)	20247_at (AC004392.4_AT)
20263_at (AB004798.1_AT)	20269_at (AC002387.237_AT)
20271_at (Z99707.27_AT)	20287_at (Y14590.5_AT)
20288_g_at (Y14590.5_G_AT)	20291_s_at (M92353.4_S_AT)
20297_at (AC007153.27_AT)	20323_at (AC004561.62_AT)
20348_at (AC005967.35_AT)	20356_at (AC004561.74_AT)
20370_at (AC004561.263_AT)	20420_at (AL024486.131_AT)
20421_at (U81294.2_AT)	20422_g_at (U81294.2_G_AT)
20432_at (U43486.2_AT)	20450_at (AJ005930.2_AT)
20461_at (AL049480.157_AT)	20462_at (U82399.2_AT)
20479_i_at (AF069495.2_I_AT)	20480_s_at (AF069495.2_S_AT)
20485_at (AC007660.131_AT)	20529_at (Z97341.125_AT)
20572_s_at (AC005560.229_S_AT)	20589_at (AF081066.3_AT)
20669_s_at (AC002388.6_S_AT)	20685_at (AL049751.46_AT)
20689_s_at (AC002335.19_S_AT)	

Table 7 Probe Sets as referred to in Tables 4a and 4b corresponding to genes, the expression of which is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis* having a mutation in a gene whose expression is important for resistance to necrotrophic fungi

11997_at (AC005967.4_AT)	12004_at (AL022023.132_AT)
12037_at (AC004005.174_AT)	12072_at (AL035396.4_AT)
12079_s_at (A71597.1_S_AT)	12081_at (AC001645.140_AT)
12115_at (AL033545.26_AT)	12136_at (AC007591.60_AT)
12150_at (AC004005.151_AT)	12216_at (AC007119.56_AT)
12317_at (AC004138.27_AT)	12323_at (AC002333.18_AT)
12332_s_at (AB023448.2_S_AT)	12369_at (AC002535.59_AT)
12400_at (X98453.1_AT)	12449_s_at (AC002343.179_S_AT)
12475_at (Y11794.1_AT)	12487_at (AC004411.126_AT)
12500_s_at (AF081067.3_S_AT)	12530_at (Z99707.184_AT)
12535_at (AL035538.156_AT)	12538_at (AF033205.2_AT)
12574_at (X82624.2_AT)	12584_at (AC004521.233_AT)
12626_at (AC006234.95_AT)	12645_at (AL021712.56_AT)
12744_at (AC001645.15_AT)	12760_g_at (AC005278.32_G_AT)
12772_at (AC005278.34_AT)	12797_s_at (AC007138.25_S_AT)
12851_s_at (ACCSYN1_S_AT)	12880_s_at (AIG2_S_AT)
12889_s_at (ASA1_S_AT)	12904_s_at (ATERF1_S_AT)
12905_s_at (ATERF2_S_AT)	12921_s_at (ATHHMGCOAR_S_AT)
12951_at (AC005489.5_AT)	12965_at (AL021711.118_AT)
12966_s_at (AL023094.197_S_AT)	12989_s_at (AC004077.149_S_AT)
13040_at (AC002392.134_AT)	13094_at (AL035523.163_AT)
13134_s_at (AC002337.9_S_AT)	13152_s_at (AC005322.24_S_AT)
13176_at (AL031394.56_AT)	13211_s_at (BCHI_S_AT)
13215_s_at (cafferoylcoAmethyltrans_S_AT)	13243_r_at (ELI32_R_AT)
13244_s_at (ELI32_S_AT)	13266_s_at (GST4_S_AT)
13275_f_at (HSP174_F_AT)	13277_i_at (HSP176A_I_AT)
13312_at (AC006223.75_AT)	13370_at (AC005322.4_AT)
13381_at (AC006580.8_AT)	13395_at (AL035528.202_AT)
13435_at (AF003102.3_AT)	13437_at (AF096371.8_AT)
13536_at (AL021636.47_AT)	13538_at (AL080254.75_AT)
13565_at (AL035601.21_AT)	13588_at (AL021961.24_AT)
13680_s_at (LOX1_S_AT)	13688_s_at (monopteros_S_AT)
13751_at (NOVARTIS127_AT)	13755_at (NOVARTIS15_AT)
13764_at (NOVARTIS22_AT)	13803_at (Z97341.376_AT)

13848_at (AC003981.31_AT)	13918_at (AC005388.29_AT)
13949_s_at (Z97343.352_S_AT)	13999_at (AF071527.56_AT)
14015_s_at (A71588.1_S_AT)	14016_s_at (A71596.1_S_AT)
14041_at (AC003970.28_AT)	14052_at (AC004122.24_AT)
14068_s_at (AC006922.197_S_AT)	14070_at (AL049658.217_AT)
14089_at (AC006223.65_AT)	14100_at (AF002109.108_AT)
14197_at (NOVARTIS71_AT)	14240_s_at (NR1_S_AT)
14450_at (AC002986.49_AT)	14461_at (AC006202.73_AT)
14475_at (AL021811.121_AT)	14584_at (AC007658.25_AT)
14609_at (AC002340.147_AT)	14663_s_at (trehalaseprecursor_RC_S_AT)
14667_s_at (TRPB_S_AT)	14673_s_at (TSB2_S_AT)
14675_s_at (VSP_S_AT)	14705_i_at (WT77_RC_I_AT)
14706_r_at (WT77_RC_R_AT)	14735_s_at (AF008124_S_AT)
14750_s_at (AF096370.12_S_AT)	14779_at (AC004680.71_AT)
14786_at (AC005397.115_AT)	14978_at (AC002333.49_AT)
15052_at (AC002332.103_AT)	15073_at (AC007069.93_AT)
15088_s_at (AC002311.37_S_AT)	15091_at (AC004683.97_AT)
15098_s_at (ATU26945_S_AT)	15124_s_at (ATU59508_S_AT)
15125_f_at (D85190_F_AT)	15137_s_at (ATU57320_S_AT)
15141_s_at (D85191_S_AT)	15154_s_at (ATHMTGDAS_S_AT)
15161_s_at (ATU90522_S_AT)	15162_s_at (U01880_S_AT)
15188_s_at (AF081202_S_AT)	15196_s_at (ATU43412_S_AT)
15211_s_at (ATH243813_S_AT)	15342_at (AC006593.101_AT)
15406_at (AC006931.179_AT)	15479_at (AL049483.205_AT)
15483_s_at (AC005819.20_S_AT)	15485_at (AC006233.109_AT)
15496_at (AC006282.167_AT)	15522_i_at (AL078637.213_I_AT)
15523_s_at (AL078637.213_S_AT)	15524_at (AC005508.25_AT)
15526_at (AC004122.16_AT)	15531_i_at (AL078637.191_I_AT)
15532_r_at (AL078637.191_R_AT)	15547_at (AC005970.122_AT)
15594_s_at (ATU56635_S_AT)	15622_s_at (ATU43945_S_AT)
15625_s_at (ATU74610_S_AT)	15632_s_at (AB012570_S_AT)
15665_s_at (AF022658_S_AT)	15670_s_at (AF061638_S_AT)
15792_at (AC002341.106_AT)	15798_at (AC002521.173_AT)
15839_at (AC005662.203_AT)	15859_at (AC006587.164_AT)
15874_at (AL022223.106_AT)	15886_at (AL078637.204_AT)
15982_s_at (AC006260.78_S_AT)	16063_s_at (AB008103_S_AT)
16073_f_at (AF062908_F_AT)	16108_s_at (D78604_S_AT)
16130_s_at (AF078683_S_AT)	16173_s_at (D78607_S_AT)

16203_at (AC007519.53_AT)	16272_at (AC006304.136_AT)
16298_at (AL021890.71_AT)	16301_s_at (AL031018.105_S_AT)
16306_at (AL049751.112_AT)	16357_at (AF149413.38_AT)
16363_at (AC004255.14_AT)	16398_s_at (AL022603.3_S_AT)
16405_at (AC005850.9_AT)	16461_i_at (AC004683.79_I_AT)
16462_s_at (AC004683.79_S_AT)	16470_s_at (AF068299.4_S_AT)
16510_at (AL034567.198_AT)	16522_at (X77500.2_AT)
16526_at (Z49227.1_AT)	16541_s_at (AB023423_S_AT)
16545_s_at (AF037229_S_AT)	16553_f_at (AF078821_F_AT)
16589_s_at (ATU26937_S_AT)	16603_s_at (ATU81293_S_AT)
16609_s_at (AB008104_S_AT)	16611_s_at (AB008782_S_AT)
16638_s_at (AF139098_S_AT)	16646_s_at (ATHDHS1_S_AT)
16649_s_at (ATHORF_S_AT)	16701_at (AC005312.61_AT)
16747_at (AL021713.3_AT)	16781_at (AC002392.100_AT)
16810_at (AC002339.46_AT)	16864_i_at (AF037367.4_I_AT)
16865_s_at (AF037367.4_S_AT)	16914_s_at (AL049500.57_S_AT)
16968_at (AL021961.93_AT)	16989_at (AL030978.46_AT)
16995_at (AC002391.188_AT)	17008_at (AC006585.212_AT)
17041_s_at (D89631_S_AT)	17066_s_at (ATHLIPOXY_S_AT)
17075_s_at (ATU09961_S_AT)	17104_s_at (D88541_S_AT)
17111_s_at (ATHACSC_S_AT)	17119_s_at (AF132212_S_AT)
17187_at (AF128396.2_AT)	17300_at (X66017.2_AT)
17323_at (U95973.69_AT)	17338_at (AC002535.97_AT)
17356_s_at (Z97338.190_S_AT)	17485_s_at (Z97340.345_S_AT)
17511_s_at (AF067605_S_AT)	17514_s_at (AF076277_S_AT)
17522_s_at (D78606_S_AT)	17533_s_at (ATU43488_S_AT)
17548_s_at (AF118823_S_AT)	17595_s_at (AF166352_S_AT)
17648_at (AL021684.43_AT)	17702_at (AC005700.212_AT)
17719_at (AC006592.17_AT)	17775_at (AC004392.2_AT)
17860_at (AL078467.4_AT)	17877_g_at (AJ007587.2_G_AT)
17893_at (AC004401.135_AT)	17945_at (Z97341.411_AT)
18109_s_at (AC002391.206_S_AT)	18121_s_at (AC002337.21_S_AT)
18122_at (AC002338.110_AT)	18148_at (AC004669.25_AT)
18176_at (AL035540.31_AT)	18213_at (AL022140.126_AT)
18224_s_at (AL021890.57_S_AT)	18228_at (X91259.1_AT)
18236_s_at (AC004683.69_S_AT)	18258_s_at (AC006439.222_S_AT)
18266_at (AC004684.33_AT)	18299_s_at (M23872.2_S_AT)
18587_s_at (AC007166.53_S_AT)	18590_at (AJ222713.4_AT)

18596_at (AC005698.13_AT)	18636_at (AC006577.22_AT)
18668_at (AJ249794_AT)	18735_s_at (Z29490_S_AT)
18782_at (AC003040.90_AT)	18803_at (AC005315.94_AT)
18888_at (AC007591.68_AT)	18899_s_at (X13434.1_S_AT)
18908_i_at (AF055848.2_I_AT)	18933_at (AC007020.48_AT)
18949_at (Z54136.1_AT)	18953_at (AF077955.1_AT)
18963_at (AC004561.99_AT)	19019_i_at (X82623.2_I_AT)
19060_at (AC003671.34_AT)	19110_s_at (X86947.2_S_AT)
19137_at (X74755.2_AT)	19257_s_at (AC000104.57_S_AT)
19284_at (AC003028.196_AT)	19288_at (AC005824.130_AT)
19325_at (AL022604.42_AT)	19364_at (AL022023.142_AT)
19383_at (AC006200.203_AT)	19395_at (AF007270.32_AT)
19409_at (AC007357.56_AT)	19432_s_at (AL035680.11_S_AT)
19451_at (AC004392.6_AT)	19460_s_at (AC000132.66_S_AT)
19546_at (AC005398.172_AT)	19591_at (AJ010735.4_AT)
19614_at (AC003970.32_AT)	19635_at (AL049746.38_AT)
19640_at (AC004561.78_AT)	19641_at (AC004561.66_AT)
19645_at (AC004561.70_AT)	19667_at (AL021710.5_AT)
19672_at (AC005687.19_AT)	19673_g_at (AC005687.19_G_AT)
19700_s_at (AL031326.154_S_AT)	19704_i_at (AJ005927.2_I_AT)
19707_s_at (Z95768.3_S_AT)	19755_at (AC006593.64_AT)
19762_at (AL035527.204_AT)	19818_i_at (AL021749.33_I_AT)
19851_at (U23794.3_AT)	19895_s_at (U77347.4_S_AT)
19956_at (AC006282.11_AT)	19960_at (AL035527.360_AT)
20023_at (AC006577.46_AT)	20051_at (AC000106.38_AT)
20053_at (AC002292.27_AT)	20096_at (AC004238.31_AT)
20133_i_at (AC007178.71_I_AT)	20134_s_at (AC007178.71_S_AT)
20144_at (AL079350.68_AT)	20179_at (AL035538.229_AT)
20189_at (AC005489.2_AT)	20194_at (AC007584.48_AT)
20247_at (AC004392.4_AT)	20263_at (AB004798.1_AT)
20291_s_at (M92353.4_S_AT)	20297_at (AC007153.27_AT)
20323_at (AC004561.62_AT)	20348_at (AC005967.35_AT)
20356_at (AC004561.74_AT)	20370_at (AC004561.263_AT)
20433_at (AC006232.147_AT)	20450_at (AJ005930.2_AT)
20479_i_at (AF069495.2_I_AT)	20485_at (AC007660.131_AT)
20572_s_at (AC005560.229_S_AT)	20646_at (AC002291.20_AT)
20656_at (AL035396.46_AT)	20658_s_at (AL050400.70_S_AT)
20669_s_at (AC002388.6_S_AT)	20686_at (Y14424.2_AT)

Table 8 Probe Sets as referred to in Table 6 corresponding to genes, the expression of which is increased after infection of wild-type *Arabidopsis* and altered after infection of at least one mutant *Arabidopsis* having a mutation in a gene that interferes with salicylic acid dependent signaling

12079_s_at (A71597.1_S_AT)	12081_at (AC001645.140_AT)
12115_at (AL033545.26_AT)	12150_at (AC004005.151_AT)
12233_at (AJ001807.1_AT)	12307_at (AC002392.162_AT)
12314_at (AC001229.28_AT)	12332_s_at (AB023448.2_S_AT)
12341_s_at (AL021637.176_S_AT)	12400_at (X98453.1_AT)
12438_at (AL021710.83_AT)	12475_at (Y11794.1_AT)
12487_at (AC004411.126_AT)	12497_at (AC006533.51_AT)
12500_s_at (AF081067.3_S_AT)	12530_at (Z99707.184_AT)
12574_at (X82624.2_AT)	12584_at (AC004521.233_AT)
12712_f_at (Z95774_F_AT)	12760_g_at (AC005278.32_G_AT)
12764_f_at (AC004138.69_F_AT)	12879_s_at (AIG1_S_AT)
12883_s_at (APX_S_AT)	12889_s_at (ASA1_S_AT)
12891_at (ATACS6_AT)	12892_g_at (ATACS6_G_AT)
12905_s_at (ATERF2_S_AT)	12911_s_at (ATG6PDHE5_S_AT)
12921_s_at (ATHHMGCOAR_S_AT)	12958_at (AC002332.249_AT)
12989_s_at (AC004077.149_S_AT)	13003_s_at (AB021936.1_S_AT)
13014_at (U93215.87_AT)	13040_at (AC002392.134_AT)
13070_at (AC006919.171_AT)	13094_at (AL035523.163_AT)
13157_at (AC002409.35_AT)	13190_s_at (ATTHIREDA_S_AT)
13211_s_at (BCHI_S_AT)	13212_s_at (BGL2_S_AT)
13219_s_at (CHI4_S_AT)	13273_s_at (HSF4_S_AT)
13275_f_at (HSP174_F_AT)	13370_at (AC005322.4_AT)
13381_at (AC006580.8_AT)	13538_at (AL080254.75_AT)
13565_at (AL035601.21_AT)	13588_at (AL021961.24_AT)
13589_at (AC000132.24_AT)	13617_at (AC006592.64_AT)
13627_at (AL035394.196_AT)	13656_at (AC007138.31_AT)
13659_at (AL022347.46_AT)	13666_s_at (INDOLE3GPS_S_AT)
13680_s_at (LOX1_S_AT)	13697_at (NI16_AT)
13751_at (NOVARTIS127_AT)	13755_at (NOVARTIS15_AT)
13763_at (NOVARTIS21_AT)	13764_at (NOVARTIS22_AT)
13818_s_at (AC006218.175_S_AT)	13880_s_at (AL049480.183_S_AT)
13920_at (AC005990.53_AT)	14015_s_at (A71588.1_S_AT)
14016_s_at (A71596.1_S_AT)	14025_s_at (AC007293.3_S_AT)
14030_at (AC005970.225_AT)	14032_at (AL035601.11_AT)

14041_at (AC003970.28_AT)	14052_at (AC004122.24_AT)
14068_s_at (AC006922.197_S_AT)	14110_i_at (AL035528.279_I_AT)
14139_at (NOVARTIS30_AT)	14148_at (NOVARTIS38_AT)
14170_at (NOVARTIS51_AT)	14214_at (NOVARTIS83_AT)
14242_s_at (NRA_S_AT)	14248_at (PAD3_AT)
14249_i_at (PAD4_I_AT)	14408_at (AC002291.14_AT)
14450_at (AC002986.49_AT)	14461_at (AC006202.73_AT)
14487_at (Z97341.343_AT)	14584_at (AC007658.25_AT)
14609_at (AC002340.147_AT)	14620_s_at (PAT1_S_AT)
14635_s_at (PR.1_S_AT)	14638_s_at (PRXCB_S_AT)
14663_s_at (trehalaseprecursor_RC_S_AT)	14667_s_at (TRPB_S_AT)
14672_s_at (TSA1_S_AT)	14673_s_at (TSB2_S_AT)
14735_s_at (AF008124_S_AT)	14763_at (X86958.1_AT)
14786_at (AC005397.115_AT)	14882_at (AL022605.63_AT)
14959_at (AC007202.26_AT)	14978_at (AC002333.49_AT)
15073_at (AC007069.93_AT)	15091_at (AC004683.97_AT)
15116_f_at (AF121356_F_AT)	15137_s_at (ATU57320_S_AT)
15162_s_at (U01880_S_AT)	15196_s_at (ATU43412_S_AT)
15199_s_at (AB005804_S_AT)	15216_s_at (ATU75191_S_AT)
15431_at (AL030978.64_AT)	15483_s_at (AC005819.20_S_AT)
15496_at (AC006282.167_AT)	15518_at (AC005322.28_AT)
15526_at (AC004122.16_AT)	15540_at (AC006585.205_AT)
15543_at (AF096371.10_AT)	15544_at (AL021633.110_AT)
15551_at (AL035440.289_AT)	15594_s_at (ATU56635_S_AT)
15622_s_at (ATU43945_S_AT)	15632_s_at (AB012570_S_AT)
15672_s_at (AF082299_S_AT)	15778_at (X98676.2_AT)
15779_g_at (X98676.2_G_AT)	15815_s_at (Z97342.366_S_AT)
15839_at (AC005662.203_AT)	15859_at (AC006587.164_AT)
15866_s_at (AC007133.59_S_AT)	15874_at (AL022223.106_AT)
15924_at (AC007138.61_AT)	15970_s_at (X71794.2_S_AT)
15978_at (X68592.6_AT)	15982_s_at (AC006260.78_S_AT)
16003_s_at (AL021749.64_S_AT)	16021_s_at (AL022224.182_S_AT)
16031_at (X94248.1_AT)	16043_at (AC005489.17_AT)
16053_i_at (Y14251.4_I_AT)	16083_s_at (AF153283_S_AT)
16091_s_at (ATHHSP83_S_AT)	16103_s_at (ATU60445_S_AT)
16105_s_at (ATU68017_S_AT)	16108_s_at (D78604_S_AT)
16130_s_at (AF078683_S_AT)	16233_at (AL080254.83_AT)
16272_at (AC006304.136_AT)	16299_at (AL024486.185_AT)

16306_at (AL049751.112_AT)	16340_at (AC004255.15_AT)
16357_at (AF149413.38_AT)	16363_at (AC004255.14_AT)
16383_at (AC006300.64_AT)	16409_at (AC004393.2_AT)
16461_i_at (AC004683.79_I_AT)	16462_s_at (AC004683.79_S_AT)
16470_s_at (AF068299.4_S_AT)	16570_s_at (ATHCDPKA_S_AT)
16578_s_at (ATHRPRP1B_S_AT)	16589_s_at (ATU26937_S_AT)
16594_s_at (ATU39783_S_AT)	16603_s_at (ATU81293_S_AT)
16609_s_at (AB008104_S_AT)	16701_at (AC005312.61_AT)
16721_at (AC006533.58_AT)	16781_at (AC002392.100_AT)
16810_at (AC002339.46_AT)	16864_i_at (AF037367.4_I_AT)
16865_s_at (AF037367.4_S_AT)	16914_s_at (AL049500.57_S_AT)
16968_at (AL021961.93_AT)	16995_at (AC002391.188_AT)
17007_at (AC005896.26_AT)	17051_s_at (AF098947_S_AT)
17066_s_at (ATHLIPOXY_S_AT)	17075_s_at (ATU09961_S_AT)
17128_s_at (ATHRPRP1A_S_AT)	17180_at (AF007270.30_AT)
17338_at (AC002535.97_AT)	17341_at (AL021713.89_AT)
17356_s_at (Z97338.190_S_AT)	17413_s_at (AJ006961.4_S_AT)
17451_at (AC002343.47_AT)	17452_g_at (AC002343.47_G_AT)
17484_at (X79052.2_AT)	17485_s_at (Z97340.345_S_AT)
17487_s_at (U18993.2_S_AT)	17533_s_at (ATU43488_S_AT)
17544_s_at (ATU40856_S_AT)	17585_s_at (AF134487_S_AT)
17653_at (AL035679.144_AT)	17752_at (AC003974.37_AT)
17758_at (AF076243.41_AT)	17775_at (AC004392.2_AT)
17781_at (AL049746.177_AT)	17840_s_at (AC002333.223_S_AT)
17893_at (AC004401.135_AT)	17899_at (Z97339.197_AT)
17930_s_at (AJ006960.4_S_AT)	17963_at (AL049730.88_AT)
18054_at (AJ238846_AT)	18148_at (AC004669.25_AT)
18194_i_at (AL096859.227_I_AT)	18213_at (AL022140.126_AT)
18242_g_at (AC006580.71_G_AT)	18255_at (AC005770.25_AT)
18258_s_at (AC006439.222_S_AT)	18508_s_at (AC006532.89_S_AT)
18544_at (AC007060.14_AT)	18590_at (AJ222713.4_AT)
18591_at (X74756.2_AT)	18596_at (AC005698.13_AT)
18604_at (AF069298.31_AT)	18622_g_at (AJ005902.2_G_AT)
18625_at (AC005278.22_AT)	18686_s_at (U18126_S_AT)
18698_s_at (X17528_S_AT)	18735_s_at (Z29490_S_AT)
18753_s_at (AF118222.28_S_AT)	18803_at (AC005315.94_AT)
18885_at (AC006921.147_AT)	18888_at (AC007591.68_AT)
18909_s_at (AF055848.2_S_AT)	18928_at (AC002333.181_AT)

18930_at (AC005990.57_AT)	18933_at (AC007020.48_AT)
18953_at (AF077955.1_AT)	18966_at (AC004561.106_AT)
19019_i_at (X82623.2_I_AT)	19137_at (X74755.2_AT)
19140_at (AC005170.24_AT)	19181_s_at (AF053065.2_S_AT)
19207_at (AC006069.117_AT)	19247_at (AF071527.44_AT)
19257_s_at (AC000104.57_S_AT)	19325_at (AL022604.42_AT)
19364_at (AL022023.142_AT)	19407_at (AC004697.81_AT)
19409_at (AC007357.56_AT)	19411_at (AC007661.104_AT)
19421_at (X70990.4_AT)	19432_s_at (AL035680.11_S_AT)
19451_at (AC004392.6_AT)	19460_s_at (AC000132.66_S_AT)
19465_at (AL021768.96_AT)	19546_at (AC005398.172_AT)
19555_at (AF058919.48_AT)	19624_at (AL049481.196_AT)
19641_at (AC004561.66_AT)	19667_at (AL021710.5_AT)
19741_at (AL049171.72_AT)	19755_at (AC006593.64_AT)
19818_i_at (AL021749.33_I_AT)	19881_at (AC004077.49_AT)
19892_at (AC005770.30_AT)	19944_at (AC002130.4_AT)
19956_at (AC006282.11_AT)	19970_s_at (AC003674.10_S_AT)
19982_at (AC002986.28_AT)	19991_at (AC007017.124_AT)
20017_at (AC004521.66_AT)	20030_at (AL078637.51_AT)
20051_at (AC000106.38_AT)	20098_at (AC004697.123_AT)
20133_i_at (AC007178.71_I_AT)	20134_s_at (AC007178.71_S_AT)
20144_at (AL079350.68_AT)	20245_s_at (AC005309.97_S_AT)
20247_at (AC004392.4_AT)	20269_at (AC002387.237_AT)
20271_at (Z99707.27_AT)	20287_at (Y14590.5_AT)
20288_g_at (Y14590.5_G_AT)	20291_s_at (M92353.4_S_AT)
20323_at (AC004561.62_AT)	20356_at (AC004561.74_AT)
20370_at (AC004561.263_AT)	20420_at (AL024486.131_AT)
20421_at (U81294.2_AT)	20422_g_at (U81294.2_G_AT)
20432_at (U43486.2_AT)	20450_at (AJ005930.2_AT)
20461_at (AL049480.157_AT)	20462_at (U82399.2_AT)
20479_i_at (AF069495.2_I_AT)	20480_s_at (AF069495.2_S_AT)
20529_at (Z97341.125_AT)	20572_s_at (AC005560.229_S_AT)
20589_at (AF081066.3_AT)	20669_s_at (AC002388.6_S_AT)
20685_at (AL049751.46_AT)	20689_s_at (AC002335.19_S_AT)

Table 9 Probe Sets corresponding to genes, the expression of which is downregulated (repressed) in an avrRpt-2-dependent manner in *Arabidopsis*

ProbeSet	Description
11991_g_at (AC002387.210_G_AT)	11991_g_at (AC002387.210_G_AT)gb AAB82645.1 (AC002387) unknown protein [Arabidopsis thaliana]
12091_at (AC004450.116_AT)	12091_at (AC004450.116_AT)gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
12124_s_at (Z97337.149_S_AT)	12124_s_at (Z97337.149_S_AT)emb CAB10270.1 (Z97337) imidazoleglycerol-phosphate dehydratase [Arabidopsis thaliana]
12125_at (Z97341.99_AT)	12125_at (Z97341.99_AT)emb CAB10421.1 (Z97341) hypothetical protein [Arabidopsis thaliana]
12160_at (AC006284.117_AT)	12160_at (AC006284.117_AT)gb AAD17436.1 (AC006284) unknown protein [Arabidopsis thaliana]
12191_at (AC006068.35_AT)	12191_at (AC006068.35_AT)gb AAD15440.1 (AC006068) unknown protein [Arabidopsis thaliana]
12193_at (AC006072.132_AT)	12193_at (AC006072.132_AT)gb AAD13708.1 (AC006072) unknown protein [Arabidopsis thaliana]
12223_s_at (AC007168.178_S_AT)	12223_s_at (AC007168.178_S_AT)gb AAF18668.1 AC007168_1 (AC007168) unknown protein [Arabidopsis thaliana]
12290_at (Y09418.2_AT)	12290_at (Y09418.2_AT)emb CAA70572.1 (Y09418) CDPK-related protein kinase [Arabidopsis thaliana]
12421_at (AJ002414.1_AT)	12421_at (AJ002414.1_AT)emb CAA05398.1 (AJ002414) hnRNP-like protein [Arabidopsis thaliana]
12460_s_at (AC006920.129_S_AT)	12460_s_at (AC006920.129_S_AT)gb AAD22284.1 AC006920_8 (AC006920) DNA-directed RNA polymerase II, third largest subunit [Arabidopsis thaliana]
12493_g_at (Y09095.1_G_AT)	12493_g_at (Y09095.1_G_AT)emb CAA70310.1 (Y09095) chloride channel [Arabidopsis thaliana]

ProbeSet	Description
12559_at (AC005727.83_AT)	12559_at (AC005727.83_AT)gb AAC79586.1 (AC005727) putative DOF zinc finger protein [Arabidopsis thaliana]
12560_at (AC005825.57_AT)	12560_at (AC005825.57_AT)gb AAD24598.1 AC005825_5 (AC005825) putative chloroplast outer membrane protein [Arabidopsis thaliana]
12561_at (AL021687.107_AT)	12561_at (AL021687.107_AT)emb CAA16701.1 (AL021687) putative protein [Arabidopsis thaliana]
12855_f_at (ADH_F_AT)	12855_f_at (ADH_F_AT)gb AAC00625.1 (AC002291) Alcohol Dehydrogenase [Arabidopsis thaliana]
12962_at (AC004697.165_AT)	12962_at (AC004697.165_AT)gb AAC28988.1 (AC004697) putative ABC transporter [Arabidopsis thaliana]
13221_at (CHS-WHOLE-SEQ_AT)	13221_at (CHS-WHOLE-SEQ_AT)gb AAF23561.1 AF112086_1 (AF112086) chalcone synthase [Arabidopsis thaliana]
13253_f_at (FPS1_F_AT)	13253_f_at (FPS1_F_AT)gb AAB49290.1 (U80605) farnesyl diphosphate synthase precursor [Arabidopsis thaliana]
13459_at (AF013294.21_AT)	13459_at (AF013294.21_AT)gb AAB62852.1 (AF013294) similar to auxin-induced protein [Arabidopsis thaliana]
13708_s_at (AC007259X_S_AT)	13708_s_at (AC007259X_S_AT)gb AAD50000.1 AC007259_1 3 (AC007259) Similar to protein kinases [Arabidopsis thaliana]
14428_s_at (AL023094.342_S_AT)	14428_s_at (AL023094.342_S_AT)emb CAA18852.1 (AL023094) putative protein [Arabidopsis thaliana]
15175_s_at (ATU28215_S_AT)	15175_s_at (ATU28215_S_AT)gb AAC62130.1 (AC005169) hexokinase (ATHXK2) [Arabidopsis thaliana]
15943_at (AC007202.16_AT)	15943_at (AC007202.16_AT)gb AAD30227.1 AC007202_9 (AC007202) Strong similarity to gb Y14272 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase from Pisum sativum. ESTs gb AA067485 and gb AI100551 come from this gene. [Arabidopsis thaliana]

ProbeSet	Description
19219_at (AC007019.185_AT)	19219_at (AC007019.185_AT)gb AAD20413.1 (AC007019) unknown protein [Arabidopsis thaliana]

Table 10A: Expression data for 9 probe sets corresponding to genes that are specifically induced during incompatible interaction within 3 hours

ProbeSet	Col					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12094_at	ud	303	ud	19	28	ud
12128_at	84	255	ud	0	181	ud
12712_f_at	10	278	ud	ud	90	20
13763_at	18	176	16	64	274	40
14882_at	24	385	11	62	457	46
16398_s_at	16	104	5	17	65	18
16536_s_at	24	346	19	ud	19	30
17180_at	50	361	26	93	367	76
19970_s_at	18	175	8	14	65	11
ProbeSet	Ws					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12094_at	ud	104	ud	ud	29	ud
12128_at	ud	77	ud	ud	29	ud
12712_f_at	ud	146	ud	ud	46	ud
13763_at	ud	90	ud	15	378	25
14882_at	19	255	7	23	291	32
16398_s_at	9	93	7	4	49	ud
16536_s_at	ud	409	ud	ud	4	8
17180_at	ud	200	ud	ud	259	ud
19970_s_at	11	146	5	4	46	6
ProbeSet	Ler					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12094_at	ud	121	ud	24	41	ud
12128_at	71	160	ud	33	145	ud
12712_f_at	19	113	11	24	46	14
13763_at	22	85	19	139	248	43
14882_at	50	227	25	121	321	41
16398_s_at	20	85	20	23	57	10

16536_s_at	13	110	29	ud	ud	78
17180_at	46	181	18	123	214	37
19970_s_at	23	140	13	32	55	22
ProbeSet	Cvi					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12094_at	18	166	ud	32	54	ud
12128_at	75	204	37	52	168	28
12712_f_at	11	92	ud	14	39	13
13763_at	42	166	21	133	344	25
14882_at	45	213	34	86	417	26
16398_s_at	12	52	16	25	67	14
16536_s_at	15	164	30	ud	8	23
17180_at	45	203	ud	152	263	ud
19970_s_at	25	142	11	19	68	13

Table 10B: Expression data for 18 probe sets corresponding to genes that are specifically induced during incompatible interaction in 6 hours (but not within 3 hours)

ProbeSet	Col					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12711_f_at	ud	ud	ud	ud	100	ud
13312_at	ud	118	ud	36	176	11
13370_at	ud	ud	ud	ud	144	ud
13818_s_at	ud	9	ud	65	476	21
14609_at	ud	11	4	23	233	21
14635_s_at	ud	ud	ud	42	360	13
14931_at	ud	ud	ud	10	284	16
15120_s_at	ud	ud	ud	ud	214	12
16357_at	8	70	6	14	102	26
16968_at	19	28	7	33	257	19
17134_at	ud	ud	ud	ud	199	ud
17371_at	ud	16	ud	31	191	19
17485_s_at	ud	ud	ud	ud	86	7
18631_at	10	105	ud	32	92	17
19451_at	ud	ud	ud	ud	116	ud
20323_at	20	51	19	12	280	14
20356_at	ud	ud	ud	ud	82	ud
20421_at	ud	ud	ud	26	685	20
ProbeSet	Ws					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12711_f_at	ud	ud	ud	ud	86	ud
13312_at	ud	34	ud	11	114	2
13370_at	ud	ud	ud	20	70	ud
13818_s_at	ud	12	8	10	422	10
14609_at	ud	12	ud	ud	184	3
14635_s_at	ud	ud	ud	ud	264	ud
14931_at	ud	ud	ud	ud	36	ud
15120_s_at	ud	13	ud	ud	89	ud
16357_at	ud	31	ud	ud	80	6
16968_at	ud	5	ud	12	54	ud

17134_at	ud	ud	ud	ud	27	ud
17371_at	ud	ud	ud	ud	133	ud
17485_s_at	ud	ud	ud	8	85	ud
18631_at	10	103	ud	17	81	10
19451_at	ud	6	ud	ud	52	ud
20323_at	ud	60	11	ud	119	ud
20356_at	ud	ud	ud	ud	96	ud
20421_at	ud	5	ud	ud	67	ud
ProbeSet	Ler					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12711_f_at	ud	ud	5	15	32	ud
13312_at	ud	48	ud	133	158	12
13370_at	ud	ud	ud	36	122	ud
13818_s_at	ud	ud	4	26	211	ud
14609_at	ud	ud	5	30	359	15
14635_s_at	ud	ud	ud	22	310	17
14931_at	ud	ud	ud	ud	149	ud
15120_s_at	ud	ud	ud	17	252	ud
16357_at	14	47	10	23	117	11
16968_at	14	18	5	ud	105	5
17134_at	ud	ud	ud	ud	112	ud
17371_at	ud	ud	ud	ud	ud	ud
17485_s_at	ud	ud	ud	ud	49	ud
18631_at	16	63	27	34	68	ud
19451_at	5	7	4	14	123	ud
20323_at	11	6	8	ud	11	ud
20356_at	ud	5	ud	17	111	ud
20421_at	ud	ud	ud	7	329	ud
ProbeSet	Cvi					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12711_f_at	ud	ud	ud	15	46	7
13312_at	10	64	5	60	116	ud
13370_at	ud	ud	18	40	88	ud
13818_s_at	4	ud	7	47	274	10

14609_at	8	23	6	127	778	ud
14635_s_at	6	ud	ud	179	519	44
14931_at	ud	ud	ud	23	182	ud
15120_s_at	ud	17	ud	31	150	ud
16357_at	17	52	16	32	132	16
16968_at	16	20	18	ud	56	3
17134_at	ud	ud	ud	ud	121	ud
17371_at	ud	ud	ud	ud	ud	ud
17485_s_at	ud	ud	ud	ud	55	ud
18631_at	11	41	10	24	85	ud
19451_at	4	6	ud	19	413	ud
20323_at	7	ud	ud	ud	11	ud
20356_at	ud	ud	ud	13	107	ud
20421_at	ud	20	ud	ud	293	ud

Table 10C: Expression data for 6 probe sets corresponding to genes that are activated by *P. syringae* in 6 hours. Most of them are compatible interaction-specific/preferential

ProbeSet	Col					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
13243_r_at	44	ud	24	123	91	14
14573_at	ud	ud	ud	234	32	23
14613_at	ud	ud	9	138	ud	10
18122_at	34	38	25	169	96	28
19150_at	ud	ud	3	97	4	6
19673_g_at	69	34	27	596	290	ud
ProbeSet	Ws					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
13243_r_at	27	38	16	132	96	17
14573_at	ud	ud	ud	377	63	12
14613_at	ud	10	ud	136	ud	ud
18122_at	33	56	30	235	76	24
19150_at	ud	ud	ud	218	9	ud
19673_g_at	21	6	ud	496	312	ud
ProbeSet	Ler					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
13243_r_at	66	52	45	149	59	7
14573_at	ud	ud	ud	22	17	9
14613_at	ud	ud	14	102	13	13
18122_at	42	58	42	136	60	20
19150_at	ud	ud	ud	24	7	ud
19673_g_at	30	2	10	426	181	ud
ProbeSet	Cvi					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
13243_r_at	62	42	55	142	116	ud
14573_at	ud	ud	ud	25	22	ud
14613_at	13	ud	13	63	ud	ud

18122_at	36	43	41	151	81	28
19150_at	ud	6	ud	11	3	ud
19673_g_at	ud	ud	26	41	184	ud

Pst/aR2 ... represents the incompatible interaction

Pst ... *P. syringae* pv. tomato

aR2 ... avrRpt2

ud ... undetectable

Table 11 Probe Sets corresponding to genes induced early after infection of different *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121 (at 3 or 6 hours) or by estradiol inducible

ProbeSet	Description
12737_f_at (Z97049_F_AT)	12737_f_at (Z97049_F_AT)emb CAA74603.1 (Y14207) R2R3-MYB transcription factor [Arabidopsis thaliana]
12908_s_at (ATERF5_S_AT)	12908_s_at (ATERF5_S_AT)dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
16398_s_at (AL022603.3_S_AT)	16398_s_at (AL022603.3_S_AT)emb CAA20204.1 (AL031187) serine/threonine kinase-like protein [Arabidopsis thaliana]
17105_s_at (AF055357_S_AT)	17105_s_at (AF055357_S_AT)gb AAC39479.1 (AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]
19970_s_at (AC003674.10_S_AT)	19970_s_at (AC003674.10_S_AT)gb AAB97120.1 (AC003674) unknown protein [Arabidopsis thaliana]
20620_g_at (AC005896.161_G_AT)	20620_g_at (AC005896.161_G_AT)gb AAC98070.1 (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
12094_at (AC006223.143_AT)	12094_at (AC006223.143_AT)gb AAD15401.1 (AC006223) putative alanine acetyl transferase [Arabidopsis thaliana]
13255_i_at (gammaglutamyltranspepti_I_AT)	13255_i_at (GAMMAGLUTAMYLTRANSPEPTI_I_AT)emb CAA89206.1 (Z49240) gamma-glutamyl transpeptidase [Arabidopsis thaliana]
12712_f_at (Z95774_F_AT)	12712_f_at (Z95774_F_AT)emb CAB09206.1 (Z95774) R2R3-MYB transcription factor [Arabidopsis thaliana]
13015_s_at (X98673.2_S_AT)	13015_s_at (X98673.2_S_AT)emb CAA67232.1 (X98674) zinc finger protein [Arabidopsis thaliana]
13842_at (AC002396.12_AT)	13842_at (AC002396.12_AT)gb AAC00572.1 (AC002396) similar to zinc metalloproteinases [Arabidopsis thaliana]

ProbeSet	Description
14235_at (NOVARTIS97_AT)	14235_at (NOVARTIS97_AT)gb AAF14671.1 AC011713_19 (AC011713) Similar to gb Z48431 DNA-binding protein from Avena fatua. [Arabidopsis thaliana]
15779_g_at (X98676.2_G_AT)	15779_g_at (X98676.2_G_AT)emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
16059_s_at (D88206_S_AT)	16059_s_at (D88206_S_AT)dbj BAA24694.1 (D88206) protein kinase [Arabidopsis thaliana]
17180_at (AF007270.30_AT)	17180_at (AF007270.30_AT)gb AAB61058.1 (AF007270) contains similarity to GATA-type zinc fingers (PS:PS00344) [Arabidopsis thaliana]
17303_s_at (AC004683.25_S_AT)	17303_s_at (AC004683.25_S_AT)gb AAC67339.2 (AC005499) putative WRKY-type DNA binding protein [Arabidopsis thaliana]
12571_s_at (AF149413.18_S_AT)	12571_s_at (AF149413.18_S_AT)gb AAD40138.1 AF149413_19 (AF149413) Arabidopsis thaliana ferrochelatase-I (SW:P42043); Pfam
12642_at (AC006920.138_AT)	12642_at (AC006920.138_AT)gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]
13177_at (AL049640.42_AT)	13177_at (AL049640.42_AT)emb CAB40989.1 (AL049640) growth factor like protein [Arabidopsis thaliana]
14162_at (NOVARTIS46_AT)	14162_at (NOVARTIS46_AT)No hits found less than or equal to 1e-15.
14214_at (NOVARTIS83_AT)	14214_at (NOVARTIS83_AT)gb AAF24849.1 AC012679_20 (AC012679) putative calmodulin-binding protein [Arabidopsis thaliana]
14217_at (NOVARTIS85_RC_AT)	14217_at (NOVARTIS85_RC_AT)gb AAF07816.1 AC011020_16 (AC011020) putative receptor protein kinase [Arabidopsis thaliana] thaliana. [Arabidopsis thaliana]
14711_s_at (ZFPL_S_AT)	14711_s_at (ZFPL_S_AT)gb AAD25930.1 AF085279_3 (AF085279) hypothetical Cys-3-His zinc finger protein [Arabidopsis thaliana]

ProbeSet	Description
14882_at (AL022605.63_AT)	14882_at (AL022605.63_AT)emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]
15431_at (AL030978.64_AT)	15431_at (AL030978.64_AT)emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
15680_s_at (ATHATPK19B_S_AT)	15680_s_at (ATHATPK19B_S_AT)dbj BAA07661.1 (D42061) ribosomal-protein S6 kinase homolog [Arabidopsis thaliana]
17379_at (AF085279.9_AT)	17379_at (AF085279.9_AT)gb AAF18728.1 AC018721_3 (AC018721) putative CCCH-type zinc finger protein [Arabidopsis thaliana]
18267_at (AC006223.23_AT)	18267_at (AC006223.23_AT)gb AAD15384.1 (AC006223) unknown protein [Arabidopsis thaliana]
18604_at (AF069298.31_AT)	18604_at (AF069298.31_AT)gb AAC19273.1 (AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3- acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]
19460_s_at (AC000132.66_S_AT)	19460_s_at (AC000132.66_S_AT)gb AAB60749.1 (AC000132) Identical to A. thaliana HEMA2 (gb U27118). [Arabidopsis thaliana]
15775_at (AL079344.196_AT)	15775_at (AL079344.196_AT)emb CAB45334.1 (AL079344) cytokinin oxidase-like protein [Arabidopsis thaliana]
16939_at (AC002334.110_AT)	16939_at (AC002334.110_AT)gb AAC04922.1 (AC002334) putative synaptobrevin [Arabidopsis thaliana]
18672_s_at (D13983_S_AT)	18672_s_at (D13983_S_AT)dbj BAA03090.1 (D13983) chloroplast envelope Ca ²⁺ -ATPase precursor [Arabidopsis thaliana]

Table 12 Probe Sets corresponding to genes repressed early after infection of *Arabidopsis* with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121

ProbeSet	Description
12212_at (AL049711.168_AT)	12212_at (AL049711.168_AT)emb[CAB41327.1 (AL049711) putative protein [Arabidopsis thaliana]
17555_s_at (ATU89296_S_AT)	17555_s_at (ATU89296_S_AT)gb AAB62404.1 (U89296) auxin response transcription factor 3; ARF3 [Arabidopsis thaliana]
17975_at (AF175998_AT)	17975_at (AF175998_AT)gb AAD53103.1 AF175998_1 (AF175998) putative transcription factor [Arabidopsis thaliana]
14386_at (AC005309.177_AT)	14386_at (AC005309.177_AT)gb AAC63645.1 (AC005309) unknown protein [Arabidopsis thaliana]
16613_s_at (AF012657_S_AT)	16613_s_at (AF012657_S_AT)gb AAC49845.1 (AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]
18916_s_at (X92393.1_S_AT)	18916_s_at (X92393.1_S_AT)emb CAA63131.1 (X92393) KNAT4 homeobox protein [Arabidopsis thaliana]
20443_s_at (AC006341.42_S_AT)	20443_s_at (AC006341.42_S_AT)gb AAD34693.1 AC006341_21 (AC006341) Similar to gb AF069494 cytochrome P450 from Sinapis alba and is a member of the PF 00067 Cytochrome P450 family. EST gb F14190 comes from this gene. [Arabidopsis thaliana]
20524_at (AC005698.12_AT)	20524_at (AC005698.12_AT)gb AAD43613.1 AC005698_12 (AC005698) T3P18.12 [Arabidopsis thaliana]
12609_at (X92975.2_AT)	12609_at (X92975.2_AT)emb CAA63553.1 (X92975) xyloglucan endo-transglycosylase [Arabidopsis thaliana]
20061_at (AC005508.23_AT)	20061_at (AC005508.23_AT)gb AAD14498.1 (AC005508) 37496 [Arabidopsis thaliana]

Table 13a Probe Sets corresponding to genes, the expression of which is induced in an incompatible interaction at 3 and/or 6 hours after infection of four *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121

ProbeSet	Description
12128_at (AC004261.157_AT)	12128_at (AC004261.157_AT)gb AAD12010.1 (AC004261) unknown protein [Arabidopsis thaliana]
12335_at (AC004411.73_AT)	12335_at (AC004411.73_AT)gb AAC34243.1 (AC004411) putative protein kinase [Arabidopsis thaliana]
12347_at (AC007258.28_AT)	12347_at (AC007258.28_AT)gb AAD39325.1 AC007258_14 (AC007258) Putative ATPase [Arabidopsis thaliana]
12497_at (AC006533.51_AT)	12497_at (AC006533.51_AT)gb AAD32284.1 AC006533_8 (AC006533) putative receptor-like protein kinase [Arabidopsis thaliana]
12759_at (AC005278.32_AT)	12759_at (AC005278.32_AT)gb AAC72120.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from <i>Daucus carota</i> . ESTs gb 84105 and gb AI100071 come from this gene. [Arabidopsis thaliana]
12790_s_at (AL021635.58_S_AT)	12790_s_at (AL021635.58_S_AT)emb CAA16554.1 (AL021635) cytochrome P450 like protein [Arabidopsis thaliana]
12801_at (AC005223.34_AT)	12801_at (AC005223.34_AT)gb AAD10652.1 (AC005223) Unknown protein [Arabidopsis thaliana]
12904_s_at (ATERF1_S_AT)	12904_s_at (ATERF1_S_AT)dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]
12909_s_at (ATERF6_S_AT)	12909_s_at (ATERF6_S_AT)emb CAB10530.1 (Z97343) EREBP-4 like protein [Arabidopsis thaliana]
12989_s_at (AC004077.149_S_AT)	12989_s_at (AC004077.149_S_AT)gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
13014_at (U93215.87_AT)	13014_at (U93215.87_AT)gb AAB63082.1 (U93215) putative lipase [Arabidopsis thaliana]

ProbeSet	Description
13110_at (AF074021.34_AT)	13110_at (AF074021.34_AT)gb AAD29776.1 AF074021_8 (AF074021) putative symbiosis-related protein [Arabidopsis thaliana]
13115_at (AC000375.44_AT)	13115_at (AC000375.44_AT)gb AAB60774.1 (AC000375) ESTs gb U75592,gb T13956,gb T43869 come from from this gene. [Arabidopsis thaliana]
13256_s_at (gammaglutamyltranspepti_S_AT)	13256_s_at (gammaglutamyltranspepti_S_AT)emb CAA89206.1 (Z49240) gamma-glutamyl transpeptidase [Arabidopsis thaliana]
13270_at (HSF21_AT)	13270_at (HSF21_AT)gb AAC31792.1 (U68561) heat shock transcription factor 21 [Arabidopsis thaliana]
13271_g_at (HSF21_G_AT)	13271_g_at (HSF21_G_AT)gb AAC31792.1 (U68561) heat shock transcription factor 21 [Arabidopsis thaliana]
13273_s_at (HSF4_S_AT)	13273_s_at (HSF4_S_AT)gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
13279_s_at (HSP176II_S_AT)	13279_s_at (HSP176II_S_AT)emb CAA45039.1 (X63443) heat shock protein 17.6-II [Arabidopsis thaliana]
13370_at (AC005322.4_AT)	13370_at (AC005322.4_AT)gb AAC97990.1 (AC005322) Strong similarity to Dsor1 protein kinase gb D13782 from Drosophila melanogaster. [Arabidopsis thaliana]
13645_at (AC000098.8_AT)	13645_at (AC000098.8_AT)gb AAB71443.1 (AC000098) EST gb ATTS0295 comes from this gene. [Arabidopsis thaliana]
13656_at (AC007138.31_AT)	13656_at (AC007138.31_AT)gb AAD22649.1 AC007138_13 (AC007138) predicted protein of unknown function [Arabidopsis thaliana]
13714_at (NOVARTIS101_RC_AT)	13714_at gb AAF18728.1 AC018721_3 (AC018721) putative CCCH-type zinc finger protein [Arabidopsis thaliana]
13806_at (AC002354.15_AT)	13806_at (AC002354.15_AT)gb AAB81668.1 (AC002354) NAM (no apical meristem)-like protein [Arabidopsis thaliana]

ProbeSet	Description
13818_s_at (AC006218.175_S_AT)	13818_s_at (AC006218.175_S_AT)gb AAD15433.1 (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]
14030_at (AC005970.225_AT)	14030_at (AC005970.225_AT)gb AAC95171.1 (AC005970) putative protein kinase [Arabidopsis thaliana]
14139_at (NOVARTIS30_AT)	14139_at gb AAD09343.1 (AF026538) ABA- responsive protein [Hordeum vulgare]
14141_at (NOVARTIS31_AT)	14141_at No hits found less than or equal to 1e-15.
14170_at (NOVARTIS51_AT)	14170_at gb AAF29406.1 AC022354_5 (AC022354) unknown protein [Arabidopsis thaliana]
14248_at (PAD3_AT)	14248_at (PAD3_AT)gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
14431_at (AL035394.279_AT)	14431_at (AL035394.279_AT)emb CAA23047.1 (AL035394) putative protein [Arabidopsis thaliana]
14605_at (AC006193.6_AT)	14605_at (AC006193.6_AT)gb AAD38247.1 AC006193_3 (AC006193) very similar to alcohol dehydrogenase [Arabidopsis thaliana]
14608_at (AC007357.49_AT)	14608_at (AC007357.49_AT)gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana]
14609_at (AC002340.147_AT)	14609_at (AC002340.147_AT)gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
14697_g_at (WT740_RC_G_AT)	14697_g_at (WT740_RC_G_AT)gb AAD23643.1 AC007119_9 (AC007119) unknown protein [Arabidopsis thaliana]
14763_at (X86958.1_AT)	14763_at (X86958.1_AT)emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]

ProbeSet	Description
14959_at (AC007202.26_AT)	14959_at (AC007202.26_AT)gb AAD30230.1 AC007202_12 (AC007202) T8K14.13 [Arabidopsis thaliana]
14978_at (AC002333.49_AT)	14978_at (AC002333.49_AT)gb AAB64024.1 (AC002333) putative glucosyltransferase [Arabidopsis thaliana]
15039_at (AF001308.67_AT)	15039_at (AF001308.67_AT)gb AAC78710.1 (AF001308) drought-induced-19-like 1 [Arabidopsis thaliana]
15040_g_at (AF001308.67_G_AT)	15040_g_at (AF001308.67_G_AT)gb AAC78710.1 (AF001308) drought-induced-19-like 1 [Arabidopsis thaliana]
15120_s_at (ATU10034_S_AT)	15120_s_at (ATU10034_S_AT)gb AAA93132.1 (U10034) glutamate decarboxylase [Arabidopsis thaliana]
15137_s_at (ATU57320_S_AT)	15137_s_at (ATU57320_S_AT)gb AAB47973.1 (U57320) blue copper-binding protein II [Arabidopsis thaliana]
15203_s_at (AB013887_S_AT)	15203_s_at (AB013887_S_AT)dbj BAA34251.1 (AB013887) RAV2 [Arabidopsis thaliana]
17376_at (AL021890.218_AT)	17376_at (AL021890.218_AT)emb CAA17164.1 (AL021890) putative protein [Arabidopsis thaliana]
17381_at (Z99708.402_AT)	17381_at (Z99708.402_AT)emb CAB16811.1 (Z99708) putative protein [Arabidopsis thaliana]
15551_at (AL035440.289_AT)	15551_at (AL035440.289_AT)emb CAB36537.1 (AL035440) putative dihydrolipoamide succinyltransferase [Arabidopsis thaliana]
15582_s_at (ATH131392_S_AT)	15582_s_at (ATH131392_S_AT)emb CAA10364.1 (AJ131392) alternative oxidase [Arabidopsis thaliana]
15665_s_at (AF022658_S_AT)	15665_s_at (AF022658_S_AT)gb AAB80922.1 (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]
15672_s_at (AF082299_S_AT)	15672_s_at (AF082299_S_AT)No hits found less than or equal to 1e-15.
15919_at (AC007060.42_AT)	15919_at (AC007060.42_AT)gb AAD25764.1 AC007060_22 (AC007060) EST gb AA721821 comes from this gene. [Arabidopsis thaliana]

ProbeSet	Description
15924_at (AC007138.61_AT)	15924_at (AC007138.61_AT)gb AAD22658.1 AC007138_22 (AC007138) predicted protein of unknown function [Arabidopsis thaliana]
15978_at (X68592.6_AT)	15978_at (X68592.6_AT)emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
16003_s_at (AL021749.64_S_AT)	16003_s_at (AL021749.64_S_AT)emb CAA16877.1 (AL021749) ADP, ATP carrier-like protein [Arabidopsis thaliana]
16053_i_at (Y14251.4_I_AT)	16053_i_at (Y14251.4_I_AT)emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]
16077_s_at (AF085230_S_AT)	16077_s_at (AF085230_S_AT)gb AAD16046.1 (AF085230) phytochelatin synthase 1 [Arabidopsis thaliana]
16134_s_at (AF132016_S_AT)	16134_s_at (AF132016_S_AT)gb AAD33584.1 AF132016_1 (AF132016) RING-H2 zinc finger protein ATL6 [Arabidopsis thaliana]
16151_s_at (ATHPRKINA_S_AT)	16151_s_at (ATHPRKINA_S_AT)gb AAA18853.1 (L07248) protein kinase [Arabidopsis thaliana]
16232_s_at (AL080252.77_S_AT)	16232_s_at (AL080252.77_S_AT)emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana]
16357_at (AF149413.38_AT)	16357_at (AF149413.38_AT)gb AAD40144.1 AF149413_25 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]
16442_s_at (AJ002551.2_S_AT)	16442_s_at (AJ002551.2_S_AT)emb CAA05547.1 (AJ002551) heat shock protein 70 [Arabidopsis thaliana]
16457_s_at (AC005397.17_S_AT)	16457_s_at (AC005397.17_S_AT)gb AAD23036.1 AC006526_ 2 (AC006526) unknown protein [Arabidopsis thaliana]
16539_s_at (AB013301_S_AT)	16539_s_at (AB013301_S_AT)emb CAB10530.1 (Z97343) EREBP-4 like protein [Arabidopsis thaliana]

ProbeSet	Description
16570_s_at (ATHCDPKA_S_AT)	16570_s_at (ATHCDPKA_S_AT)gb AAF27092.1 AC011809_1 (AC011809) calcium-dependent protein kinase 1 [Arabidopsis thaliana]
16620_s_at (AF051338_S_AT)	16620_s_at (AF051338_S_AT)gb AAC05572.1 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]
16638_s_at (AF139098_S_AT)	16638_s_at (AF139098_S_AT)gb AAD37511.1 AF139098_1 (AF139098) putative zinc finger protein [Arabidopsis thaliana]
16712_at (AC006068.67_AT)	16712_at (AC006068.67_AT)gb AAD15444.1 (AC006068) putative glycogenin [Arabidopsis thaliana]
16721_at (AC006533.58_AT)	16721_at (AC006533.58_AT)gb AAD32285.1 AC006533_9 (AC006533) putative poly(ADP-ribose) glycohydrolase [Arabidopsis thaliana]
16753_at (AL031032.110_AT)	16753_at (AL031032.110_AT)emb CAA19874.1 (AL031032) putative protein [Arabidopsis thaliana]
16916_s_at (X77199.8_S_AT)	16916_s_at (X77199.8_S_AT)emb CAA54420.1 (X77199) heat shock cognate 70-2 [Arabidopsis thaliana]
16968_at (AL021961.93_AT)	16968_at (AL021961.93_AT)emb CAA17559.1 (AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]
17051_s_at (AF098947_S_AT)	17051_s_at (AF098947_S_AT)gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]
17323_at (U95973.69_AT)	17323_at (U95973.69_AT)gb AAB65477.1 (U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
17352_at (AC007127.33_AT)	17352_at (AC007127.33_AT)gb AAD25140.1 AC007127_6 (AC007127) putative protein kinase [Arabidopsis thaliana]
17477_s_at (X63443.2_S_AT)	17477_s_at (X63443.2_S_AT)emb CAA45039.1 (X63443) heat shock protein 17.6-II [Arabidopsis thaliana]
17579_s_at (AF093753_S_AT)	17579_s_at (AF093753_S_AT)gb AAD50593.1 AF093753_1 (AF093753) phytochelatin synthase [Arabidopsis thaliana]

ProbeSet	Description
17775_at (AC004392.2_AT)	17775_at (AC004392.2_AT)gb AAC28500.1 (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
17840_s_at (AC002333.223_S_AT)	17840_s_at (AC002333.223_S_AT)gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
17886_at (AC004484.151_AT)	17886_at (AC004484.151_AT)gb AAC14530.1 (AC004484) unknown protein [Arabidopsis thaliana]
17894_at (AC005724.44_AT)	17894_at (AC005724.44_AT)gb AAD08938.1 (AC005724) unknown protein [Arabidopsis thaliana]
17907_s_at (AC004684.165_S_AT)	17907_s_at (AC004684.165_S_AT)gb AAC23645.1 (AC004684) unknown protein [Arabidopsis thaliana]
17990_at (AF178075_AT)	17990_at (AF178075_AT)emb CAB41312.1 (AL049711) putative calmodulin [Arabidopsis thaliana]
18167_s_at (AL021711.23_S_AT)	18167_s_at (AL021711.23_S_AT)emb CAA16745.1 (AL021711) heat shock transcription factor-like protein [Arabidopsis thaliana]
18255_at (AC005770.25_AT)	18255_at (AC005770.25_AT)gb AAC79625.1 (AC005770) unknown protein [Arabidopsis thaliana]
18263_at (AC005724.36_AT)	18263_at (AC005724.36_AT)gb AAD08937.1 (AC005724) unknown protein [Arabidopsis thaliana]
18284_at (AL021961.67_AT)	18284_at (AL021961.67_AT)emb CAA17557.1 (AL021961) putative protein [Arabidopsis thaliana]
18544_at (AC007060.14_AT)	18544_at (AC007060.14_AT)gb AAD25749.1 AC007060_7 (AC007060) Strong similarity to F19I3.8 gi 3033381 putative UDP-galactose-4-epimerase from Arabidopsis thaliana BAC gb AC004238 and is a member of PF01370 the NAD dependent epimerase/dehydratase family. EST gb AA597338 comes from this gene.
18600_at (L76926.1_AT)	18600_at (L76926.1_AT)gb AAC77829.1 (L76926) putative zinc finger protein [Arabidopsis thaliana]
18662_s_at (AC002343.20_S_AT)	18662_s_at (AC002343.20_S_AT)gb AAB63608.1 (AC002343) unknown protein [Arabidopsis thaliana]
18896_at (AC002329.51_AT)	18896_at (AC002329.51_AT)gb AAA67317.1 (L19262) 3-hydroxy-3-methylglutaryl-CoA reductase [Arabidopsis thaliana]

ProbeSet	Description
19247_at (AF071527.44_AT)	19247_at (AF071527.44_AT)gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
19411_at (AC007661.104_AT)	19411_at (AC007661.104_AT)gb AAD32774.1 AC007661_11 (AC007661) unknown protein [Arabidopsis thaliana]
19451_at (AC004392.6_AT)	19451_at (AC004392.6_AT)gb AAC28502.1 (AC004392) Similar to F4I1.26 putative beta-glucosidase gi 3128187 from A. thaliana BAC gb AC004521. ESTs gb N97083, gb F19868 and gb F15482 come from this gene. [Arabidopsis thaliana]
19462_s_at (AF001168.2_S_AT)	19462_s_at (AF001168.2_S_AT)emb CAB75467.1 (AL138659) serine/threonine-specific kinase lecRK1 precursor, lectin
19640_at (AC004561.78_AT)	19640_at (AC004561.78_AT)gb AAC95192.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
19916_at (AC006577.34_AT)	19916_at (AC006577.34_AT)gb AAD25781.1 AC006577_17 (AC006577) EST gb R64848 comes from this gene. [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	19991_at (AC007017.124_AT)gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
20051_at (AC000106.38_AT)	20051_at (AC000106.38_AT)gb AAB70412.1 (AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb Z49209). ESTs gb T44436,gb 42252 come from this gene. [Arabidopsis thaliana]
20142_at (AL035521.155_AT)	20142_at (AL035521.155_AT)emb CAB36716.1 (AL035521) extra-large G-protein-like [Arabidopsis thaliana]
20199_at (AL050300.89_AT)	20199_at (AL050300.89_AT)emb CAB43428.1 (AL050300) putative protein [Arabidopsis thaliana]
20269_at (AC002387.237_AT)	20269_at (AC002387.237_AT)gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
20335_s_at (Y14208.2_S_AT)	20335_s_at (Y14208.2_S_AT)emb CAA74604.1 (Y14208) R2R3-MYB transcription factor [Arabidopsis thaliana]

ProbeSet	Description
20356_at (AC004561.74_AT)	20356_at (AC004561.74_AT)gb AAC95191.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
20372_at (AL021713.24_AT)	20372_at (AL021713.24_AT)emb CAA16792.1 (AL021713) putative protein [Arabidopsis thaliana]
20421_at (U81294.2_AT)	20421_at (U81294.2_AT)emb CAB10242.1 (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]
20590_at (AL035540.159_AT)	20590_at (AL035540.159_AT)emb CAB37511.1 (AL035540) Phospholipase like protein [Arabidopsis thaliana]
20619_at (AC005896.161_AT)	20619_at (AC005896.161_AT)gb AAC98070.1 (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
20686_at (Y14424.2_AT)	20686_at (Y14424.2_AT)emb CAA74766.1 (Y14424) hypothetical protein [Arabidopsis thaliana]
20689_s_at (AC002335.19_S_AT)	20689_s_at (AC002335.19_S_AT)gb AAB64310.1 (AC002335) putative calcium binding protein [Arabidopsis thaliana]

Table 13b Probe Sets corresponding to genes, the expression of which is decreased in an incompatible interaction at 3 and/or 6 hours after infection of four *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121

ProbeSet	Description
12048_at (AF001308.46_AT)	12048_at (AF001308.46_AT)gb AAC78704.1 (AF001308) predicted glycosyl transferase [Arabidopsis thaliana]
12218_at (AJ242588.2_AT)	12218_at (AJ242588.2_AT)emb CAB43344.1 (AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase [Arabidopsis thaliana]
12727_f_at (Z95799_F_AT)	12727_f_at (Z95799_F_AT)gb AAD53097.1 AF175992_1 (AF175992) putative transcription factor [Arabidopsis thaliana]
13144_at (AC007017.246_AT)	13144_at (AC007017.246_AT)gb AAD21471.1 (AC007017) unknown protein [Arabidopsis thaliana]

ProbeSet	Description
13161_at (AF002109.89_AT)	13161_at (AF002109.89_AT)gb AAB95278.1 (AF002109) putative isoamylase [Arabidopsis thaliana]
13220_s_at (CHS-EXON1_S_AT)	13220_s_at (CHS-EXON1_S_AT)gb AAA32771.1 (M20308) chalcone synthase [Arabidopsis thaliana]
13482_at (AC005896.195_AT)	13482_at (AC005896.195_AT)gb AAC98071.1 (AC005896) nodulin-like protein [Arabidopsis thaliana]
13547_s_at (AC004450.15_S_AT)	13547_s_at (AC004450.15_S_AT)gb AAC64299.1 (AC004450) 3-isopropylmalate dehydratase, small subunit [Arabidopsis thaliana]
13637_at (AL049482.9_AT)	13637_at (AL049482.9_AT)emb CAB39634.1 (AL049482) AX110P-like protein [Arabidopsis thaliana]
13651_at (AL035538.320_AT)	13651_at (AL035538.320_AT)emb CAB37556.1 (AL035538) putative protein [Arabidopsis thaliana]
15832_at (AC004561.255_AT)	15832_at (AC004561.255_AT)gb AAC95217.1 (AC004561) unknown protein [Arabidopsis thaliana]
16110_s_at (AB004822_S_AT)	16110_s_at (AB004822_S_AT)dbj BAA22215.1 (AB004822) plastid RNA polymerase sigma-subunit [Arabidopsis thaliana]
16229_at (AL049638.148_AT)	16229_at (AL049638.148_AT)emb CAB40944.1 (AL049638) putative transport protein [Arabidopsis thaliana]
16351_at (AL021684.194_AT)	16351_at (AL021684.194_AT)emb CAA16688.1 (AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
16468_at (AF049870.5_AT)	16468_at (AF049870.5_AT)gb AAD02499.1 (AF049870) thaumatin-like protein [Arabidopsis thaliana]
16548_s_at (AF054617_S_AT)	16548_s_at (AF054617_S_AT)gb AAC25108.1 (AF054617) one helix protein [Arabidopsis thaliana]
16978_g_at (AF076641.2_G_AT)	16978_g_at (AF076641.2_G_AT)gb AAD46064.1 AF076641_1 (AF076641) homeodomain leucine-zipper protein ATHB16 [Arabidopsis thaliana]
17018_s_at (ATU18929_S_AT)	17018_s_at (ATU18929_S_AT)gb AAA79982.1 (U18929) cytochrome p450 dependent monooxygenase [Arabidopsis thaliana]
17494_s_at (ATU30478_S_AT)	17494_s_at (ATU30478_S_AT)gb AAB38071.1 (U30478) expansin At-EXP5 [Arabidopsis thaliana]

ProbeSet	Description
17823_s_at (AC006555.10_S_AT)	17823_s_at (AC006555.10_S_AT)gb AAD26909.1 AC007233_1 (AC007233) putative beta-1,3-glucanase [Arabidopsis thaliana]
18215_at (Z97335.114_AT)	18215_at (Z97335.114_AT)emb CAB46000.1 (Z97335) selenium-binding protein like [Arabidopsis thaliana]
18301_s_at (AL022223.48_S_AT)	18301_s_at (AL022223.48_S_AT)emb CAA18218.1 (AL022223) fructose-bisphosphate aldolase [Arabidopsis thaliana]
18471_at (AC006533.103_AT)	18471_at (AC006533.103_AT)gb AAD32293.1 AC006533_17 (AC006533) putative glucosyltransferase [Arabidopsis thaliana]
18634_s_at (Z97343.468_S_AT)	18634_s_at (Z97343.468_S_AT)emb CAB10536.1 (Z97343) hypothetical protein [Arabidopsis thaliana]
18976_at (AC000106.31_AT)	18976_at (AC000106.31_AT)gb AAB70409.1 (AC000106) Contains similarity to Rhodococcus amidase (gb D16207). ESTs gb T20504,gb H36650,gb N97423,gb H36595 come from this gene. [Arabidopsis thaliana]
18984_at (AC003096.100_AT)	18984_at (AC003096.100_AT)gb AAC16266.1 (AC003096) unknown protein [Arabidopsis thaliana]
19494_at (AC007296.26_AT)	19494_at (AC007296.26_AT)gb AAD30251.1 AC007296_12 (AC007296) Strong similarity to gb X95759 soluble-starch-synthase precursor (SSIII) from Solanum tuberosum. [Arabidopsis thaliana]
20442_i_at (AC006341.42_I_AT)	20442_i_at (AC006341.42_I_AT)gb AAD34693.1 AC006341_21 (AC006341) Similar to gb AF069494 cytochrome P450 from Sinapis alba and is a member of the PF 00067 Cytochrome P450 family. EST gb F14190 comes from this gene. [Arabidopsis thaliana]

Table 14 Probe Sets as referred to in Table 3 corresponding to genes with promoters conferring low basal expression in all ecotypes (Col, Ler, Ws, and Cvi) and high inducibility in Col

ProbeSet	Description
20421_at (U81294.2_AT)	see Table 3
20142_at (AL035521.155_AT)	see Table 3
14635_s_at (PR.1_S_AT)	see Table 3
12908_s_at (ATERF5_S_AT)	see Table 11
20620_g_at (AC005896.161_G_AT)	see Table 11

Table 15 Probe Sets as referred to in Table 3 corresponding to genes with promoters inducing expression in *Pseudomonas syringae* pv. *maculiola*-infected *Arabidopsis*

12891_at (ATACS6_AT)	13015_s_at (X98673.2_S_AT)
13100_at (AC003680.50_AT)	13115_at (AC000375.44_AT)
13217_s_at (CALMODULINLIKE_S_AT)	13467_at (AL096860.198_AT)
13645_at (AC000098.8_AT)	13818_s_at (AC006218.175_S_AT)
14032_at (AL035601.11_AT)	14248_at (PAD3_AT)
14609_at (AC002340.147_AT)	15116_f_at (AF121356_F_AT)
15622_s_at (ATU43945_S_AT)	16173_s_at (D78607_S_AT)
17485_s_at (Z97340.345_S_AT)	17511_s_at (AF067605_S_AT)
17548_s_at (AF118823_S_AT)	17775_at (AC004392.2_AT)
17930_s_at (AJ006960.4_S_AT)	19284_at (AC003028.196_AT)
19546_at (AC005398.172_AT)	19640_at (AC004561.78_AT)
20134_s_at (AC007178.71_S_AT)	20194_at (AC007584.48_AT)
20348_at (AC005967.35_AT)	12892_g_at (ATACS6_G_AT)
12904_s_at (ATERF1_S_AT)	12989_s_at (AC004077.149_S_AT)
13215_s_at (cafferoylcoAmethyltrans_S_AT)	13565_at (AL035601.21_AT)
13627_at (AL035394.196_AT)	16649_s_at (ATHORF_S_AT)
16914_s_at (AL049500.57_S_AT)	16995_at (AC002391.188_AT)
19991_at (AC007017.124_AT)	20356_at (AC004561.74_AT)

Table 16 Probe Sets corresponding to genes with promoters inducing expression in *Botrytis cinerea*-infected *Arabidopsis*

Probe Set	Description
12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]
12574_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]
12989_s_at (AC004077.149_S_AT)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
13015_s_at (X98673.2_S_AT)	emb CAA67232.1 (X98674) zinc finger protein [Arabidopsis thaliana]
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
13215_s_at (cafferoylcoAmethyltrans_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
13565_at (AL035601.21_AT)	emb CAB38206.1 (AL035601) auxin-responsive GH3-like protein [Arabidopsis thaliana]
14015_s_at (A71588.1_S_AT)	emb CAB42612.1 (A71639) unnamed protein product [Arabidopsis thaliana]
14016_s_at (A71596.1_S_AT)	emb CAB42592.1 (A71596) unnamed protein product [Arabidopsis thaliana]
14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
16638_s_at (AF139098_S_AT)	gb AAD37511.1 AF139098_1 (AF139098) putative zinc finger protein [Arabidopsis thaliana]
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
16892_at (U37336.3_AT)	gb AAC49135.1 (U37336) senescence-specific cysteine protease
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]
17533_s_at (ATU43488_S_AT)	gb AAB18367.1 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]
17744_s_at (AC004684.168_S_AT)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]

Probe Set	Description
18716_at (X91916_AT)	
18888_at (AC007591.68_AT)	gb AAD39666.1 AC007591_31 (AC007591) Is a member of the PF 00903 glyoxalase family. ESTs gb T44721, gb T21844 and gb AA395404 come from this gene. [Arabidopsis thaliana]
19019_i_at (X82623.2_I_AT)	emb CAA57943.1 (X82623) SRG2At [Arabidopsis thaliana]
19284_at (AC003028.196_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
20356_at (AC004561.74_AT)	gb AAC95191.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Table 17 Probe sets which correspond to genes downregulated in response to infection by 5 different viruses

Probe Set	Description	Function	Blast
17191_i_at (AL021961.178_I_AT)	emb CAA17564.1 (AL021961) putative protein [Arabidopsis thaliana]	DNA binding protein	MyB TF
18866_at (AC005917.178_AT)	gb AAD10163.1 (AC005917) putative Tal 1-like non-LTR retroelement protein [Arabidopsis thaliana]	transposon	
20678_at (AC007296.30_AT)	gb AAD30253.1 AC007296_14 (AC007296) ESTs gb R65381 and gb T44635 come from this gene. [Arabidopsis thaliana]	unknown	unknown
12356_at (X99952.1_AT)	emb CAA68212.1 (X99952) peroxidase [Arabidopsis thaliana]	metabolic protein	
12448_at (AC002337.58_AT)	gb AAB63824.1 (AC002337) putative acyl-CoA synthetase [Arabidopsis thaliana]	metabolic protein	
12854_s_at (ACS1_S_AT)	gb AAA96006.1 (U26542) 1- aminocyclopropane-1- carboxylate synthase-like protein [Arabidopsis thaliana]	hormone response	
13812_s_at (AC005275.104_S_AT)	gb AAD14468.1 (AC005275) putative GH3-like protein [Arabidopsis thaliana]	hormone response	
14530_at (AL021889.231_AT)	emb CAA17145.1 (AL021889) putative protein [Arabidopsis thaliana]	unknown	unknown
16461_i_at (AC004683.79_I_AT)	gb AAC28766.1 (AC004683) peroxidase [Arabidopsis thaliana]	metabolic protein	
16462_s_at (AC004683.79_S_AT)	gb AAC28766.1 (AC004683) peroxidase [Arabidopsis thaliana]	metabolic protein	
17305_at (U25649.3_AT)	gb AAC50023.1 (U25649) ATPME2 precursor [Arabidopsis thaliana]	cell wall polymer	
14965_at (AC002329.22_AT)	gb AAB86507.1 (AC002329) unknown protein [Arabidopsis thaliana]	unknown	unknown

Probe Set	Description	Function	Blast
15578_s_at (AF004213_S_AT)	gb AAC49746.1 (AF004213) ethylene-insensitive3-like1 [Arabidopsis thaliana]	hormone response	
16062_s_at (AB007789_S_AT)	gb AAD15976.1 (AF074601) CRT/DRE binding factor 2 [Arabidopsis thaliana]	stress response	
16111_f_at (AB007788_F_AT)	dbj BAA33435.1 (AB013816) DREB1B [Arabidopsis thaliana] [Arabidopsis thaliana]	stress response	
16434_at (AL021711.157_AT)	emb CAA16754.1 (AL021711) putative protein [Arabidopsis thaliana]	metabolic protein	similar to APG (non proline-rich region) [Arabidopsis thaliana] /putative GDSL- motif lipase/hydrolase
16891_s_at (AF080120.33_S_AT)	gb AAC35539.1 (AF080120) contains similarity to glycosyl hydrolases family 9 (Pfam: glycosyl_hydro5.hmm, score: 88.03) [Arabidopsis thaliana]	cell wall polymer	
16990_at (AC004684.91_AT)	gb AAC23634.1 (AC004684) putative expansin [Arabidopsis thaliana]	cell wall polymer	
17577_g_at (AF087820_G_AT)	gb AAD52697.1 AF087820_1 (AF087820) auxin transport protein [Arabidopsis thaliana]	hormone response	
17743_at (AC002341.99_AT)	gb AAB67624.1 (AC002341) putative peroxidase [Arabidopsis thaliana]	metabolic protein	
19017_at (AL035709.69_AT)	emb CAB38928.1 (AL035709) endo-xyloglucan transferase-like protein [Arabidopsis thaliana]	cell wall polymer	
19396_at (AJ001855.2_AT)	emb CAA05054.1 (AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]	structural protein	
19660_at (AC002336.29_AT)	gb AAB87577.1 (AC002336) putative expansin [Arabidopsis thaliana]	cell wall polymer	

Probe Set	Description	Function	Blast
20675_at (AC006234.204_AT)	gb AAD20920.1 (AC006234) beta-expansin [Arabidopsis thaliana]	cell wall polymer	
12086_s_at (AC002409.88_S_AT)	gb AAB86456.1 (AC002409) unknown protein [Arabidopsis thaliana]	unknown	
13728_at (NOVARTIS111_AT)	gb AAF27057.1 AC008262_6 (AC008262) F4N2.12 [Arabidopsis thaliana]	unknown	unknown
14770_s_at (AC002338.167_S_AT)	gb AAB63092.1 (U93215) putative MYB family transcription factor [Arabidopsis thaliana]	DNA binding protein	
15067_at (AC004683.36_AT)	gb AAC28758.1 (AC004683) unknown protein [Arabidopsis thaliana]	membrane protein	transporter or ferroportin
15154_s_at (ATHMTGDAS_S_AT)	emb CAB51206.1 (AL096860) glutamine-dependent asparagine synthetase [Arabidopsis thaliana]	metabolic protein	
15544_at (AL021633.110_AT)	emb CAA16532.1 (AL021633) predicted protein [Arabidopsis thaliana]	membrane protein	E. coli cation transporter ChaC
15631_s_at (AB005805_S_AT)	dbj BAA28625.1 (AB005805) aldehyde oxidase [Arabidopsis thaliana]	metabolic protein	
16048_at (X78586.2_AT)	emb CAA55323.1 (X78586) Dr4 [Arabidopsis thaliana]	stress response	
16090_s_at (ATHFAD8A_S_AT)	gb AAB60302.1 (U08216) chloroplast linoleate desaturase [Arabidopsis thaliana]	metabolic protein	
16164_s_at (ATU47029_S_AT)	gb AAC49302.1 (U47029) ERECTA [Arabidopsis thaliana]	receptor/kinase	
16241_at (AL022604.84_AT)	emb CAA18733.1 (AL022604) putative protein [Arabidopsis thaliana]	unknown	unknown
16327_at (AC002334.12_AT)	gb AAF18589.1 AC002332_1 (AC002332) putative myosin heavy chain [Arabidopsis thaliana]	structural protein	

Probe Set	Description	Function	Blast
16406_at (AC006921.33_AT)	gb AAD21431.1 (AC006921) putative protein kinase [Arabidopsis thaliana]	receptor/kinase	
16868_at (AL035679.123_AT)	emb CAB38821.1 (AL035679) putative endo-1, 4-beta- glucanase [Arabidopsis thaliana]	cell wall polymer	
17362_s_at (Z97338.181_S_AT)	emb CAB10305.1 (Z97338) glucosyltransferase [Arabidopsis thaliana]	metabolic protein	
17916_at (U22428.2_AT)	gb AAB03100.1 (U22428) starch branching enzyme class II [Arabidopsis thaliana]	metabolic protein	
18515_at (AC007063.215_AT)	gb AAF24822.1 AC007592_15 (AC007592) F12K11.17 [Arabidopsis thaliana]	metabolic protein	putative 1,3- beta-D-glucan synthase [Arabidopsis thaliana]
18635_at (AC004005.44_AT)	gb AAC23401.1 (AC004005) unknown protein [Arabidopsis thaliana]	metabolic protein	methyl C1 transferase
18667_at (AJ249442_AT)	emb CAB55758.1 (AJ249442) putative AUX1-like permease [Arabidopsis thaliana]	hormone response	
18683_s_at (L27158_S_AT)	gb AAB60302.1 (U08216) chloroplast linoleate desaturase [Arabidopsis thaliana]	metabolic protein	
18694_s_at (U89272_S_AT)	gb AAB61458.1 (U89272) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana]	membrane protein	
19870_s_at (AL021811.48_S_AT)	emb CAA16958.1 (AL021811) putative protein [Arabidopsis thaliana]	unknown	unknown

Table 18 Probe sets which correspond to genes upregulated in response to infection by 5 different viruses

Probeset	Description	Time	Function	Blast
12904_s_at (ATERF1_S_AT)	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]	5dpi	hormone response	
16063_s_at (AB008103_S_AT)	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]	5dpi	hormone response	
12906_s_at (ATERF3_S_AT)	dbj BAA32420.1 (AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]	1dpi	stress response	
16537_s_at (AB008111_S_AT)	dbj BAA28953.1 (AB008111) Atrboh F [Arabidopsis thaliana]	4dpi	stress response	
16610_s_at (AB008490_S_AT)	dbj BAA34729.1 (AB008490) response regulator 7 [Arabidopsis thaliana]	1dpi	signaling not kinase	
13645_at (AC000098.8_AT)	gb AAB71443.1 (AC000098) EST gb ATTS0295 comes from this gene. [Arabidopsis thaliana]	4-5dpi	unknown	unknown
19388_at (AC000104.61_AT)	gb AAB70450.1 (AC000104) ESTs gb N65789,gb T04628 come from this gene. [Arabidopsis thaliana]	4dpi	kinase/recep tor	prenylated Rab receptor
19368_at (AC000348.22_AT)	gb AAB61497.1 (AC000348) T7N9.21 [Arabidopsis thaliana]	5dpi	unknown	unknown
13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592,gb T13956,gb T4386 9 come from from this gene. [Arabidopsis thaliana]	4dpi	DNA binding protein	putative WRKY DNA binding protein [Oryza sativa]
14964_at (AC001229.8_AT)	gb AAB60905.1 (AC001229) F5I14.4 gene product [Arabidopsis thaliana]	5dpi	unknown	unknown
17840_s_at (AC002333.223_S_AT)	gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]	5dpi	stress response	

Probeset	Description	Time	Function	Blast
15379_at (AC002335.182_AT)	gb AAB64323.1 (AC002335) unknown protein [Arabidopsis thaliana]	1dpi	unknown	unknown
20689_s_at (AC002335.19_S_AT)	gb AAB64310.1 (AC002335) putative calcium binding protein [Arabidopsis thaliana]	5dpi	stress response	
12449_s_at (AC002343.179_S_AT)	gb AAB63623.1 (AC002343) cellulose synthase isolog [Arabidopsis thaliana]	4-5dpi	cell wall polymer	
13842_at (AC002396.12_AT)	gb AAC00572.1 (AC002396) similar to zinc metalloproteinases [Arabidopsis thaliana]	5dpi	protein processing	
19424_at (AC002396.44_AT)	gb AAC00588.1 (AC002396) glucose-6-phosphate 1- dehydrogenase [Arabidopsis thaliana]	5dpi	metabolic protein	
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]	5dpi	metabolic protein	
16365_at (AC003974.136_AT)	gb AAC04495.1 (AC003974) putative disease resistance protein [Arabidopsis thaliana]	2-5dpi	stress response	
17752_at (AC003974.37_AT)	gb AAC04483.1 (AC003974) putative protein kinase [Arabidopsis thaliana]	4dpi	kinase/recep tor	
20409_g_at (AC004077.132_G_AT)	emb CAB40383.1 (AJ131180) ribosomal protein S14 [Arabidopsis thaliana]	5dpi	protein processing	
13048_s_at (AC004138.22_S_AT)	gb AAC32906.1 (AC004138) putative basic blue protein (plantacyanin) [Arabidopsis thaliana]	4dpi	stress response	
12764_f_at (AC004138.69_F_AT)	gb AAC32912.1 (AC004138) putative glutathione S- transferase [Arabidopsis thaliana]	5dpi	stress response	
13895_at (AC004218.63_AT)	gb AAC27833.1 (AC004218) putative phospholipase [Arabidopsis thaliana]	4dpi	signaling not kinase	

Probeset	Description	Time	Function	Blast
20477_at (AC004238.154_AT)	gb AAC12841.1 (AC004238) putative UDP-N- acetylglucosamine pyrophosphorylase [Arabidopsis thaliana]	5dpi	metabolic protein	
16972_at (AC004261.89_AT)	gb AAA87347.1 (M88307) calmodulin [Brassica juncea]	5dpi	signaling not kinase	
19848_s_at (AC004261.94_S_AT)	dbj BAA08282.1 (D45848) calmodulin-related protein [Arabidopsis thaliana]	5dpi	signaling not kinase	
19044_at (AC004392.38_AT)	gb AAC28514.1 (AC004392) Strong similarity to gi 2160138 F19K23.6 gene product from A. thaliana BAC gb AC000375. [Arabidopsis thaliana]	5dpi	unknown	unknown
19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	5dpi	stress response	
20491_at (AC004561.146_AT)	gb AAC95203.1 (AC004561) putative tropinone reductase [Arabidopsis thaliana]	5dpi	metabolic protein	
16888_s_at (AC004684.174_S_AT)	gb AAC23647.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]	4dpi	stress response	
15389_at (AC004786.100_AT)	gb AAC32433.1 (AC004786) unknown protein [Arabidopsis thaliana]	4dpi	unknown	unknown
18844_at (AC005315.131_AT)	gb AAC33239.1 (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]	4dpi	signaling not kinase	
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis	5dpi	stress response	
17894_at (AC005724.44_AT)	gb AAD08938.1 (AC005724) unknown protein [Arabidopsis thaliana]	5dpi	unknown	unknown
18263_at (AC005724.36_AT)	gb AAD08937.1 (AC005724) unknown protein [Arabidopsis thaliana]	5dpi	unknown	unknown

Probeset	Description	Time	Function	Blast
15539_at (AC005770.21_AT)	gb AAC79601.1 (AC005770) unknown protein [Arabidopsis thaliana]	2dpi 4dpi	unknown	unknown
13920_at (AC005990.53_AT)	gb AAC98026.1 (AC005990) EST gb AA597511 comes from this gene. [Arabidopsis thaliana]	5dpi	unknown	unknown
18267_at (AC006223.23_AT)	gb AAD15384.1 (AC006223) unknown protein [Arabidopsis thaliana]	4dpi	unknown	unknown
12627_at (AC006533.99_AT)	gb AAD32292.1 AC006533_16 (AC006533) putative protein kinase [Arabidopsis thaliana]	1dpi	kinase/recep tor	
12497_at (AC006533.51_AT)	gb AAD32284.1 AC006533_8 (AC006533) putative receptor- like protein kinase [Arabidopsis thaliana]	5dpi	kinase/recep tor	
12656_at (AC006569.43_AT)	gb AAD21751.1 (AC006569) unknown protein [Arabidopsis thaliana]	5dpi	unknown	unknown
17008_at (AC006585.212_AT)	gb AAD23027.1 AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]	4-5dpi	metabolic protein	
19386_at (AC006592.51_AT)	No hits found less than or equal to 1e-15.	2dpi	metabolic protein	
13617_at (AC006592.64_AT)	gb AAD22351.1 AC006592_8 (AC006592) putative mitochondrial dicarboxylate carrier protein [Arabidopsis thaliana]	5dpi	unknown	unknown
15473_at (AC006836.125_AT)	gb AAD20072.1 (AC006836) putative ubiquinone biosynthesis protein [Arabidopsis thaliana]	5dpi	metabolic protein	
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]	5dpi	metabolic protein	putative xyloglucan fucosyltransf erase [Arabidopsis thaliana]
15921_s_at (AC007067.1_S_AT)	gb AAD39561.1 AC007067_1 (AC007067) T10O24.1 [Arabidopsis thaliana]	4dpi	unknown	unknown

Probeset	Description	Time	Function	Blast
14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from <i>Arabidopsis thaliana</i> and is a member of the PF00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.	5dpi	metabolic protein	
19903_at (AC007660.40_AT)	gb AAD32803.1 AC007660_4 (AC007660) unknown protein [<i>Arabidopsis thaliana</i>]	4dpi	unknown	unknown
15487_at (AC007661.87_AT)	gb AAD32771.1 AC007661_8 (AC007661) unknown protein [<i>Arabidopsis thaliana</i>]	5dpi	unknown	unknown
13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [<i>Arabidopsis thaliana</i>]	4dpi	unknown	unknown
13246_at (ERECTAL_AT)	gb AAF26067.1 AC012562_22 (AC012562) putative protein kinase [<i>Arabidopsis thaliana</i>]	4dpi	kinase/receptor	
14636_s_at (PR5_S_AT)	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [<i>Arabidopsis thaliana</i>]	2-5dpi	stress response	
16153_s_at (ATHRPRP1C_S_AT)	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [<i>Arabidopsis thaliana</i>]	2-5dpi	stress response	
16617_s_at (AF029980_S_AT)	gb AAD01897.1 (AF029980) A37 [<i>Arabidopsis thaliana</i>]	5dpi	unknown	unknown
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [<i>Arabidopsis thaliana</i>]	4dpi	cell wall polymer	
18681_at (L23573_AT)	gb AAD02548.1 (AF049922) PGP169-12 [<i>Petunia x hybrida</i>]	4dpi	membrane protein	
19181_s_at (AF053065.2_S_AT)	gb AAC39464.1 (AF053065) late embryogenesis abundant protein homolog [<i>Arabidopsis thaliana</i>]	5dpi	stress response	

Probeset	Description	Time	Function	Blast
19555_at (AF058919.48_AT)	gb AAC13630.1 (AF058919) F6N23.8 gene product [Arabidopsis thaliana]	4dpi	metabolic protein	probable methylene- tetrahydrofol- ate dehydrogenas e (NADP+)
15515_r_at (AF058919.32_R_AT)	gb AAC13627.1 (AF058919) F6N23.26 gene product [Arabidopsis thaliana]	5dpi	metabolic protein	putative phosphoribos- ylanthranilate transferase [Arabidopsis thaliana]
15606_s_at (AF061517_S_AT)	gb AAC15807.1 (AF061517) putative copper/zinc superoxide dismutase copper chaperone [Arabidopsis thaliana]	5dpi	stress response	
18604_at (AF069298.31_AT)	gb AAC19273.1 (AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]	5dpi	stress response	
12002_at (AF069442.47_AT)	gb AAC79112.1 (AF069442) hypothetical protein [Arabidopsis thaliana]	4-5dpi	protein processing	ubiquitin-like
20480_s_at (AF069495.2_S_AT)	emb CAB38908.1 (AL035708) cytochrome P450-like protein [Arabidopsis thaliana]	4-5dpi	metabolic protein	
20479_i_at (AF069495.2_I_AT)	emb CAB38908.1 (AL035708) cytochrome P450-like protein [Arabidopsis thaliana]	5dpi	metabolic protein	
19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]	4-5dpi	unknown	Ankyrin repeats
12500_s_at (AF081067.3_S_AT)	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]	4-5dpi	hormone response	

Probeset	Description	Time	Function	Blast
14711_s_at (ZFPL_S_AT)	gb AAD25930.1 AF085279_3 (AF085279) hypothetical Cys-3- His zinc finger protein [Arabidopsis thaliana]	5dpi	DNA binding protein	
20345_at (AF104919.16_AT)	gb AAC72865.1 (AF104919) similar to class I chitinases (Pfam: PF00182, E=1.2e-142, N=1) [Arabidopsis thaliana]	4dpi	stress response	
17589_at (AF156783_AT)	gb AAF00612.1 AF156783_1 (AF156783) apyrase [Arabidopsis thaliana]	5dpi	membrane protein	
18010_s_at (AJ001264_S_AT)	emb CAA77109.1 (Y18291) uncoupling protein [Arabidopsis thaliana]	5dpi	stress response	
12421_at (AJ002414.1_AT)	emb CAA05398.1 (AJ002414) hnRNP-like protein [Arabidopsis thaliana]	2dpi	RNA processing	
13284_s_at (HSP70_S_AT)	emb CAA05547.1 (AJ002551) heat shock protein 70 [Arabidopsis thaliana]	2dpi 5dpi	heat shock	
16442_s_at (AJ002551.2_S_AT)	emb CAA05547.1 (AJ002551) heat shock protein 70 [Arabidopsis thaliana]	2dpi	heat shock	
19591_at (AJ010735.4_AT)	emb CAA09330.1 (AJ010735) gr1-protein [Arabidopsis thaliana]	4dpi	stress response	
20507_at (AL021635.67_AT)	emb CAA16557.1 (AL021635) glycoprotein endopeptidase - like protein [Arabidopsis thaliana]	5dpi	metabolic protein	
19531_at (AL021960.91_AT)	emb CAA17531.1 (AL021960) amino acid transport protein AAT1 [Arabidopsis thaliana]	5dpi	membrane protein	
14595_at (AL022580.163_AT)	emb CAA18626.1 (AL022580) putative protein [Arabidopsis thaliana]	4dpi	membrane protein	putative integral membrane protein
14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]	2dpi	protein processing	vacuole processing
20142_at (AL035521.155_AT)	emb CAB36716.1 (AL035521) extra-large G-protein-like [Arabidopsis thaliana]	5dpi	signaling not kinase	

Probeset	Description	Time	Function	Blast
20516_at (AL035523.64_AT)	emb CAB36736.1 (AL035523) ubiquitin activating enzyme-like protein [Arabidopsis thaliana]	4dpi	unknown	unknown
13094_at (AL035523.163_AT)	emb CAB36745.1 (AL035523) putative protein [Arabidopsis thaliana]	5dpi	protein processing	
14032_at (AL035601.11_AT)	emb CAB38204.1 (AL035601) cytochrome P450-like protein [Arabidopsis thaliana]	2dpi 5dpi	metabolic protein	
13147_at (AL035678.99_AT)	emb CAB38794.1 (AL035678) putative protein [Arabidopsis thaliana]	5dpi	metabolic protein	HpnA protein, oxidoreducta se/cinnamyl- alcohol dehydrogenas e
19624_at (AL049481.196_AT)	emb CAB39628.1 (AL049481) cytochrome c [Arabidopsis thaliana]	4dpi	metabolic protein	
14036_at (AL049655.54_AT)	emb CAB41088.1 (AL049655) protein disulfide-isomerase-like protein [Arabidopsis thaliana]	4dpi	protein processing	
14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]	5dpi	stress response	stress
14250_r_at (PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]	5dpi	stress response	stress
16232_s_at (AL080252.77_S_AT)	emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana]	5dpi	signaling not kinase	protein phosphatase 2C, putative Ser/The phosphatase 2C
13212_s_at (BGL2_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]	2-5dpi	stress response	
16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]	2-5dpi	stress response	
15622_s_at (ATU43945_S_AT)	gb AAB40594.1 (U43945) strictosidine synthase [Arabidopsis thaliana]	4dpi	stress response	

Probeset	Description	Time	Function	Blast
14145_at (NOVARTIS35_AT)	dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]	4dpi	DNA binding protein	
15680_s_at (ATHATPK19B_S_AT)	dbj BAA07661.1 (D42061) ribosomal-protein S6 kinase homolog [Arabidopsis thaliana]	5dpi	signaling not kinase	
16173_s_at (D78607_S_AT)	dbj BAA28539.1 (D78607) cytochrome P450 monooxygenase [Arabidopsis thaliana]	4dpi	metabolic protein	
12832_f_at (U33014.2_M_F_AT)	gb AAD03342.1 (L81140) ubiquitin [Pisum sativum]	1dpi	protein degradation	
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]	5dpi	heat shock	
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]	5dpi	heat shock	
13722_at (NOVARTIS108_AT)	No hits found less than or equal to 1e-15.	5dpi	DNA binding protein	transcription factor
13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	5dpi	stress response	
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	5dpi	stress response	
13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	5dpi	stress response	
16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	5dpi	stress response	
17544_s_at (ATU40856_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]	5dpi	stress response	
12880_s_at (AIG2_S_AT)	gb AAC49283.1 (U40857) AIG2 [Arabidopsis thaliana]	1dpi	stress response	
17097_s_at (ATU66345_S_AT)	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana]	5dpi	protein processing	

Probeset	Description	Time	Function	Blast
17027_s_at (ATU72958_S_AT)	gb AAB38795.1 (U72958) AtHSP23.6-mito [Arabidopsis thaliana] protein (AtHSP23.6- mito) [Arabidopsis thaliana]	5dpi	heat shock	
14998_at (U93215.42_AT)	gb AAB63078.1 (U93215) unknown protein [Arabidopsis thaliana]	5dpi	DNA binding protein	Petroselinum crispum transcription factor (WRKY3) WRKY3 DNA- binding protein, TMV response- related gene product
13275_f_at (HSP174_F_AT)	emb CAA35182.1 (X17293) heat shock protein (AA 1 - 156) [Arabidopsis thaliana]	4-5dpi	heat shock	
12831_f_at (U33014.2_5_F_AT)	emb CAA40323.1 (X57003) polyubiquitin protein [Helianthus annuus]	1dpi	protein degradation	
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]	4dpi	metabolic protein	
15118_s_at (ATHGLUGRFS_S_AT)	emb CAA53051.1 (X75303) glutathione S-transferase [Arabidopsis thaliana]	5dpi	stress response	
17484_at (X79052.2_AT)	emb CAA55654.1 (X79052) SRG1 [Arabidopsis thaliana]	5dpi	stress response	
16236_g_at (X92657.3_G_AT)	emb CAA63346.1 (X92657) cationic amino acid transporter [Arabidopsis thaliana]	5dpi	membrane protein	
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]	5dpi	DNA binding protein	salt-tolerance zinc finger protein
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]	5dpi	DNA binding protein	A.thaliana mRNA for salt-tolerance zinc finger protein

Probeset	Description	Time	Function	Blast
20660_s_at (X97488.2_S_AT)	emb CAA66120.1 (X97488) beta-transducin like protein [Arabidopsis thaliana]	4dpi	signaling not kinase	
13015_s_at (X98673.2_S_AT)	emb CAA67232.1 (X98674) zinc finger protein [Arabidopsis thaliana]	5dpi	DNA binding protein	
16465_at (Y08892.1_AT)	emb CAA70105.1 (Y08892) Hsc70-G8 protein [Arabidopsis thaliana]	4-5dpi	heat shock	
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]	2-5dpi	heat shock	
16054_s_at (Y14251.4_S_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]	5dpi	stress response	
20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]	4-5dpi	stress response	
19178_at (Y18227.2_AT)	dbj BAA86999.1 (AB035137) blue copper binding protein [Arabidopsis thaliana]	5dpi	metabolic protein	
16943_s_at (Z97339.466_S_AT)	emb CAB10370.1 (Z97339) drought-induced protein like [Arabidopsis thaliana]	5dpi	stress response	
13803_at (Z97341.376_AT)	emb CAB10444.1 (Z97341) cyanohydrin lyase like protein [Arabidopsis thaliana]	4dpi	metabolic protein	
18140_at (Z97341.319_AT)	emb CAB10440.1 (Z97341) growth regulator like protein [Arabidopsis thaliana]	5dpi	hormone response	

Table 19 Correlation of SEQ ID NOs:1-953 (#) representing genes, the expression of which is altered after pathogen infection of *Arabidopsis* with ProbeSet designations

#	ProbeSet	#	ProbeSet
1	11991_g_at (AC002387.210_G_AT)	33	12218_at (AJ242588.2_AT)
2	11997_at (AC005967.4_AT)		12223_s_at
3	12002_at (AF069442.47_AT)	34	(AC007168.178_S_AT)
4	12004_at (AL022023.132_AT)	35	12227_at (AC007576.18_AT)
5	12007_at (Z99708.249_AT)	36	12233_at (AJ001807.1_AT)
6	12037_at (AC004005.174_AT)	37	12278_at (AJ011674.2_AT)
7	12048_at (AF001308.46_AT)	38	12290_at (Y09418.2_AT)
8	12051_at (AL021889.94_AT)	39	12307_at (AC002392.162_AT)
9	12062_at (AC006069.147_AT)	40	12314_at (AC001229.28_AT)
10	12068_at (AF118223.24_AT)	41	12317_at (AC004138.27_AT)
11	12072_at (AL035396.4_AT)	42	12323_at (AC002333.18_AT)
12	12079_s_at (A71597.1_S_AT)	43	12332_s_at (AB023448.2_S_AT)
13	12081_at (AC001645.140_AT)	44	12335_at (AC004411.73_AT)
14	12086_s_at (AC002409.88_S_AT)		12341_s_at
15	12091_at (AC004450.116_AT)	45	(AL021637.176_S_AT)
16	12092_at (AC004793.13_AT)	46	12347_at (AC007258.28_AT)
17	12094_at (AC006223.143_AT)	47	12349_s_at (X84728.6_S_AT)
18	12115_at (AL033545.26_AT)	48	12356_at (X99952.1_AT)
19	12124_s_at (Z97337.149_S_AT)	49	12369_at (AC002535.59_AT)
20	12125_at (Z97341.99_AT)	50	12400_at (X98453.1_AT)
21	12128_at (AC004261.157_AT)	51	12421_at (AJ002414.1_AT)
22	12136_at (AC007591.60_AT)	52	12438_at (AL021710.83_AT)
23	12150_at (AC004005.151_AT)	53	12448_at (AC002337.58_AT)
24	12160_at (AC006284.117_AT)		12449_s_at
25	12187_at (AC005489.31_AT)	54	(AC002343.179_S_AT)
26	12191_at (AC006068.35_AT)	55	12454_at (AC006232.164_AT)
27	12193_at (AC006072.132_AT)		12460_s_at
28	12198_at (AC006954.90_AT)	56	(AC006920.129_S_AT)
29	12203_at (AL021710.268_AT)	57	12475_at (Y11794.1_AT)
30	12212_at (AL049711.168_AT)	58	12487_at (AC004411.126_AT)
31	12216_at (AC007119.56_AT)	59	12493_g_at (Y09095.1_G_AT)
32	12217_at (AJ223804.1_AT)	60	12497_at (AC006533.51_AT)
		61	12500_s_at (AF081067.3_S_AT)
		62	12521_at (AF049236.28_AT)

#	ProbeSet	#	ProbeSet
63	12525_at (AC006587.85_AT)	96	12832_f_at (U33014.2_M_F_AT)
64	12530_at (Z99707.184_AT)	97	12851_s_at (ACCSYN1_S_AT)
65	12535_at (AL035538.156_AT)	98	12854_s_at (ACS1_S_AT)
66	12538_at (AF033205.2_AT)	99	12855_f_at (ADH_F_AT)
67	12559_at (AC005727.83_AT)	100	12879_s_at (AIG1_S_AT)
68	12560_at (AC005825.57_AT)	101	12880_s_at (AIG2_S_AT)
69	12561_at (AL021687.107_AT)	102	12883_s_at (APX_S_AT)
70	12571_s_at (AF149413.18_S_AT)	103	12889_s_at (ASA1_S_AT)
71	12574_at (X82624.2_AT)	104	12891_at (ATACS6_AT)
72	12584_at (AC004521.233_AT)	105	12892_g_at (ATACS6_G_AT)
73	12609_at (X92975.2_AT)	106	12904_s_at (ATERF1_S_AT)
74	12626_at (AC006234.95_AT)	107	12905_s_at (ATERF2_S_AT)
75	12627_at (AC006533.99_AT)	108	12906_s_at (ATERF3_S_AT)
76	12642_at (AC006920.138_AT)	109	12908_s_at (ATERF5_S_AT)
77	12645_at (AL021712.56_AT)	110	12909_s_at (ATERF6_S_AT)
78	12656_at (AC006569.43_AT)		12911_s_at
79	12698_at (AC000106.42_AT)	111	(ATG6PDHE5_S_AT)
80	12711_f_at (Z95773_F_AT)		12921_s_at
81	12712_f_at (Z95774_F_AT)	112	(ATHHMGCOAR_S_AT)
82	12727_f_at (Z95799_F_AT)	113	12930_s_at (ATLLS1_S_AT)
83	12736_f_at (Z97048_F_AT)	114	12951_at (AC005489.5_AT)
84	12737_f_at (Z97049_F_AT)	115	12958_at (AC002332.249_AT)
85	12744_at (AC001645.15_AT)	116	12962_at (AC004697.165_AT)
86	12759_at (AC005278.32_AT)	117	12965_at (AL021711.118_AT)
87	12760_g_at (AC005278.32_G_AT)		12966_s_at
88	12764_f_at (AC004138.69_F_AT)	118	(AL023094.197_S_AT)
89	12772_at (AC005278.34_AT)		12989_s_at
90	12776_at (AL021811.156_AT)	119	(AC004077.149_S_AT)
91	12790_s_at (AL021635.58_S_AT)	120	13003_s_at (AB021936.1_S_AT)
92	12797_s_at (AC007138.25_S_AT)	121	13005_at (AC004683.61_AT)
93	12801_at (AC005223.34_AT)	122	13014_at (U93215.87_AT)
94	12802_at (AL022373.153_AT)	123	13015_s_at (X98673.2_S_AT)
95	12831_f_at (U33014.2_5_F_AT)	124	13025_at (AL050400.20_AT)
		125	13040_at (AC002392.134_AT)
			13048_s_at
		126	(AC004138.22_S_AT)
		127	13070_at (AC006919.171_AT)

#	ProbeSet	#	ProbeSet
128	13094_at (AL035523.163_AT)	156	13243_r_at (ELI32_R_AT)
129	13100_at (AC003680.50_AT)	157	13244_s_at (ELI32_S_AT)
130	13110_at (AF074021.34_AT)	158	13246_at (ERECTAL_AT)
131	13115_at (AC000375.44_AT)	159	13253_f_at (FPS1_F_AT)
132	13119_at (AC007260.23_AT)		13255_i_at
133	13128_at (AL049607.47_AT)	160	(gammaglutamyltranspepti_I_AT)
134	13134_s_at (AC002337.9_S_AT)		13256_s_at
135	13137_at (AC007169.86_AT)	161	(gammaglutamyltranspepti_S_AT)
136	13144_at (AC007017.246_AT)		13259_s_at
137	13147_at (AL035678.99_AT)	162	(glutathioneperoxidase1_S_AT)
	13152_s_at		13261_s_at
138	(AC005322.24_S_AT)	163	(glutathionereductase1_S_AT)
	13154_s_at	164	13263_s_at (GST1_RC_S_AT)
139	(AC002333.210_S_AT)	165	13266_s_at (GST4_S_AT)
140	13157_at (AC002409.35_AT)	166	13270_at (HSF21_AT)
141	13161_at (AF002109.89_AT)	167	13271_g_at (HSF21_G_AT)
	13163_s_at	168	13273_s_at (HSF4_S_AT)
142	(AC005560.223_S_AT)	169	13275_f_at (HSP174_F_AT)
143	13176_at (AL031394.56_AT)	170	13277_i_at (HSP176A_I_AT)
144	13177_at (AL049640.42_AT)	171	13279_s_at (HSP176II_S_AT)
145	13187_i_at (ATTHIRED4_I_AT)	172	13284_s_at (HSP70_S_AT)
	13188_r_at	173	13285_s_at (HSP83_S_AT)
146	(ATTHIRED4_R_AT)	174	13312_at (AC006223.75_AT)
	13189_s_at	175	13367_at (AC004680.97_AT)
147	(ATTHIRED4_S_AT)	176	13370_at (AC005322.4_AT)
148	13190_s_at (ATTHIREDA_S_AT)	177	13381_at (AC006580.8_AT)
149	13211_s_at (BCHI_S_AT)	178	13395_at (AL035528.202_AT)
150	13212_s_at (BGL2_S_AT)	179	13435_at (AF003102.3_AT)
	13215_s_at	180	13437_at (AF096371.8_AT)
151	(CAFFEROYLCOAMETHYLTR ANS_S_AT)	181	13450_at (AL049657.33_AT)
	13217_s_at	182	13459_at (AF013294.21_AT)
152	(CALMODULINLIKE_S_AT)	183	13467_at (AL096860.198_AT)
153	13219_s_at (CHI4_S_AT)	184	13480_at (AC005223.15_AT)
	13220_s_at (CHS-	185	13482_at (AC005896.195_AT)
154	EXON1_S_AT)	186	13534_at (AF149413.36_AT)
	13221_at (CHS-WHOLE-	187	13536_at (AL021636.47_AT)
155	SEQ_AT)	188	13538_at (AL080254.75_AT)

#	ProbeSet	#	ProbeSet
189	13547_s_at (AC004450.15_S_AT)	220	13755_at (NOVARTIS15_AT)
190	13564_at (AC005312.113_AT)	221	13763_at (NOVARTIS21_AT)
191	13565_at (AL035601.21_AT)	222	13764_at (NOVARTIS22_AT)
192	13584_at (AC007127.23_AT)	223	13789_at (AJ132436.2_AT)
193	13588_at (AL021961.24_AT)	224	13803_at (Z97341.376_AT)
194	13589_at (AC000132.24_AT)	225	13806_at (AC002354.15_AT)
195	13604_at (AC000104.20_AT)		13812_s_at
196	13605_at (AL078470.75_AT)	226	(AC005275.104_S_AT)
197	13617_at (AC006592.64_AT)		13818_s_at
198	13627_at (AL035394.196_AT)	227	(AC006218.175_S_AT)
199	13637_at (AL049482.9_AT)	228	13825_s_at (AF104919.22_S_AT)
200	13645_at (AC000098.8_AT)	229	13834_at (AL080237.29_AT)
201	13647_at (AF000657.22_AT)	230	13842_at (AC002396.12_AT)
202	13651_at (AL035538.320_AT)	231	13848_at (AC003981.31_AT)
203	13656_at (AC007138.31_AT)		13880_s_at
204	13659_at (AL022347.46_AT)	232	(AL049480.183_S_AT)
	13666_s_at	233	13895_at (AC004218.63_AT)
205	(INDOLE3GPS_S_AT)	234	13896_at (AC004473.8_AT)
206	13680_s_at (LOX1_S_AT)	235	13908_s_at (A71590.1_S_AT)
207	13685_s_at (MLOLIKE2_S_AT)	236	13918_at (AC005388.29_AT)
	13688_s_at	237	13920_at (AC005990.53_AT)
208	(MONOPTEROS_S_AT)	238	13944_at (U89959.24_AT)
209	13697_at (NI16_AT)	239	13949_s_at (Z97343.352_S_AT)
210	13705_s_at (AC003671X_S_AT)	240	13963_at (AL021711.26_AT)
211	13706_s_at (AC005724X_S_AT)	241	13964_at (AL021889.3_AT)
212	13708_s_at (AC007259X_S_AT)	242	13966_at (AL022023.172_AT)
	13714_at	243	13999_at (AF071527.56_AT)
213	(NOVARTIS101_RC_AT)	244	14015_s_at (A71588.1_S_AT)
	13716_at	245	14016_s_at (A71596.1_S_AT)
214	(NOVARTIS103_RC_AT)	246	14025_s_at (AC007293.3_S_AT)
	13718_at	247	14026_at (AC000106.5_AT)
215	(NOVARTIS105_RC_AT)	248	14030_at (AC005970.225_AT)
216	13722_at (NOVARTIS108_AT)	249	14032_at (AL035601.11_AT)
217	13728_at (NOVARTIS111_AT)	250	14036_at (AL049655.54_AT)
	13746_at	251	14041_at (AC003970.28_AT)
218	(NOVARTIS121_RC_AT)	252	14052_at (AC004122.24_AT)
219	13751_at (NOVARTIS127_AT)		

#	ProbeSet	#	ProbeSet
	14068_s_at	286	14448_at (AC002387.243_AT)
253	(AC006922.197_S_AT)	287	14450_at (AC002986.49_AT)
254	14070_at (AL049658.217_AT)	288	14459_at (AC006200.69_AT)
255	14083_at (AC005662.56_AT)	289	14460_at (AC006201.21_AT)
256	14089_at (AC006223.65_AT)	290	14461_at (AC006202.73_AT)
257	14100_at (AF002109.108_AT)	291	14468_at (AC007576.62_AT)
258	14110_i_at (AL035528.279_I_AT)	292	14475_at (AL021811.121_AT)
259	14116_at (AF077407.30_AT)	293	14487_at (Z97341.343_AT)
260	14122_at (AF058826.23_AT)	294	14498_at (AC004261.51_AT)
261	14139_at (NOVARTIS30_AT)	295	14530_at (AL021889.231_AT)
262	14141_at (NOVARTIS31_AT)	296	14573_at (AF069298.35_AT)
263	14145_at (NOVARTIS35_AT)	297	14584_at (AC007658.25_AT)
264	14148_at (NOVARTIS38_AT)	298	14591_at (AL035440.107_AT)
265	14162_at (NOVARTIS46_AT)	299	14595_at (AL022580.163_AT)
266	14170_at (NOVARTIS51_AT)	300	14605_at (AC006193.6_AT)
267	14197_at (NOVARTIS71_AT)	301	14608_at (AC007357.49_AT)
268	14214_at (NOVARTIS83_AT)	302	14609_at (AC002340.147_AT)
	14217_at	303	14613_at (AC004669.20_AT)
269	(NOVARTIS85_RC_AT)	304	14614_at (AC004165.66_AT)
270	14223_at (NOVARTIS9_AT)	305	14620_s_at (PAT1_S_AT)
271	14235_at (NOVARTIS97_AT)	306	14635_s_at (PR.1_S_AT)
272	14240_s_at (NR1_S_AT)	307	14636_s_at (PR5_S_AT)
273	14242_s_at (NRA_S_AT)	308	14638_s_at (PRXCB_S_AT)
274	14248_at (PAD3_AT)		14640_s_at
275	14249_i_at (PAD4_I_AT)	309	(PUTATIVEMLOHI_S_AT)
276	14250_r_at (PAD4_R_AT)	310	14643_s_at (RAR047_S_AT)
277	14254_s_at (PAL1-MRNA_S_AT)		14660_s_at
	14256_f_at (PAL1-	311	(THIOREDOXL_S_AT)
278	INTRON_F_AT)		14663_s_at
279	14257_s_at (PAL2-MRNA_S_AT)		(TREHALASEPRECUSOR_RC_
280	14320_at (AC005956.54_AT)	312	S_AT)
281	14381_at (AC002521.68_AT)	313	14667_s_at (TRPB_S_AT)
282	14386_at (AC005309.177_AT)	314	14672_s_at (TSA1_S_AT)
283	14408_at (AC002291.14_AT)	315	14673_s_at (TSB2_S_AT)
	14428_s_at	316	14675_s_at (VSP_S_AT)
284	(AL023094.342_S_AT)		14682_i_at
285	14431_at (AL035394.279_AT)	317	(WT1012A_RC_I_AT)

#	ProbeSet	#	ProbeSet
318	14686_s_at (WT1073_S_AT)	352	15067_at (AC004683.36_AT)
319	14696_at (WT740_RC_AT)	353	15073_at (AC007069.93_AT)
320	14697_g_at (WT740_RC_G_AT)		15085_s_at
321	14705_i_at (WT77_RC_I_AT)	354	(AL031018.274_S_AT)
322	14706_r_at (WT77_RC_R_AT)	355	15088_s_at (AC002311.37_S_AT)
323	14711_s_at (ZFPL_S_AT)	356	15091_at (AC004683.97_AT)
324	14735_s_at (AF008124_S_AT)	357	15098_s_at (ATU26945_S_AT)
325	14750_s_at (AF096370.12_S_AT)	358	15116_f_at (AF121356_F_AT)
326	14763_at (X86958.1_AT)		15118_s_at
	14770_s_at	359	(ATHGLUGRFS_S_AT)
327	(AC002338.167_S_AT)	360	15120_s_at (ATU10034_S_AT)
328	14779_at (AC004680.71_AT)	361	15123_s_at (ATU40857_S_AT)
329	14780_at (AC004683.103_AT)	362	15124_s_at (ATU59508_S_AT)
330	14786_at (AC005397.115_AT)	363	15125_f_at (D85190_F_AT)
331	14793_at (AC006202.10_AT)	364	15129_s_at (AF030386_S_AT)
332	14838_s_at (M96073.6_S_AT)	365	15132_s_at (AF121878_S_AT)
333	14882_at (AL022605.63_AT)	366	15137_s_at (ATU57320_S_AT)
334	14884_at (AL031032.95_AT)	367	15140_s_at (ATU93845_S_AT)
335	14895_s_at (Z97344.138_S_AT)	368	15141_s_at (D85191_S_AT)
336	14900_at (AC000348.12_AT)		15154_s_at
337	14923_at (AC006283.158_AT)	369	(ATHMTGDAS_S_AT)
338	14924_at (AC006283.46_AT)	370	15161_s_at (ATU90522_S_AT)
339	14928_at (AC006569.88_AT)	371	15162_s_at (U01880_S_AT)
340	14931_at (AC006951.173_AT)	372	15175_s_at (ATU28215_S_AT)
341	14959_at (AC007202.26_AT)	373	15188_s_at (AF081202_S_AT)
342	14964_at (AC001229.8_AT)	374	15192_s_at (ATHERD1_S_AT)
343	14965_at (AC002329.22_AT)	375	15196_s_at (ATU43412_S_AT)
344	14972_at (AC005499.38_AT)	376	15197_s_at (ATU52851_S_AT)
345	14978_at (AC002333.49_AT)	377	15199_s_at (AB005804_S_AT)
346	14998_at (U93215.42_AT)	378	15203_s_at (AB013887_S_AT)
347	15032_at (AC002294.8_AT)	379	15211_s_at (ATH243813_S_AT)
348	15039_at (AF001308.67_AT)	380	15216_s_at (ATU75191_S_AT)
	15040_g_at	381	15342_at (AC006593.101_AT)
349	(AF001308.67_G_AT)	382	15379_at (AC002335.182_AT)
350	15042_at (AL021961.3_AT)	383	15389_at (AC004786.100_AT)
351	15052_at (AC002332.103_AT)	384	15406_at (AC006931.179_AT)

#	ProbeSet	#	ProbeSet
385	15431_at (AL030978.64_AT)	415	15622_s_at (ATU43945_S_AT)
386	15463_at (AL031326.226_AT)	416	15625_s_at (ATU74610_S_AT)
387	15473_at (AC006836.125_AT)	417	15629_s_at (AB003280_S_AT)
388	15479_at (AL049483.205_AT)	418	15631_s_at (AB005805_S_AT)
	15483_s_at	419	15632_s_at (AB012570_S_AT)
389	(AC005819.20_S_AT)	420	15641_s_at (AF117063_S_AT)
390	15485_at (AC006233.109_AT)	421	15646_s_at (ATHSAT1G_S_AT)
391	15487_at (AC007661.87_AT)	422	15665_s_at (AF022658_S_AT)
392	15496_at (AC006282.167_AT)	423	15669_s_at (AF047834_S_AT)
	15515_r_at	424	15670_s_at (AF061638_S_AT)
393	(AF058919.32_R_AT)	425	15672_s_at (AF082299_S_AT)
394	15518_at (AC005322.28_AT)	426	15674_s_at (AF091844_S_AT)
395	15522_i_at (AL078637.213_I_AT)		15680_s_at
	15523_s_at	427	(ATHATPK19B_S_AT)
396	(AL078637.213_S_AT)	428	15775_at (AL079344.196_AT)
397	15524_at (AC005508.25_AT)	429	15778_at (X98676.2_AT)
398	15526_at (AC004122.16_AT)	430	15779_g_at (X98676.2_G_AT)
	15531_i_at	431	15792_at (AC002341.106_AT)
399	(AL078637.191_I_AT)	432	15798_at (AC002521.173_AT)
	15532_r_at	433	15815_s_at (Z97342.366_S_AT)
400	(AL078637.191_R_AT)	434	15832_at (AC004561.255_AT)
401	15539_at (AC005770.21_AT)	435	15839_at (AC005662.203_AT)
402	15540_at (AC006585.205_AT)	436	15859_at (AC006587.164_AT)
403	15543_at (AF096371.10_AT)	437	15866_s_at (AC007133.59_S_AT)
404	15544_at (AL021633.110_AT)	438	15874_at (AL022223.106_AT)
405	15547_at (AC005970.122_AT)	439	15886_at (AL078637.204_AT)
406	15551_at (AL035440.289_AT)	440	15900_at (AC005311.74_AT)
407	15578_s_at (AF004213_S_AT)	441	15919_at (AC007060.42_AT)
408	15580_s_at (AF057043_S_AT)	442	15921_s_at (AC007067.1_S_AT)
409	15582_s_at (ATH131392_S_AT)	443	15924_at (AC007138.61_AT)
410	15594_s_at (ATU56635_S_AT)	444	15943_at (AC007202.16_AT)
411	15606_s_at (AF061517_S_AT)	445	15970_s_at (X71794.2_S_AT)
	15613_s_at	446	15978_at (X68592.6_AT)
412	(ATHHOMEOA_S_AT)		15982_s_at
	15614_s_at	447	(AC006260.78_S_AT)
413	(ATHMER15B_S_AT)	448	16001_at (AF035385.2_AT)
414	15617_s_at (ATHSAR1_S_AT)		

#	ProbeSet	#	ProbeSet
	16003_s_at	481	16173_s_at (D78607_S_AT)
449	(AL021749.64_S_AT)	482	16203_at (AC007519.53_AT)
	16021_s_at	483	16229_at (AL049638.148_AT)
450	(AL022224.182_S_AT)	484	16230_at (AL049655.78_AT)
451	16031_at (X94248.1_AT)		16232_s_at
452	16043_at (AC005489.17_AT)	485	(AL080252.77_S_AT)
453	16048_at (X78586.2_AT)	486	16233_at (AL080254.83_AT)
454	16053_i_at (Y14251.4_I_AT)	487	16236_g_at (X92657.3_G_AT)
455	16054_s_at (Y14251.4_S_AT)	488	16241_at (AL022604.84_AT)
456	16058_s_at (ATU94495_S_AT)	489	16272_at (AC006304.136_AT)
457	16059_s_at (D88206_S_AT)	490	16288_at (AF024504.17_AT)
458	16062_s_at (AB007789_S_AT)	491	16298_at (AL021890.71_AT)
459	16063_s_at (AB008103_S_AT)	492	16299_at (AL024486.185_AT)
460	16073_f_at (AF062908_F_AT)		16301_s_at
461	16077_s_at (AF085230_S_AT)	493	(AL031018.105_S_AT)
462	16080_f_at (AF118822_F_AT)	494	16306_at (AL049751.112_AT)
463	16083_s_at (AF153283_S_AT)	495	16327_at (AC002334.12_AT)
	16087_s_at		16329_s_at
464	(ATHATPK6A_S_AT)	496	(AF013294.17_S_AT)
465	16090_s_at (ATHFAD8A_S_AT)	497	16335_at (AL079347.105_AT)
466	16091_s_at (ATHHSP83_S_AT)	498	16340_at (AC004255.15_AT)
467	16092_s_at (ATHKAT1_S_AT)	499	16351_at (AL021684.194_AT)
468	16103_s_at (ATU60445_S_AT)	500	16357_at (AF149413.38_AT)
469	16105_s_at (ATU68017_S_AT)	501	16363_at (AC004255.14_AT)
470	16108_s_at (D78604_S_AT)	502	16365_at (AC003974.136_AT)
471	16110_s_at (AB004822_S_AT)	503	16383_at (AC006300.64_AT)
472	16111_f_at (AB007788_F_AT)	504	16391_at (AL050351.194_AT)
473	16130_s_at (AF078683_S_AT)	505	16398_s_at (AL022603.3_S_AT)
474	16133_s_at (AF089810_S_AT)	506	16405_at (AC005850.9_AT)
475	16134_s_at (AF132016_S_AT)	507	16406_at (AC006921.33_AT)
	16151_s_at	508	16409_at (AC004393.2_AT)
476	(ATHPRKINA_S_AT)	509	16434_at (AL021711.157_AT)
	16153_s_at		16440_s_at
477	(ATHRPRP1C_S_AT)	510	(AF002109.137_S_AT)
478	16159_s_at (ATU37697_S_AT)	511	16442_s_at (AJ002551.2_S_AT)
479	16161_s_at (ATU39072_S_AT)		16457_s_at
480	16164_s_at (ATU47029_S_AT)	512	(AC005397.17_S_AT)

#	ProbeSet	#	ProbeSet
513	16461_i_at (AC004683.79_I_AT)	547	16649_s_at (ATHORF_S_AT)
	16462_s_at	548	16701_at (AC005312.61_AT)
514	(AC004683.79_S_AT)	549	16712_at (AC006068.67_AT)
515	16465_at (Y08892.1_AT)	550	16721_at (AC006533.58_AT)
516	16468_at (AF049870.5_AT)	551	16747_at (AL021713.3_AT)
517	16470_s_at (AF068299.4_S_AT)	552	16753_at (AL031032.110_AT)
518	16483_at (X68053_AT)	553	16781_at (AC002392.100_AT)
519	16496_s_at (AF030386.1_S_AT)	554	16810_at (AC002339.46_AT)
520	16510_at (AL034567.198_AT)	555	16817_s_at (AL096882.91_S_AT)
521	16522_at (X77500.2_AT)	556	16859_at (AL035523.135_AT)
522	16524_at (AC006577.38_AT)	557	16864_i_at (AF037367.4_I_AT)
523	16526_at (Z49227.1_AT)	558	16865_s_at (AF037367.4_S_AT)
524	16536_s_at (AB008107_S_AT)	559	16868_at (AL035679.123_AT)
525	16537_s_at (AB008111_S_AT)		16888_s_at
526	16538_s_at (AB010259_S_AT)	560	(AC004684.174_S_AT)
527	16539_s_at (AB013301_S_AT)		16891_s_at
528	16541_s_at (AB023423_S_AT)	561	(AF080120.33_S_AT)
529	16545_s_at (AF037229_S_AT)	562	16892_at (U37336.3_AT)
530	16548_s_at (AF054617_S_AT)	563	16902_at (AC007119.67_AT)
531	16553_f_at (AF078821_F_AT)		16903_g_at
	16568_s_at	564	(AC007119.67_G_AT)
532	(ATHATCDPK_S_AT)	565	16908_at (AC002396.22_AT)
533	16570_s_at (ATHCDPKA_S_AT)	566	16914_s_at (AL049500.57_S_AT)
534	16578_s_at (ATHRPRP1B_S_AT)	567	16916_s_at (X77199.8_S_AT)
535	16589_s_at (ATU26937_S_AT)	568	16927_s_at (AF035384.2_S_AT)
536	16594_s_at (ATU39783_S_AT)	569	16939_at (AC002334.110_AT)
537	16603_s_at (ATU81293_S_AT)		16940_g_at
538	16609_s_at (AB008104_S_AT)	570	(AC002334.110_G_AT)
539	16610_s_at (AB008490_S_AT)	571	16943_s_at (Z97339.466_S_AT)
540	16611_s_at (AB008782_S_AT)	572	16951_i_at (AC005662.30_I_AT)
541	16613_s_at (AF012657_S_AT)	573	16952_s_at (AC005662.30_S_AT)
542	16617_s_at (AF029980_S_AT)	574	16955_at (AL031326.215_AT)
543	16620_s_at (AF051338_S_AT)	575	16968_at (AL021961.93_AT)
544	16635_s_at (AF126057_S_AT)	576	16970_s_at (Y18291.5_S_AT)
545	16638_s_at (AF139098_S_AT)	577	16972_at (AC004261.89_AT)
546	16646_s_at (ATHDHS1_S_AT)	578	16978_g_at (AF076641.2_G_AT)
		579	16981_s_at (U35829.2_S_AT)

#	ProbeSet	#	ProbeSet
580	16989_at (AL030978.46_AT)	613	17362_s_at (Z97338.181_S_AT)
581	16990_at (AC004684.91_AT)	614	17371_at (AF076243.44_AT)
582	16995_at (AC002391.188_AT)	615	17376_at (AL021890.218_AT)
583	17007_at (AC005896.26_AT)	616	17379_at (AF085279.9_AT)
584	17008_at (AC006585.212_AT)	617	17380_at (AL021961.39_AT)
585	17009_at (AL021633.163_AT)	618	17381_at (Z99708.402_AT)
586	17018_s_at (ATU18929_S_AT)	619	17398_at (AC002535.143_AT)
587	17027_s_at (ATU72958_S_AT)	620	17413_s_at (AJ006961.4_S_AT)
588	17039_s_at (D78602_S_AT)	621	17451_at (AC002343.47_AT)
589	17041_s_at (D89631_S_AT)		17452_g_at
590	17051_s_at (AF098947_S_AT)	622	(AC002343.47_G_AT)
	17066_s_at	623	17458_at (AC006260.91_AT)
591	(ATHLIPOXY_S_AT)	624	17464_at (AC000132.72_AT)
592	17073_s_at (ATT54391_S_AT)	625	17477_s_at (X63443.2_S_AT)
593	17075_s_at (ATU09961_S_AT)	626	17482_s_at (Z97343.441_S_AT)
594	17083_s_at (ATU18770_S_AT)	627	17484_at (X79052.2_AT)
595	17097_s_at (ATU66345_S_AT)	628	17485_s_at (Z97340.345_S_AT)
596	17104_s_at (D88541_S_AT)	629	17487_s_at (U18993.2_S_AT)
597	17105_s_at (AF055357_S_AT)	630	17490_s_at (M90416.2_S_AT)
598	17111_s_at (ATHACSC_S_AT)	631	17494_s_at (ATU30478_S_AT)
599	17119_s_at (AF132212_S_AT)		17500_s_at
	17128_s_at	632	(ATHCALLGA_S_AT)
600	(ATHRPRP1A_S_AT)	633	17511_s_at (AF067605_S_AT)
601	17134_at (AC000106.53_AT)	634	17514_s_at (AF076277_S_AT)
602	17180_at (AF007270.30_AT)	635	17516_s_at (AF072536_S_AT)
603	17187_at (AF128396.2_AT)	636	17522_s_at (D78606_S_AT)
	17191_i_at	637	17533_s_at (ATU43488_S_AT)
604	(AL021961.178_I_AT)	638	17544_s_at (ATU40856_S_AT)
605	17300_at (X66017.2_AT)	639	17548_s_at (AF118823_S_AT)
	17303_s_at	640	17555_s_at (ATU89296_S_AT)
606	(AC004683.25_S_AT)	641	17577_g_at (AF087820_G_AT)
607	17305_at (U25649.3_AT)	642	17578_at (AF093604_AT)
608	17323_at (U95973.69_AT)	643	17579_s_at (AF093753_S_AT)
609	17338_at (AC002535.97_AT)	644	17585_s_at (AF134487_S_AT)
610	17341_at (AL021713.89_AT)	645	17589_at (AF156783_AT)
611	17352_at (AC007127.33_AT)	646	17595_s_at (AF166352_S_AT)
612	17356_s_at (Z97338.190_S_AT)		

#	ProbeSet	#	ProbeSet
647	17636_at (AF077409.7_AT)	679	17975_at (AF175998_AT)
648	17648_at (AL021684.43_AT)	680	17990_at (AF178075_AT)
649	17653_at (AL035679.144_AT)	681	18010_s_at (AJ001264_S_AT)
650	17702_at (AC005700.212_AT)	682	18012_s_at (AJ002295_S_AT)
651	17719_at (AC006592.17_AT)	683	18045_at (AJ011976_AT)
652	17743_at (AC002341.99_AT)	684	18054_at (AJ238846_AT)
	17744_s_at		18109_s_at
653	(AC004684.168_S_AT)	685	(AC002391.206_S_AT)
654	17752_at (AC003974.37_AT)	686	18121_s_at (AC002337.21_S_AT)
655	17758_at (AF076243.41_AT)	687	18122_at (AC002338.110_AT)
656	17775_at (AC004392.2_AT)	688	18140_at (Z97341.319_AT)
657	17781_at (AL049746.177_AT)	689	18148_at (AC004669.25_AT)
	17823_s_at		18167_s_at
658	(AC006555.10_S_AT)	690	(AL021711.23_S_AT)
	17840_s_at	691	18176_at (AL035540.31_AT)
659	(AC002333.223_S_AT)		18194_i_at
660	17854_at (Z99707.366_AT)	692	(AL096859.227_I_AT)
661	17860_at (AL078467.4_AT)	693	18213_at (AL022140.126_AT)
662	17876_at (AJ007587.2_AT)	694	18215_at (97335.114_AT)
663	17877_g_at (J007587.2_G_AT)	695	18216_at (X95573.2_AT)
664	17881_at (AC002391.54_AT)	696	18217_g_at (X95573.2_G_AT)
665	17882_at (AL035523.49_AT)		18224_s_at
666	17886_at (AC004484.151_AT)	697	(AL021890.57_S_AT)
667	17893_at (AC004401.135_AT)		18226_s_at
668	17894_at (AC005724.44_AT)	698	(AC002343.142_S_AT)
669	17899_at (Z97339.197_AT)	699	18228_at (X91259.1_AT)
	17900_s_at	700	18234_at (AC000348.3_AT)
670	(AC000106.13_S_AT)		18236_s_at
	17907_s_at	701	(AC004683.69_S_AT)
671	(AC004684.165_S_AT)	702	18241_at (AC006580.71_AT)
672	17916_at (U22428.2_AT)		18242_g_at
673	17930_s_at (AJ006960.4_S_AT)	703	(AC006580.71_G_AT)
674	17945_at (Z97341.411_AT)	704	18255_at (AC005770.25_AT)
675	17955_at (AL021768.242_AT)		18258_s_at
676	17956_i_at (AC005967.32_I_AT)	705	(AC006439.222_S_AT)
677	17963_at (AL049730.88_AT)	706	18263_at (18263_AT)
678	17967_at (AL096859.32_AT)	707	18266_at (AC004684.33_AT)
		708	18267_at (AC006223.23_AT)

#	ProbeSet	#	ProbeSet
709	18268_s_at (AC006418.38_S_AT)	742	18681_at (L23573_AT)
710	18280_at (AC007369.2_AT)	743	18683_s_at (L27158_S_AT)
711	18284_at (AL021961.67_AT)	744	18686_s_at (U18126_S_AT)
712	18287_at (AC007661.142_AT)	745	18694_s_at (U89272_S_AT)
713	18299_s_at (M23872.2_S_AT)	746	18698_s_at (X17528_S_AT)
714	18301_s_at (AL022223.48_S_AT)	747	18716_at (X91916_AT)
715	18314_i_at (AL078579.83_I_AT)	748	18720_s_at (X92419_S_AT)
716	18348_at (AL022603.104_AT)	749	18735_s_at (Z29490_S_AT)
	18456_s_at		18753_s_at
717	(AC004697.159_S_AT)	750	(AF118222.28_S_AT)
718	18471_at (AC006533.103_AT)	751	18782_at (AC003040.90_AT)
719	18508_s_at (AC006532.89_S_AT)	752	18803_at (AC005315.94_AT)
720	18515_at (AC007063.215_AT)	753	18844_at (AC005315.131_AT)
721	18544_at (AC007060.14_AT)	754	18866_at (AC005917.178_AT)
722	18582_s_at (AC003671.36_S_AT)	755	18885_at (AC006921.147_AT)
723	18587_s_at (AC007166.53_S_AT)	756	18888_at (AC007591.68_AT)
724	18590_at (AJ222713.4_AT)	757	18896_at (AC002329.51_AT)
725	18591_at (X74756.2_AT)	758	18899_s_at (X13434.1_S_AT)
726	18596_at (AC005698.13_AT)	759	18908_i_at (AF055848.2_I_AT)
727	18597_at (AL080282.74_AT)	760	18909_s_at (AF055848.2_S_AT)
728	18600_at (L76926.1_AT)	761	18916_s_at (X92393.1_S_AT)
	18601_s_at	762	18928_at (AC002333.181_AT)
729	(AC002387.279_S_AT)	763	18930_at (AC005990.57_AT)
730	18604_at (AF069298.31_AT)	764	18933_at (AC007020.48_AT)
731	18622_g_at (AJ005902.2_G_AT)	765	18936_at (AJ003119.4_AT)
732	18625_at (AC005278.22_AT)	766	18949_at (Z54136.1_AT)
733	18631_at (AC002510.112_AT)	767	18953_at (AF077955.1_AT)
734	18634_s_at (Z97343.468_S_AT)	768	18963_at (AC004561.99_AT)
735	18635_at (AC004005.44_AT)	769	18966_at (AC004561.106_AT)
736	18636_at (AC006577.22_AT)	770	18976_at (AC000106.31_AT)
	18650_s_at	771	18980_at (U78721.20_AT)
737	(AF013294.25_S_AT)	772	18984_at (AC003096.100_AT)
	18662_s_at	773	19017_at (AL035709.69_AT)
738	(AC002343.20_S_AT)	774	19019_i_at (X82623.2_I_AT)
739	18667_at (AJ249442_AT)	775	19044_at (AC004392.38_AT)
740	18668_at (AJ249794_AT)	776	19060_at (AC003671.34_AT)
741	18672_s_at (D13983_S_AT)		

#	ProbeSet	#	ProbeSet
777	19092_at (AL078606.188_AT)	811	19451_at (AC004392.6_AT)
778	19110_s_at (X86947.2_S_AT)		19460_s_at
	19132_s_at	812	(AC000132.66_S_AT)
779	(AL022603.298_S_AT)	813	19462_s_at (AF001168.2_S_AT)
780	19137_at (X74755.2_AT)	814	19464_at (AC005560.51_AT)
781	19140_at (AC005170.24_AT)	815	19465_at (AL021768.96_AT)
782	19150_at (AC006577.20_AT)	816	19494_at (AC007296.26_AT)
783	19161_at (AL078579.9_AT)	817	19531_at (AL021960.91_AT)
784	19171_at (AC002335.160_AT)	818	19546_at (AC005398.172_AT)
785	19178_at (Y18227.2_AT)	819	19555_at (AF058919.48_AT)
786	19181_s_at (AF053065.2_S_AT)	820	19591_at (AJ010735.4_AT)
787	19182_at (AL031804.245_AT)	821	19614_at (AC003970.32_AT)
788	19207_at (AC006069.117_AT)	822	19623_at (AF000657.40_AT)
789	19219_at (AC007019.185_AT)	823	19624_at (AL049481.196_AT)
790	19230_at (AC003113.15_AT)		19625_s_at
791	19247_at (AF071527.44_AT)	824	(AC002311.26_S_AT)
792	19257_s_at (AC000104.57_S_AT)	825	19635_at (AL049746.38_AT)
793	19284_at (AC003028.196_AT)	826	19639_at (AL080252.22_AT)
794	19288_at (AC005824.130_AT)	827	19640_at (AC004561.78_AT)
795	19325_at (AL022604.42_AT)	828	19641_at (AC004561.66_AT)
796	19364_at (AL022023.142_AT)	829	19645_at (AC004561.70_AT)
797	19368_at (AC000348.22_AT)		19646_s_at
798	19376_at (AF024504.11_AT)	830	(AC005819.55_S_AT)
799	19383_at (AC006200.203_AT)	831	19655_at (Y14199.1_AT)
800	19386_at (AC006592.51_AT)	832	19660_at (AC002336.29_AT)
801	19388_at (AC000104.61_AT)	833	19667_at (AL021710.5_AT)
802	19395_at (AF007270.32_AT)	834	19672_at (AC005687.19_AT)
803	19396_at (AJ001855.2_AT)		19673_g_at
804	19405_at (AJ223803.1_AT)	835	(AC005687.19_G_AT)
805	19407_at (AC004697.81_AT)		19700_s_at
806	19409_at (AC007357.56_AT)	836	(AL031326.154_S_AT)
807	19411_at (AC007661.104_AT)		19701_s_at
808	19421_at (X70990.4_AT)	837	(AC005724.67_S_AT)
809	19424_at (AC002396.44_AT)	838	19704_i_at (AJ005927.2_I_AT)
	19432_s_at	839	19707_s_at (Z95768.3_S_AT)
810	(AL035680.11_S_AT)	840	19741_at (AL049171.72_AT)
		841	19755_at (AC006593.64_AT)

#	ProbeSet	#	ProbeSet
842	19762_at (AL035527.204_AT)	875	20142_at (AL035521.155_AT)
843	19818_i_at (AL021749.33_I_AT)	876	20144_at (AL079350.68_AT)
	19819_s_at	877	20165_at (AC002311.16_AT)
844	(AL021749.33_S_AT)	878	20179_at (AL035538.229_AT)
845	19844_at (AJ007588.2_AT)	879	20189_at (AC005489.2_AT)
846	19845_g_at (AJ007588.2_G_AT)	880	20194_at (AC007584.48_AT)
	19848_s_at	881	20199_at (AL050300.89_AT)
847	(AC004261.94_S_AT)	882	20200_at (AL050400.67_AT)
848	19851_at (U23794.3_AT)	883	20215_s_at (AF117125.2_S_AT)
	19870_s_at	884	20223_at (AL022347.145_AT)
849	(AL021811.48_S_AT)	885	20238_at (X74514.2_AT)
850	19878_at (AL080252.102_AT)	886	20239_g_at (X74514.2_G_AT)
851	19879_s_at (Z97338.342_S_AT)		20245_s_at
852	19881_at (AC004077.49_AT)	887	(AC005309.97_S_AT)
853	19892_at (AC005770.30_AT)	888	20246_s_at (AF084037.3_S_AT)
854	19894_at (AJ001809.1_AT)	889	20247_at (AC004392.4_AT)
855	19895_s_at (U77347.4_S_AT)	890	20258_at (AF130252.1_AT)
856	19903_at (AC007660.40_AT)	891	20262_at (AC002294.26_AT)
857	19916_at (AC006577.34_AT)	892	20263_at (AB004798.1_AT)
858	19944_at (AC002130.4_AT)	893	20269_at (AC002387.237_AT)
859	19946_at (AC004482.14_AT)	894	20271_at (Z99707.27_AT)
860	19956_at (AC006282.11_AT)		20285_s_at
861	19960_at (AL035527.360_AT)	895	(AC003674.18_S_AT)
	19970_s_at	896	20287_at (Y14590.5_AT)
862	(AC003674.10_S_AT)	897	20288_g_at (Y14590.5_G_AT)
863	19982_at (AC002986.28_AT)	898	20291_s_at (M92353.4_S_AT)
864	19991_at (AC007017.124_AT)	899	20297_at (AC007153.27_AT)
865	20017_at (AC004521.66_AT)	900	20323_at (AC004561.62_AT)
866	20023_at (AC006577.46_AT)	901	20335_s_at (Y14208.2_S_AT)
867	20030_at (AL078637.51_AT)	902	20345_at (AF104919.16_AT)
868	20051_at (AC000106.38_AT)	903	20346_at (L031135.156_AT)
869	20053_at (AC002292.27_AT)	904	20348_at (AC005967.35_AT)
870	20061_at (AC005508.23_AT)	905	20356_at (AC004561.74_AT)
871	20096_at (AC004238.31_AT)	906	20365_s_at (AC005850.19_S_AT)
872	20098_at (AC004697.123_AT)	907	20370_at (AC004561.263_AT)
873	20133_i_at (AC007178.71_I_AT)	908	20372_at (AL021713.24_AT)
874	20134_s_at (AC007178.71_S_AT)		

#	ProbeSet	#	ProbeSet
909	20382_s_at (AC002338.35_S_AT)	933	20572_s_at (AC005560.229_S_AT)
910	20409_g_at (AC004077.132_G_AT)	934	20577_at (AL078464.72_AT)
911	20420_at (AL024486.131_AT)	935	20584_at (AC004450.75_AT)
912	20421_at (U81294.2_AT)		20586_i_at
913	20422_g_at (U81294.2_G_AT)	936	(AC005824.195_I_AT)
914	20432_at (U43486.2_AT)		20587_s_at
915	20433_at (AC006232.147_AT)	937	(AC005824.195_S_AT)
916	20442_i_at (AC006341.42_I_AT)	938	20589_at (AF081066.3_AT)
917	20443_s_at (AC006341.42_S_AT)	939	20590_at (AL035540.159_AT)
918	20450_at (AJ005930.2_AT)	940	20591_at (AL080252.115_AT)
919	20461_at (20461_AT)	941	20619_at (AC005896.161_AT)
920	20462_at (U82399.2_AT)		20620_g_at
921	20477_at (AC004238.154_AT)	942	(AC005896.161_G_AT)
922	20479_i_at (AF069495.2_I_AT)	943	20646_at (AC002291.20_AT)
923	20480_s_at (AF069495.2_S_AT)	944	20656_at (AL035396.46_AT)
924	20485_at (AC007660.131_AT)		20658_s_at
925	20491_at (AC004561.146_AT)	945	(2AL050400.70_S_AT)
926	20507_at (AL021635.67_AT)	946	20660_s_at (X97488.2_S_AT)
927	20511_at (AC007290.24_AT)	947	20669_s_at (AC002388.6_S_AT)
928	20516_at (AL035523.64_AT)	948	20675_at (AC006234.204_AT)
929	20517_at (Y17722.7_AT)	949	20678_at (AC007296.30_AT)
930	20524_at (AC005698.12_AT)	950	20685_at (AL049751.46_AT)
931	20529_at (Z97341.125_AT)	951	20686_at (Y14424.2_AT)
932	20551_at (AC006081.211_AT)		20689_s_at
		952	(AC002335.19_S_AT)
		953	20715_at (AF079183.1_AT)

Table 20a: cDNA-AFLP gene fragments with similarity to other known proteins

cDNA***	Known protein	Organism	Related accession number**	Blast score*
DESCA1	no significant similarity	-	-	-
DESCA2	ser/thr kinase	bean	AF078082	2e-12
DESCA3	endo-1,4-betaglucanase	rape	AJ242807	4e-19
DESCA4	pdr 5-abc transporter	duckweed	Z70524	1e-27
DESCA5	transcriptional regulator	yeast	NP 014933	9e-1
DESCA6	kinase	Arabidopsis	T00502	7e-1
DESCA7	salicylate-induced glucosyltransferase IS5a	tobacco	T03747	2e-21
DESCA8	nbs-LRR	rice	AAF82158	5e-2
DESCA9	cytochrome p450 monooxygenase	tobacco	X96784	7e-31
DESCA10	MRP-like ABC transporter	Arabidopsis	U96399	8e-7
DESCA11	phosphoribosylanthranilate transferase	Arabidopsis	AAF18518	8e-17
DESCA12	hypersensitivity-related 201	tobacco	X95343	3e-23
DESCA13	integral membrane glycoprotein	puffer fish	AF013613	9e-1
7a tgaa	no significant similarity	-	-	-
10d tcg	hypothetical protein F3F9.18	Arabidopsis	AC013430	7e-15
11a tgca	no significant similarity	-	-	-
c.r. actin	actin	C. rubrum	X92353	7e-45

* NCBI BLASTX translated search (Altschul et al., 1997)

** Accession numbers are listed in SEQ ID Nos 1967-1980

*** DESCA sequences are listed in SEQ ID Nos 1954-1966

Table 20b: Relative gene expression fold changes of cDNA-AFLP gene fragments with similarity to other known proteins at different time points during viral infections as determined by quantitative RT-PCR

cDNA	Gene expression fold changes				
	<i>C. amaranticolor</i>			TRV ²	<i>C. quinoa</i>
	TMV ¹				TMV ³
	4dai	7dai	11dai		4dai
DESCA1	200	180	6.1	278	not detectable
DESCA2	36	25	27	10	700
DESCA3	23	15	2.7	19	46
DESCA4	21	9.2	4.5	6.8	52
DESCA5	19	8.0	9.1	15	1100
DESCA6	8.4	9.6	12	2.1	not detectable
DESCA7	8.9	2.8	5.6	53	150
DESCA8	5.9	3.2	2.0	5.8	120
DESCA9	5.1	5.9	4.2	3.1	not detectable
DESCA10	5.6	1.9	0.95	4.1	not detectable
DESCA11	5.5	3.6	3.0	3.9	230
DESCA12	5.0	2.4	1.7	5.6	7.9
DESCA13	2.9	1.8	1.9	3.3	34
7a tgaa	1.5	1.4	1.7	not tested	not tested
10d tcg	2.2	0.75	0.25	not tested	not tested
11a tgca	1.6	0.54	0.18	not tested	not tested
c.r. actin	1.0	1.0	1.0	1.0	1.0

¹ Values are the fold increases in gene expression of TMV-MGfus infected compared to mock-inoculated plants.

² Values are the fold increases in gene expression of TRV infected compared to mock-inoculated plants.

³ Values are the fold increases in gene expression of TMV infected compared to mock-inoculated plants.

Table 21 Known plant/pathogen interactions

Plant	Pathogen
Tomato	Cladosporium fulvum
Maize	Rust fungus
Antirrhinium	Rust fungus
Flax	<i>Melampsora lini</i>
Lettuce	Downy mildew
Arabidopsis	<i>Peronospora parasitica</i>
Tomato	Nematode
Corn	Cochliobolus carbonum
Tomato	Pseudomonas syringae
Rice	Xanthomonas oryzae pv. Oryzae
Rice	Pyricularia oryzae
Tobacco	Tobacco Mosaic Virus

Table 22 Rice Open Reading Frames (ORFs) orthologous to specific Arabidopsis ORFs and corresponding rice promoter regions

AORF SEQ ID NO of a specific Arabidopsis ORF

RH SEQ ID NO of homologous rice ORF(s)

RP SEQ ID NO of the rice promoter linked to a homologous rice ORF

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
3	2808	4884		3475	5551		4307	6383
	3066	5142		3567	5643		4458	6534
	3820	5896		3632	5708	52	3035	5111
	4655	6731		3769	5845		3157	5233
6	2757	4833		3916	5992		3379	5455
	3013	5089		4298	6374		3626	5702
	3393	5469	19	3184	5260		3990	6066
	3899	5975	20	2678	4754	55	2687	4763
7	3227	5303		2926	5002		2869	4945
	3579	5655		3736	5812		2984	5060
	3851	5927		3864	5940		3054	5130
	3890	5966		4124	6200		3180	5256
	4516	6592		4414	6490		3561	5637
8	3086	5162	22	2805	4881		4306	6382
	3341	5417		3997	6073		4326	6402
	3762	5838		4126	6202		4460	6536
	3767	5843		4153	6229		4476	6552
	4285	6361		4311	6387		4521	6597
	4487	6563		4639	6715		4603	6679
	4488	6564	32	3718	5794	57	4005	6081
	4489	6565		4345	6421	59	2922	4998
10	3629	5705	37	4493	6569		3833	5909
	3914	5990	42	3479	5555		3967	6043
	4291	6367		4208	6284		4202	6278
	4424	6500		4236	6312	60	2706	4782
11	3996	6072	46	3891	5967		4125	6201
	4555	6631	49	4645	6721		4720	6796
14	2809	4885	50	4210	6286	65	2815	4891
	3160	5236	51	2864	4940		4112	6188
	3201	5277		2964	5040		4288	6364
	3455	5531		4218	6294	67	2716	4792

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
	2928	5004	75	2920	4996		3198	5274
	2940	5016		3417	5493		3319	5395
	3182	5258		3742	5818		3797	5873
	3333	5409		3927	6003		4048	6124
	3351	5427		4061	6137		4184	6260
	3386	5462	78	2705	4781		4259	6335
	3387	5463		2737	4813	102	3563	5639
	3445	5521		2738	4814		3683	5759
	3530	5606		4654	6730		4108	6184
	3581	5657		4681	6757		4168	6244
	3727	5803	85	3163	5239		4232	6308
	3825	5901		3525	5601	110	2876	4952
	3915	5991		3965	6041		3099	5175
	4120	6196		4114	6190		3367	5443
	4170	6246	91	3138	5214		3610	5686
	4267	6343		3745	5821		4363	6439
	4280	6356		3803	5879		4618	6694
	4350	6426		4233	6309		4656	6732
	4479	6555		4275	6351	111	2747	4823
	4713	6789	93	4325	6401		2766	4842
68	2764	4840	95	2903	4979		2955	5031
	3072	5148		3230	5306		3450	5526
	3192	5268		3676	5752		3988	6064
	3290	5366		4480	6556	112	2779	4855
	3546	5622		4631	6707		3345	5421
	3553	5629	97	2959	5035		3799	5875
	3658	5734		3105	5181		3801	5877
	3747	5823		3222	5298		4216	6292
	3972	6048		3838	5914	113	3371	5447
	4543	6619		4026	6102		3372	5448
70	3173	5249		4224	6300		3373	5449
72	3245	5321		4523	6599		4022	6098
	4329	6405		4646	6722		4319	6395
	4412	6488	100	2667	4743	115	2707	4783
73	2862	4938		2751	4827		2871	4947
	3012	5088		2948	5024		3261	5337
	3506	5582		3167	5243		3452	5528

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
116	4513	6589	127	4496	6572	137	3761	5837
	2833	4909		4593	6669		3869	5945
	2939	5015		4629	6705		4609	6685
	3200	5276		2981	5057		2723	4799
	3571	5647		3199	5275		3220	5296
118	4031	6107	128	3467	5543	138	4173	6249
	2944	5020		3963	6039		3024	5100
	3186	5262		4053	6129		3487	5563
	3631	5707		3267	5343		3583	5659
	3633	5709		4182	6258		4503	6579
119	3697	5773	130	4530	6606	139	4591	6667
	3726	5802		2890	4966		2699	4775
	4009	6085		3293	5369		3463	5539
	4597	6673		3312	5388		3584	5660
	3169	5245		3326	5402		4451	6527
121	3637	5713	133	3812	5888	140	4595	6671
	3638	5714		3889	5965		3042	5118
	3639	5715		4134	6210		3175	5251
	3656	5732		4254	6330		4337	6413
	4692	6768		2799	4875		3558	5634
122	3041	5117	134	3008	5084	148	3655	5731
	3179	5255		3208	5284		4084	6160
	3291	5367		3706	5782		3107	5183
	4269	6345		3765	5841		3560	5636
	4633	6709		3005	5081		4146	6222
124	3388	5464	135	3145	5221	151	4398	6474
	3410	5486		3146	5222		4399	6475
	3469	5545		3328	5404		4368	6444
	4316	6392		3511	5587		4483	6559
	4449	6525		4572	6648		4550	6627
126	3215	5291	135	4584	6660	152	4551	6628
	3557	5633		2832	4908		4616	6692
	3575	5651		3073	5149		3023	5099
	3847	5923		3257	5333		3880	5956
	4044	6120		3352	5428		4237	6313
	4400	6476		3378	5454	159	4492	6568
	4444	6520		3555	5631		2720	4796

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
	3115	5191	172	3389	5465	189	2778	4854
	3383	5459		3509	5585		3514	5590
	3844	5920		3603	5679		4662	6738
	3989	6065		3664	5740	190	3020	5096
	4157	6233		3665	5741		3088	5164
	4627	6703	173	4608	6684		3605	5681
162	2813	4889	175	3754	5830		3606	5682
	2927	5003		3835	5911		3992	6068
	3346	5422		4015	6091	199	2873	4949
	3423	5499		4198	6274		2942	5018
	3682	5758		4420	6496		3492	5568
	3781	5857	179	2684	4760		3671	5747
	3830	5906		4394	6470		3856	5932
	4225	6301	180	3158	5234		4030	6106
	4475	6551		3635	5711		4100	6176
	4622	6698		4557	6633		4253	6329
164	3232	5308		4558	6634		4680	6756
	3491	5567	181	2696	4772	202	2711	4787
	4590	6666		3850	5926		3015	5091
	4625	6701		4549	6625		3774	5850
165	3271	5347	185	3110	5186		3906	5982
	3322	5398		3304	5380		3943	6019
	3406	5482		3518	5594	203	3135	5211
	3681	5757		3594	5670		3318	5394
	3973	6049		3853	5929		3443	5519
	4231	6307	187	2730	4806		3523	5599
	4324	6400		2893	4969		3911	5987
166	2767	4843		3087	5163		3924	6000
	2781	4857		3176	5252		4596	6672
	3347	5423		4234	6310	204	2851	4927
	4093	6169	188	3068	5144		2852	4928
	4130	6206		3082	5158		3151	5227
171	2733	4809		3644	5720		3152	5228
	2761	4837		4344	6420		4186	6262
	3049	5125		4427	6503	205	3078	5154
	3402	5478		4468	6544		3984	6060
	3945	6021		4636	6712		4085	6161

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
206	3051	5127	219	2789	4865	247	3971	6047
	3075	5151		2801	4877	250	2971	5047
	3117	5193		2802	4878		3696	5772
	3527	5603		2803	4879		3719	5795
	3756	5832		3703	5779		4035	6111
209	3091	5167		4222	6298		4273	6349
	3505	5581	220	2885	4961		4675	6751
	3602	5678		3394	5470	252	2909	4985
	3921	5997		3395	5471		3738	5814
	4679	6755		3396	5472		3831	5907
210	3628	5704		3499	5575		3904	5980
	4129	6205	221	2918	4994		4039	6115
212	2736	4812		3225	5301		4219	6295
	2966	5042		4453	6529		4246	6322
	3888	5964		4534	6610		4467	6543
	4240	6316		4553	6630		4495	6571
	4484	6560	225	3634	5710	254	2771	4847
213	2822	4898		3673	5749		2874	4950
	2916	4992		3920	5996		3413	5489
	2961	5037		4440	6516		3510	5586
	3102	5178		4668	6744		4143	6219
	3255	5331	229	2731	4807	255	2664	4740
215	2709	4785		3466	5542		2740	4816
	2804	4880		3897	5973		2792	4868
	2993	5069		4395	6471		3171	5247
	3174	5250		4664	6740		3368	5444
	3852	5928	237	2847	4923		3425	5501
216	2662	4738		3126	5202		3788	5864
	2695	4771		3237	5313		4183	6259
	3457	5533		3508	5584		4206	6282
	3504	5580		3704	5780		4439	6515
	3842	5918		3930	6006	256	2798	4874
	4580	6656		4006	6082		3109	5185
	4583	6659	239	2924	5000		3566	5642
218	3338	5414		4707	6783		3901	5977
	3951	6027	240	3211	5287		4190	6266
	4051	6127		3751	5827		4501	6577

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
	4579	6655		4333	6409		3953	6029
	4601	6677		4377	6453		3966	6042
258	2952	5028	271	3979	6055		4025	6101
	3283	5359		4570	6646		4161	6237
	4001	6077		4571	6647		4544	6620
	4040	6116	274	3426	5502	289	2668	4744
	4397	6473		3534	5610		2746	4822
260	3438	5514	275	2951	5027		3147	5223
	3886	5962		3268	5344		3284	5360
	4070	6146		3909	5985		3285	5361
	4215	6291		4277	6353		3878	5954
	4703	6779		4490	6566		4373	6449
263	2752	4828	285	3336	5412		4457	6533
	3098	5174		3987	6063	290	2780	4856
	3276	5352		4431	6507		2896	4972
	3625	5701	286	3430	5506		3569	5645
	4309	6385	287	2703	4779		4486	6562
265	2701	4777		3028	5104		4731	6807
	2861	4937		3329	5405	295	2785	4861
	3164	5240		3595	5671		2807	4883
	4187	6263		3667	5743		2921	4997
	4270	6346		3895	5971		2957	5033
267	2866	4942		4598	6674		3281	5357
	2941	5017		4602	6678		3303	5379
	3002	5078		4688	6764		3477	5553
	4330	6406	288	2820	4896		3792	5868
270	2875	4951		2977	5053		3925	6001
	3001	5077		2991	5067		3946	6022
	3061	5137		3007	5083		4175	6251
	3282	5358		3057	5133	296	2689	4765
	3590	5666		3097	5173		2995	5071
	3608	5684		3155	5231		2996	5072
	3618	5694		3170	5246		3133	5209
	3817	5893		3464	5540		4058	6134
	3969	6045		3528	5604		4185	6261
	4211	6287		3532	5608		4695	6771
	4265	6341		3872	5948	298	2685	4761

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
	2769	4845		3256	5332		4381	6457
	2777	4853		3385	5461		4430	6506
	3122	5198		3539	5615		4533	6609
	3153	5229		3541	5617	331	2760	4836
	3187	5263		4145	6221		2848	4924
	3323	5399	314	2839	4915		3103	5179
	4542	6618		3240	5316		3419	5495
299	2915	4991		3485	5561		3740	5816
	3705	5781		3643	5719		3999	6075
	4313	6389		3848	5924		4023	6099
	4353	6429		3957	6033		4352	6428
	4415	6491		4406	6482		4735	6811
	4600	6676		4514	6590	333	2796	4872
	4721	6797	316	3119	5195		2958	5034
300	3380	5456		3142	5218		3191	5267
	3381	5457		3251	5327		3365	5441
	3456	5532		3274	5350		3687	5763
	3755	5831		3619	5695		3932	6008
	4027	6103	318	2972	5048		4342	6418
301	2679	4755		3875	5951		4360	6436
	2865	4941		4152	6228	339	3011	5087
	3565	5641		4375	6451		3296	5372
	4029	6105		4461	6537		3624	5700
	4272	6348	319	4197	6273		3948	6024
302	2836	4912		4334	6410		4620	6696
	3236	5312	324	3033	5109		4733	6809
304	2960	5036		3771	5847	341	3248	5324
	3111	5187		3910	5986		3942	6018
	3252	5328	326	2934	5010	346	4299	6375
	3884	5960		3114	5190	348	3000	5076
	3885	5961		3806	5882		3137	5213
305	2899	4975		4359	6435		3866	5942
	3074	5150		4520	6596		4038	6114
	3431	5507	330	3401	5477		4327	6403
	3713	5789		3804	5880		4425	6501
	4008	6084		4098	6174	360	2989	5065
312	2721	4797		4331	6407		2990	5066

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
	3090	5166		4546	6622	391	2671	4747
	3100	5176		4587	6663		3862	5938
	3436	5512	370	4056	6132		3863	5939
	3515	5591	372	3414	5490		3955	6031
	3522	5598		3471	5547		3956	6032
	3636	5712		4247	6323		4133	6209
	3883	5959		4482	6558	393	3010	5086
	3977	6053		4650	6726		3802	5878
	4028	6104	374	2776	4852		3839	5915
	4199	6275		3497	5573		3923	5999
	4201	6277		3645	5721		4421	6497
	4223	6299		3728	5804		4556	6632
	4317	6393		3837	5913		4614	6690
	4354	6430	378	3808	5884	394	3069	5145
	4408	6484		4045	6121		3159	5235
	4450	6526		4308	6384		3870	5946
	4509	6585		4525	6601		4147	6223
365	3678	5754	380	3207	5283		4512	6588
	3941	6017		3773	5849	398	2976	5052
	4547	6623		4701	6777		3680	5756
	4577	6653		4715	6791	404	4217	6293
	4684	6760		4716	6792	405	4116	6192
	4714	6790	381	4034	6110	410	2754	4830
366	2691	4767	382	4405	6481		3260	5336
	3614	5690		4537	6613	411	3824	5900
	3711	5787	385	3490	5566		4004	6080
	3763	5839		4065	6141	412	2967	5043
	3975	6051		4104	6180		2988	5064
369	2708	4784		4454	6530		3887	5963
	3125	5201		4456	6532		3935	6011
	3144	5220		4730	6806		4462	6538
	3190	5266	389	2750	4826	418	3223	5299
	3370	5446		3529	5605		4376	6452
	3432	5508		3620	5696		4504	6580
	4067	6143		4575	6651		4505	6581
	4355	6431		4694	6770		4663	6739
	4410	6486		4723	6799	419	2854	4930

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
	3085	5161		4640	6716		4049	6125
	3442	5518	438	2818	4894		4158	6234
	3537	5613		2863	4939		4164	6240
	3552	5628		3344	5420		4466	6542
	4200	6276		3454	5530	457	4382	6458
	4378	6454		3613	5689	460	3166	5242
420	3321	5397		4683	6759		3592	5668
	3517	5593	439	2819	4895		4107	6183
	3544	5620		2905	4981		4128	6204
	3689	5765		2935	5011	463	2850	4926
	4243	6319		3949	6025		3488	5564
422	3228	5304		3958	6034		3489	5565
	3249	5325		4413	6489		3578	5654
	3250	5326		4417	6493		3849	5925
	3709	5785		4465	6541		4517	6593
	4589	6665	441	3330	5406		4624	6700
426	2919	4995		3708	5784	464	3657	5733
	2943	5019		3836	5912		3752	5828
	3022	5098		3898	5974		4251	6327
	3273	5349		4419	6495		4372	6448
	3739	5815	448	2715	4791		4726	6802
	4409	6485		2773	4849	465	3071	5147
428	2753	4829		3053	5129		3270	5346
	2897	4973		3408	5484		3533	5609
	3096	5172		3415	5491		3796	5872
	3500	5576		3538	5614		3905	5981
	4438	6514		3900	5976		4418	6494
431	3193	5269		4358	6434		4605	6681
432	3029	5105	450	3398	5474		4674	6750
	3219	5295		3795	5871	467	3640	5716
	3375	5451	451	2992	5068		3734	5810
	3376	5452		3183	5259		4447	6523
	3623	5699		3269	5345		4464	6540
	3968	6044		3300	5376		4515	6591
437	2855	4931		3478	5554	472	3462	5538
	2937	5013		4000	6076		3591	5667
	4341	6417		4018	6094		3823	5899

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
	4212	6288		3503	5579		3929	6005
	4349	6425		3776	5852		4052	6128
475	2739	4815		4685	6761		4081	6157
	2772	4848	497	3669	5745		4089	6165
	3168	5244	500	3444	5520		4314	6390
	3382	5458		4226	6302		4628	6704
	3451	5527		4370	6446	525	4162	6238
	3865	5941		4621	6697	526	2840	4916
	3974	6050		4651	6727		2994	5070
	3982	6058	501	3481	5557		3003	5079
	4364	6440		4239	6315		4020	6096
476	2829	4905	502	4610	6686		4653	6729
	3343	5419	503	3857	5933	528	3004	5080
	3593	5669		4611	6687		3433	5509
	3741	5817	505	3165	5241		3674	5750
	3829	5905		3242	5318		3789	5865
482	2853	4929		3749	5825		4638	6714
	4062	6138		4383	6459	533	3044	5120
	4106	6182		4718	6794		3241	5317
	4127	6203	507	2763	4839		3646	5722
484	2702	4778		3026	5102		3961	6037
	3302	5378		3409	5485		4518	6594
	3327	5403		3468	5544	535	3859	5935
	3701	5777		3983	6059		4328	6404
	4502	6578	509	2759	4835	536	3286	5362
487	3143	5219		3418	5494		3545	5621
	3677	5753		3912	5988		3659	5735
	4075	6151		4079	6155		4117	6193
	4443	6519		4470	6546		4149	6225
	4710	6786	517	2672	4748	539	3641	5717
489	2841	4917		2690	4766		4248	6324
	3188	5264		2727	4803		4286	6362
	3686	5762		2846	4922	540	3093	5169
	3867	5943		3278	5354		3127	5203
	4673	6749		3337	5413		3325	5401
493	3032	5108		3526	5602	541	2888	4964
	3480	5556		3730	5806		3037	5113

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
543	3116	5192		4136	6212		3822	5898
	3434	5510	553	2666	4742		4010	6086
	3435	5511		2945	5021	581	2765	4841
	4087	6163		3101	5177		3065	5141
	4088	6164		3224	5300		3513	5589
546	2791	4867		4459	6535		4043	6119
	2933	5009	556	2929	5005		4416	6492
	3735	5811		3810	5886	582	3212	5288
	3970	6046		3811	5887		3411	5487
	4154	6230		4046	6122		3841	5917
	4213	6289		4548	6624		4169	6245
	4292	6368	559	2734	4810		4293	6369
	4401	6477		3611	5687	583	2712	4788
549	3369	5445		3737	5813		2713	4789
	3420	5496		4179	6255		2725	4801
	3421	5497		4647	6723		2812	4888
	3441	5517	560	3598	5674		3031	5107
	3559	5635		3599	5675		3794	5870
	4069	6145		3600	5676		4274	6350
	4300	6376		3712	5788		4699	6775
	4301	6377		4388	6464	586	3746	5822
	4561	6637	566	2953	5029		4672	6748
550	3141	5217		2954	5030	595	2821	4897
	3361	5437		3615	5691		3275	5351
	3377	5453		4386	6462		3473	5549
	3939	6015		4387	6463		3877	5953
	3960	6036	569	2786	4862		4097	6173
	4091	6167		3019	5095		4312	6388
551	3340	5416		3233	5309		4362	6438
	3363	5439		3307	5383		4554	6626
	4142	6218		4469	6545	599	3055	5131
	4159	6235	572	2674	4750		3213	5289
	4436	6512		4099	6175		4166	6242
552	3805	5881		4366	6442		4167	6243
	3993	6069	577	2825	4901		4562	6638
	4016	6092		3006	5082	601	3079	5155
	4077	6153		3136	5212		3424	5500

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
	4241	6317		2999	5075	642	3039	5115
	4321	6397		3353	5429		4082	6158
602	4083	6159		3362	5438		4238	6314
603	2775	4851		3472	5548		4437	6513
	3685	5761		3723	5799		4563	6639
	3934	6010	628	2898	4974	647	2758	4834
	4235	6311		3106	5182		2879	4955
	4351	6427		3108	5184		3214	5290
	4657	6733		4539	6615		3476	5552
605	2724	4800		4540	6616		3564	5640
	2784	4860	631	3247	5323		3661	5737
	3052	5128	633	3294	5370		3772	5848
	3288	5364		3295	5371	651	2867	4943
	3422	5498		3391	5467		3244	5320
	3731	5807		3453	5529		4017	6093
	3944	6020		3621	5697		4191	6267
	4007	6083	634	2710	4786		4242	6318
	4346	6422		2756	4832	653	3077	5153
	4389	6465		3148	5224	654	2663	4739
609	3311	5387		3470	5546		2835	4911
	3791	5867		3572	5648		3459	5535
610	4011	6087		4078	6154		3908	5984
	4522	6598		4221	6297		4582	6658
612	2795	4871		4365	6441	656	3660	5736
	3130	5206		4404	6480		3893	5969
	3574	5650	635	3040	5116		4012	6088
	4315	6391		3258	5334		4021	6097
	4529	6605		3339	5415		4508	6584
613	3162	5238	640	3568	5644	657	4139	6215
619	2974	5050		3790	5866	658	2878	4954
	3717	5793		3821	5897		3437	5513
620	3650	5726		4511	6587		3486	5562
	3653	5729	641	2719	4795		4002	6078
	3675	5751		2793	4869		4160	6236
	4526	6602		3556	5632	660	3132	5208
623	2849	4925		3714	5790		3292	5368
	2936	5012		3991	6067		4426	6502

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
662	4632	6708	676	3622	5698	686	2907	4983
	4687	6763		3940	6016		2917	4993
	2969	5045		4367	6443		3540	5616
	3535	5611		2963	5039		3892	5968
	4260	6336		3084	5160		3937	6013
664	4261	6337	677	3112	5188	687	3779	5855
	4262	6338		3221	5297		3902	5978
	2704	4780		3332	5408		4569	6645
	3766	5842		3507	5583		4615	6691
	4094	6170		3570	5646		4722	6798
665	4689	6765	678	3699	5775	688	3297	5373
	4732	6808		4138	6214		4095	6171
	2741	4817		4390	6466		4282	6358
	2827	4903		3439	5515		4433	6509
	3056	5132		3440	5516		4446	6522
672	3181	5257	680	3952	6028	691	2837	4913
	3448	5524		4072	6148		3238	5314
	3520	5596		4073	6149		3364	5440
	3882	5958		2810	4886		3542	5618
	4080	6156		2883	4959		3768	5844
675	4101	6177	683	3195	5271	692	3585	5661
	4171	6247		3266	5342		3586	5662
	4176	6252		3427	5503		4658	6734
	4205	6281		2797	4873		4659	6735
	4264	6340		3750	5826		2806	4882
677	4278	6354	684	4588	6664	693	2923	4999
	4507	6583		2735	4811		3043	5119
	4676	6752		2970	5046		3229	5305
	4691	6767		3760	5836		3320	5396
	4734	6810		3778	5854		4258	6334
678	3104	5180	685	4560	6636	695	2842	4918
	3907	5983		4320	6396		2843	4919
	4141	6217		3140	5216		2844	4920
	4612	6688		3587	5663		2908	4984
	4669	6745		3876	5952		2949	5025
679	2717	4793	686	4119	6195	696	3554	5630
	3149	5225		4727	6803		3670	5746

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
700	3926	6002	715	4538	6614	731	3725	5801
	4338	6414		4607	6683		4189	6265
	2947	5023		4704	6780		4402	6478
	3246	5322		4705	6781		2688	4764
	4180	6256		4706	6782		2900	4976
702	4441	6517	718	3757	5833	732	2962	5038
	4666	6742		3936	6012		2979	5055
	4667	6743		4229	6305		3016	5092
	3216	5292		4230	6306		3048	5124
	3549	5625		4528	6604		3070	5146
706	3654	5730	719	3047	5123	740	3092	5168
	3733	5809		2817	4893		3589	5665
	4132	6208		2894	4970		3617	5693
	2697	4773		3076	5152		3720	5796
	2770	4846		3314	5390		3782	5858
707	2788	4864	720	3759	5835	741	3962	6038
	2845	4921		4092	6168		4155	6231
	3156	5232		4271	6347		4174	6250
	3234	5310		4302	6378		4474	6550
	3744	5820		4303	6379		4510	6586
712	4013	6089	725	4304	6380	744	4545	6621
	2983	5059		4305	6381		4729	6805
	3582	5658		4455	6531		3027	5103
	3642	5718		4473	6549		3064	5140
	4059	6135		2930	5006		3710	5786
712	4076	6152	729	3062	5138	741	4524	6600
	4194	6270		3172	5248		4566	6642
	4686	6762		3289	5365		3861	5937
	3038	5114		4384	6460		3196	5272
	3392	5468		4228	6304		3871	5947
712	3400	5476	729	2787	4863	744	2732	4808
	3512	5588		2975	5051		3210	5286
	3758	5834		3095	5171		4255	6331
	4110	6186		3494	5570		4256	6332
	4118	6194		3495	5571		4347	6423
712	4177	6253	729	3496	5572	744	4374	6450
	4422	6498		3702	5778		4500	6576

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
	4626	6702		4144	6220	782	3783	5859
745	2892	4968		4196	6272		3834	5910
	4428	6504		4295	6371		3854	5930
752	2686	4762		4396	6472		4165	6241
	2830	4906		4724	6800		4586	6662
	2831	4907	765	3231	5307	788	2677	4753
	2932	5008		3627	5703		3573	5649
	4623	6699		4268	6344		4192	6268
756	3094	5170		4361	6437		4434	6510
	3484	5560		4661	6737	790	3349	5425
	3597	5673	767	3777	5853		3793	5869
	3652	5728	768	3813	5889		4263	6339
	3860	5936		3814	5890	792	2877	4953
	3879	5955	770	2913	4989		2901	4977
	3964	6040		3354	5430		3516	5592
757	2826	4902		3355	5431		3918	5994
	2910	4986		3903	5979		3947	6023
	3017	5093		4527	6603		4019	6095
	3030	5106	771	2906	4982		4279	6355
	3067	5143		2911	4987		4296	6372
	3080	5156		3131	5207		4356	6432
	3113	5189		3458	5534		4643	6719
	3178	5254		3874	5950	793	2698	4774
	3272	5348	772	2856	4932		2794	4870
	3482	5558		2973	5049		2811	4887
	4585	6661		3083	5159		3350	5426
	4671	6747		3197	5273	794	3919	5995
	4711	6787		3217	5293		3954	6030
763	2868	4944		3502	5578		3986	6062
	3124	5200		4003	6079		4448	6524
	3679	5755		4565	6641		4665	6741
	4203	6279		4604	6680	795	2676	4752
	4432	6508	776	2670	4746		3058	5134
	4498	6574		3209	5285		3139	5215
	4712	6788		3780	5856		3690	5766
764	3301	5377		4209	6285		3691	5767
	3715	5791		4485	6561		3692	5768

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
	3693	5769		4559	6635		4369	6445
	3928	6004	816	2768	4844	832	2790	4866
	4214	6290		3150	5226	833	2824	4900
797	2700	4776		3846	5922		2889	4965
	2828	4904		3894	5970		2956	5032
	2882	4958		4057	6133		3360	5436
	3306	5382	820	3648	5724		3397	5473
	3695	5771		3855	5931		3521	5597
	4135	6211		4257	6333		3647	5723
798	3358	5434	823	3800	5876		3698	5774
	3405	5481	825	2870	4946		4357	6433
	3407	5483		4096	6172		4423	6499
	3460	5536		4283	6359		4637	6713
	3596	5672		4284	6360	836	3243	5319
803	3194	5270		4564	6640		3262	5338
	3239	5315	826	2931	5007		3263	5339
	3299	5375		3331	5407		3404	5480
	3588	5664		3429	5505		4131	6207
	3612	5688		3601	5677		4322	6398
	4736	6812		4103	6179		4348	6424
804	2692	4768		4494	6570		4592	6668
	3059	5135		4541	6617	838	3045	5121
	3399	5475	827	2814	4890		3154	5230
	3721	5797		3707	5783		3357	5433
	3729	5805		3784	5860	840	2800	4876
808	2904	4980		3785	5861		3843	5919
	3280	5356		4188	6264		3933	6009
	3827	5903	829	3786	5862		3978	6054
	4429	6505	830	2673	4749		3998	6074
	4660	6736		2982	5058	841	3089	5165
809	2872	4948		3390	5466		3279	5355
	4717	6793		4435	6511		3335	5411
811	4033	6109		4649	6725		4641	6717
814	2880	4956		4690	6766	848	2749	4825
	2987	5063	831	3334	5410		2912	4988
	3416	5492		3543	5619		3254	5330
	4055	6131		3743	5819		3976	6052

AORF	RH	RP	AORF	RH	RP	AORF	RH	RP
852	4708	6784	868	4452	6528	901	3985	6061
	2680	4756		4599	6675		4391	6467
	2859	4935		2681	4757		4617	6693
	2860	4936		2895	4971		3265	5341
	3118	5194		2980	5056		3672	5748
	3313	5389		4193	6269		3775	5851
	4047	6123		4477	6553		3873	5949
	4379	6455		4478	6554		4635	6711
856	4532	6608	871	4696	6772	904	4266	6342
	3366	5442		3308	5384	908	2891	4967
	4481	6557		3309	5385		3009	5085
857	3501	5577	876	3310	5386		3536	5612
	3609	5685		4567	6643		3950	6026
	3931	6007		4576	6652	909	4071	6147
	4336	6412		3021	5097		3348	5424
859	4702	6778	883	3161	5237		3651	5727
	3412	5488		3206	5282		4102	6178
	3694	5770		3607	5683		4578	6654
	4156	6232		4024	6100		4613	6689
	4499	6575		3384	5460	911	2823	4899
861	4568	6644	887	3819	5895		2857	4933
	2665	4741		3832	5908		3226	5302
	3120	5196		3868	5944		3938	6014
	3121	5197		4318	6394		4294	6370
	4109	6185		3018	5094	912	2718	4794
863	4140	6216	889	3913	5989		2816	4892
	4163	6239		4066	6142		3185	5261
	4574	6650		4407	6483		3662	5738
	2729	4805		4725	6801		4393	6469
	2925	5001		4204	6280	914	2728	4804
867	3576	5652	891	2834	4910		3177	5253
	4148	6224		3298	5374		3483	5559
	4195	6271		3815	5891		3809	5885
	2726	4802	892	4151	6227	918	4339	6415
	4310	6386		4252	6328		2968	5044
	4332	6408		3129	5205		3577	5653
	4442	6518		3342	5418		3787	5863

AORF	RH	RP	AORF	RH	RP
	4297	6373		3981	6057
	4445	6521	944	2997	5073
919	2985	5061		3046	5122
	3356	5432	950	3519	5595
	3881	5957		3980	6056
	4090	6166		4250	6326
	4652	6728		4471	6547
921	2887	4963		4535	6611
926	2946	5022	952	2714	4790
	3128	5204		2774	4850
	3649	5725		3287	5363
	3858	5934		3716	5792
928	4121	6197		4122	6198
	4392	6468		4123	6199
	4552	6629		4531	6607
929	2743	4819		4536	6612
	2745	4821		4573	6649
	3666	5742		4634	6710
	4276	6352	953	2683	4759
	4343	6419		3531	5607
	4630	6706		3668	5744
930	4249	6325		3826	5902
932	2965	5041		4150	6226
	3014	5090		SEQ	
	3840	5916		ID	
	4041	6117		NO:	
	4137	6213			
	4506	6582			
934	3616	5692			
	3816	5892			
	4105	6181			
	4111	6187			
	4172	6248			
943	2881	4957			
	2998	5074			
	3203	5279			
	3818	5894			

Table 23 Plant Open Reading Frames (ORFs) orthologous to specific Arabidopsis ORFs

SEQ ID NO: 2	
AAD17487.1 AF049347	Berberis stolonifera Catalyzes the oxidative cyclization of the N-methyl group of (S)-reticuline into the berberine bridge carbon (C-8) of (S)-scoulerine. berberine bridge enzyme. bbe1. Covalently flavinylated oxidase of isoquinoline alkaloid biosynthesis in plants.
AAB20352.1 S65550	Eschscholzia californica (S)-reticuline:oxygen oxidoreductase (methylene-bridge-forming). /gene="(S)-reticuline:oxygen oxidoreductase. This sequence comes from Fig 2; berberine bridge enzyme.
AAC39358.1 AF005655	Eschscholzia californica oxidizes the N-methyl group of (S)-reticuline to the berberine bridge carbon C-8 of (S)-scoulerine in berberine and benzophenanthridine alkaloid biosynthesis. berberine bridge enzyme. bbe1. covalently-bound FAD-dependent oxidase; elicitor-inducible.
AAC61839.1 AF025430	Papaver somniferum berberine bridge enzyme. bbe1. (S)-reticuline:oxygen oxidoreductase (methylene bridge forming).
SEQ ID NO: 19	
AAC83458.1 AF023140	Thlaspi goesingense imidazoleglycerol phosphate dehydratase. THB1.
AAB67738.1 U49978	Pisum sativum imidazoleglycerol-phosphate dehydratase. PSHIS3.
AAA93197.1 U02690	Triticum aestivum imidazoleglycerolphosphate dehydratase. partial interval represents the confirmed coding region based on homology to sequence U02689, maybe a chimeric molecule.
CAB55393.1 AL117264	Oryza sativa zwh0009.1. similar to wheat imidazoleglycerol-phosphate dehydratase (P34048); Method: conceptual translation with partial peptide sequencing.
SEQ ID NO: 32	
CAA45066.2 X63464	Pisum sativum dihydrolipoamide dehydrogenase. lpd.
CAA44729.1 X62995	Pisum sativum lipoamide dehydrogenase.
AAG17888.1 AF295339	Solanum tuberosum dihydrolipoamide dehydrogenase precursor. lpd2. NADH; E3 isoform.
BAB39219.1 AP002869	Oryza sativa putative dihydrolipoamide dehydrogenase precursor. P0554D10.3. contains ESTs C98433(E0148),AU101058(E0148).
SEQ ID NO: 33	
CAC03581.1 AJ297566	Zea mays putative 1-deoxy-D-xylulose 5-phosphate reductoisomerase. dxr.
AAD24768.1 AF116825	Mentha x piperita 1-deoxy-D-xylulose-5-phosphate reductoisomerase. DXR.

AAF65154.1 AF250235 *Catharanthus roseus*
catalyzes the formation of 2-C-methyl-D-erythritol 4-phosphate from 1-deoxy-D-xylulose-5-phosphate. 1-deoxy-D-xylulose-5-phosphate reductoisomerase. dxr.

AAD56391.2 AF182287 *Artemisia annua*
catalyzes the formation of 2-C-methyl-D-erythritol 4-phosphate from 1-deoxy-D-xylulose-5-phosphate. 1-deoxy-D-xylulose-5-phosphate reductoisomerase. DXR1.

BAB16915.1 AP002863 *Oryza sativa*
1-deoxy-d-xylulose-5-phosphate reductoisomerase. P0005A05.19. contains ESTs AU108198(S11168), D46469(S11168).

SEQ ID NO: 37

AAD21872.1 AF078082 *Phaseolus vulgaris*
receptor-like protein kinase homolog RK20-1.

CAA73134.1 Y12531 *Brassica oleracea*
serine/threonine kinase. BRLK.

AAB93834.1 U82481 *Zea mays*
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

CAA67145.1 X98520 *Brassica oleracea*
receptor-like kinase. SFR2.

AAC23542.1 U20948 *Ipomoea trifida*
receptor protein kinase. IRK1.

CAA73133.1 Y12530 *Brassica oleracea*
serine /threonine kinase. ARLK.

CAB41878.1 Y18259 *Brassica oleracea*
SRK5 protein. SRK5. receptor-like kinase.

CAB41879.1 Y18260 *Brassica oleracea*
SRK15 protein. SRK15. receptor-like kinase.

CAA74661.1 Y14285 *Brassica oleracea*
SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.

CAA74662.1 Y14286 *Brassica oleracea*
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.

AAA33000.1 M76647 *Brassica oleracea*
receptor protein kinase. SKR6.

BAA23676.1 AB000970 *Brassica rapa*
receptor kinase 1. BcRK1.

AAA33008.1 M97667 *Brassica napus*
serine/threonine kinase receptor.

AAA62232.1 U00443 *Brassica napus*
S-receptor kinase. protein contains an immunoglobulin-like domain.

CAB89179.1 AJ245479 *Brassica napus* subsp. *napus*
ser /thr kinase. S-locus receptor kinase. srk.

BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrk1.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
CAA79324.1	Z18884	Brassica oleracea	S-receptor kinase related protein.
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.

AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
SEQ ID NO: 38			
CAA58750.1	X83869	Daucus carota	CDPK-related protein kinase. CRK (or PK421).
BAA12692.1	D84508	Zea mays	CDPK-related protein kinase. Does not require calcium for its activity.
AAG01179.1	AF289237	Zea mays	calcium/calmodulin dependent protein kinase MCK2. MCK2.
AAB47181.1	S82324	Zea mays	/gene="calcium/calmodulin-dependent protein kinase. This sequence comes from Fig. 1.
BAA12691.1	D84507	Zea mays	CDPK-related protein kinase. Does not require calcium for its activity (by similarity).
BAA22410.1	D38452	Zea mays	calcium-dependent protein kinase-related kinase.
AAC24961.1	AF009337	Tradescantia virginiana	CDPK-related protein kinase. CRK1.
AAF23901.2	AF194414	Oryza sativa	calcium-dependent protein kinase. CDPK5. OsCDPK5.
AAF23900.1	AF194413	Oryza sativa	calcium-dependent protein kinase. CDPK1. OsCDPK1.
AAC78558.1	AF030879	Solanum tuberosum	protein kinase CPK1.
CAA57157.1	X81394	Oryza sativa	calcium-dependent protein kinase. OSCPK2.
BAB21081.1	AP002819	Oryza sativa	putative calcium-dependent protein kinase. P0501G01.10.
AAC25423.1	AF072908	Nicotiana tabacum	calcium-dependent protein kinase. CDPK1.
BAA12715.1	D85039	Zea mays	calcium-dependent protein kinase.
AAB49984.1	U90262	Cucurbita pepo	calcium-dependent calmodulin-independent protein kinase CDPK. cpCPK1. serine/threonine protein kinase that is activated by direct binding of calcium.
AAA69507.1	U28376	Zea mays	calcium-dependent protein kinase. MZECDPK2.
AAD17800.1	AF090835	Mesembryanthemum crystallinum	Ca ²⁺ -dependent protein kinase. CPK1. serine/threonine protein kinase.

AAB80693.1	U69174	Glycine max	calmodulin-like domain protein kinase isoenzyme gamma. CDPK gamma.
BAA81751.1	AB017517	Marchantia polymorpha	calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.
BAA81749.1	AB017515	Marchantia polymorpha	calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.
CAA39936.1	X56599	Daucus carota	calcium- dependent protein kinase. DcPK431.
BAA81748.1	AB017515	Marchantia polymorpha	calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
BAA81750.1	AB017516	Marchantia polymorpha	calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
AAA61682.1	L27484	Zea mays	calcium-dependent protein kinase. CDPK.
BAB16888.1	AB042550	Oryza sativa	OsCDPK7. oscdpk7.
AAB88537.1	AF035944	Fragaria x ananassa	calcium-dependent protein kinase. MAX17.
AAD28192.2	AF115406	Solanum tuberosum	calcium-dependent protein kinase. CDPK; catalytic domain.
CAA07481.1	AJ007366	Zea mays	calcium-dependent protein kinase.
BAA12338.1	D84408	Zea mays	calcium dependent protein kinase. ZmCDPK1.
BAA13440.1	D87707	Ipomoea batatas	calcium dependent protein kinase. CDPK.
BAA13232.1	D87042	Zea mays	Calcium-dependent protein kinase.
CAA65500.1	X96723	Medicago sativa	protein kinase. CDPK.
AAB70706.1	U82087	Tortula ruralis	calmodulin-like domain protein kinase. TrCPK1.
AAC49405.1	U08140	Vigna radiata	calcium dependent protein kinase. CDPK.
BAA85396.1	AP000615	Oryza sativa	ESTs C22369(C12239),C22370(C12239), AU057852(S21844),AU057853(S21844) correspond to a region of the predicted gene.; similar to calcium dependent protein kinase. (AF048691).
CAA57156.1	X81393	Oryza sativa	calcium-dependent protein kinase. OSCPKII.
AAC05270.1	AF048691	Oryza sativa	calcium dependent protein kinase. CDPK12.

AAF21062.1	AF216527	Dunaliella tertiolecta	calcium-dependent protein kinase. CPK1; CDPK.
AAB80692.1	U69173	Glycine max	calmodulin-like domain protein kinase isoenzyme beta. CDPK beta.
AAK26164.1	AY027885	Cucumis sativus	calcium-dependent calmodulin-independent protein kinase 5. CDPK5. CsCDPK5.
AAA33443.1	L15390	Zea mays	calcium-dependent protein kinase. CDPK.
CAA89202.1	Z49233	Chlamydomonas eugametos	calcium-stimulated protein kinase.
AAG46110.1	AC073166	Oryza sativa	calcium-dependent protein kinase. OSJNBb0064P21.2.
BAA02698.1	D13436	Oryza sativa	calcium-dependent protein kinase. spk.
BAA90814.1	AP001168	Oryza sativa	ESTs AU030197(E50746),AU030196(E50746) correspond to a region of the predicted gene.; Similar to calcium-dependent calmodulin-independent protein kinase CDPK (U90262).
CAB46228.1	Y18055	Arachis hypogaea	calcium dependent protein kinase. CDPK.
AAC49008.1	U24188	Lilium longiflorum	calcium/calmodulin-dependent phosphorylation activity. calcium/calmodulin-dependent protein kinase. CCaMK. serine/threonine kinase; binds to calcium and calmodulin.
AAF19401.1	AF203479	Glycine max	phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca ²⁺ /CaM kinase family; lacks the autoinhibitory region and EF hands.
AAF06970.1	AF162662	Kalanchoe fedtschenkoi	phosphoenolpyruvate carboxylase kinase. calcium-independent protein kinase.
SEQ ID NO: 39			
AAG00510.1	AF285172	Phaseolus vulgaris	leaf senescence-associated receptor-like protein kinase. SARK.
BAB21175.1	AP002909	Oryza sativa	putative serine/threonine-specific receptor protein kinase. P0044F08.3.
CAB51480.1	Y14600	Sorghum bicolor	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
AAF59905.1	AF197946	Glycine max	receptor protein kinase-like protein. CLV1A.
AAF59906.1	AF197947	Glycine max	receptor protein kinase-like protein. CLV1B.
AAB61708.1	U93048	Daucus carota	somatic embryogenesis receptor-like kinase. SERK.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).

AAC36318.1	AF053127	Malus x domestica	leucine-rich receptor-like protein kinase. LRPKml.
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAF91324.1	AF244890	Glycine max	receptor-like protein kinase 3. RLK3. GmRLK3.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
AAF91323.1	AF244889	Glycine max	receptor-like protein kinase 2. RLK2. GmRLK2.
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
BAB40094.1	AP003210	Oryza sativa	putative receptor protein kinase. OSJNBa0010K01.7.
CAA61510.1	X89226	Oryza sativa	leucine-rich repeat/receptor protein kinase. lrk2.
BAA87852.1	AP000816	Oryza sativa	Similar to putative Ser/Thr protein kinase. (AC004218).
BAA92221.1	AP001278	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
AAF91322.1	AF244888	Glycine max	receptor-like protein kinase 1. RLK1. GmRLK1.
AAK11569.1	AF318493	Lycopersicon hirsutum	Pto-like protein kinase D. LhirPtoD.
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).
AAC48932.1	U13923	Lycopersicon pimpinellifolium	Fen. putative serine/threonine protein kinase; similar to product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.
AAF76307.1	AF220602	Lycopersicon pimpinellifolium	Fen kinase.
AAB47424.1	U59317	Lycopersicon pimpinellifolium	serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.
AAK11566.1	AF318490	Lycopersicon hirsutum	Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.

AAB47423.1	U59315	Lycopersicon pimpinellifolium	serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
AAC48914.1	U02271	Lycopersicon pimpinellifolium	protein kinase.
AAF76306.1	AF220602	Lycopersicon pimpinellifolium	Pto kinase.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
AAF76313.1	AF220603	Lycopersicon esculentum	Pto kinase. LescPth5.
AAB47421.1	U59316	Lycopersicon esculentum	serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
AAF76314.1	AF220603	Lycopersicon esculentum	Fen kinase. Lescfen.
AAK11568.1	AF318492	Lycopersicon hirsutum	Pto-like protein kinase B. LhirPtoB.
AAB47422.1	U59318	Lycopersicon esculentum	serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
BAA06538.1	D31737	Nicotiana tabacum	protein-serine/threonine kinase.
AAK11567.1	AF318491	Lycopersicon hirsutum	Pto-like protein kinase F. LhirPtoF.
AAF34426.1	AF172282	Oryza sativa	leucine rich repeat containing protein kinase. DUPR11.16.
AAG25966.1	AF302082	Nicotiana tabacum	cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
SEQ ID NO: 41			
AAG12987.1	AF166498	Lycopersicon esculentum	sucrose transporter-like protein. SUT2. sucrose sensor.

AAF08330.1	AF021809	Vitis vinifera	putative sucrose transporter. VvSUC12.
BAA24071.1	D87819	Oryza sativa	sucrose transporter. OsSUT1.
AAF90181.1	AF280050	Oryza sativa subsp. indica	sucrose proton symporter. sucrose transporter. SUT1.
BAA83501.1	AB008464	Zea mays	Sucrose Transporter. ZmSUT1.
CAB75882.1	AJ272309	Hordeum vulgare	Transport sucrose through membrane. sucrose transporter 1. sut1.
AAD55269.1	AF182445	Vitis vinifera	sucrose transporter.
CAA83436.1	Z31561	Ricinus communis	sucrose transport. sucrose carrier. Scr1.
CAA76368.1	Y16767	Daucus carota	sucrose/H ⁺ symporter. SUT1b.
CAA76367.1	Y16766	Daucus carota	sucrose/H ⁺ symporter. SUT1a.
CAC19688.1	AJ303198	Daucus carota	essential for sucrose transport. sucrose/proton symporter. sut1a.
AAG25923.1	AF237780	Solanum tuberosum	sucrose transporter SUT4.
AAF08329.1	AF021808	Vitis vinifera	putative sucrose transporter. VvSUC11.
AAG09270.1	AF176950	Lycopersicon esculentum	sucrose transporter. SUT4.
AAF65765.1	AF242307	Euphorbia esula	sucrose transport protein.
AAF04295.1	AF191025	Alonsoa meridionalis	sucrose transporter 1. SUT1.
CAA57727.1	X82276	Nicotiana tabacum	sucrose transporter. NtSUT1a. Var. SNN bp 1-1346, Var. SR1 bp 1172-1614.
BAA89458.1	AB036758	Daucus carota	sucrose transporter protein. cSUT.
CAB75881.1	AJ272308	Hordeum vulgare	transport sucrose through membrane. sucrose transporter 2. sut2.
CAA76369.1	Y16768	Daucus carota	sucrose/H ⁺ symporter. SUT2.
CAC19689.1	AJ303199	Daucus carota	essential for sucrose transport. sucrose/proton symporter. sut2.
CAB07811.1	Z93774	Vicia faba	sugar transport. sucrose transport protein. sut.

CAA47604.1	X67125	Spinacia oleracea	sucrose permease. S21.
CAA48915.1	X69165	Solanum tuberosum	sucrose transport protein. SUT1.
AAD41024.1	AF109922	Pisum sativum	sucrose transport protein SUT1.
AAD53000.1	U64967	Beta vulgaris	sucrose-proton symporter. Bv8-6.
AAF08331.1	AF021810	Vitis vinifera	putative sucrose transporter. VvSUC27.
CAA58730.1	X83850	Beta vulgaris	sucrose/proton-symporter. sut1.
AAC99332.1	AF063400	Apium graveolens	sucrose transporter. SUT1.
AAD45391.1	AF167416	Apium graveolens	sucrose transporter SUT2B. SUT2B.
AAD45390.1	AF167415	Apium graveolens	sucrose transporter SUT2A. SUT2A.
AAF04294.1	AF191024	Asarina barclaiana	sucrose transporter 1. SUT1.
CAA59113.1	X84379	Plantago major	SUC1-sucrose proton symporter. SUC1.
AAD34610.1	AF149981	Nicotiana tabacum	sucrose transporter-like protein. SUT3.
CAA57726.1	X82275	Lycopersicon esculentum	sucrose transporter. LeSUT1.
CAA12256.1	AJ224961	Ricinus communis	Sucrose transport. Sucrose carrier. SUT1.
CAC33492.1	AJ310643	Ricinus communis	sucrose carrier. sucrose carrier. scr1.
AAD45932.1	AF168771	Betula pendula	sucrose transport protein. SUC1.
CAA53390.1	X75764	Plantago major	sucrose transporter. ptp1.
AAF22281.1	AF167417	Apium graveolens	putative sucrose transporter SUT1. SUT1.
BAA76434.1	AB025006	Cicer arietinum	sucrose transport protein.
SEQ ID NO: 42			
AAC64184.1	AF095577	Prunus persica	endopolygalacturonase.

CAA54150.1	X76735	Prunus persica	endopolygalacturonase.
AAC28906.1	AF001003	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 5. TAPG5. expressed in abscission.
AAC28947.1	AF029230	Lycopersicon esculentum	polygalacturonase. TPG6.
AAC70951.1	AF072732	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella. polygalacturonase 7. specifically and abundantly expressed in pistils.
AAC28905.1	AF001002	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 4. TAPG4. expressed in abscission.
AAA80489.1	U23053	Lycopersicon esculentum	polygalacturonase precursor.
AAC28903.1	AF001000	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 1. TAPG1. expressed in abscission.
AAB09575.1	U70480	Lycopersicon esculentum	abscission polygalacturonase. TAPG2.
AAC28904.1	AF001001	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 2. TAPG2. expressed in abscission.
AAB09576.1	U70481	Lycopersicon esculentum	abscission polygalacturonase. TAPG4.
AAC28902.2	AF000999	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 3. TAPG3. expressed in abscission.
AAC26510.1	AF062465	Cucumis melo	polygalacturonase precursor. MPG1.
AAC26511.1	AF062466	Cucumis melo	polygalacturonase precursor. MPG2.
BAB21092.1	AP002819	Oryza sativa	putative endopolygalacturonase. P0501G01.21.
AAA62286.1	U20431	Medicago sativa	polygalacturonase.
AAA82167.1	U09717	Gossypium hirsutum	polygalacturonase.
AAA58322.1	U09805	Gossypium barbadense	polygalacturonase.
CAA50336.1	X71018	Nicotiana tabacum	polygalacturonase. NPG. Protein sequence is in conflict with the conceptual translation; G27Y.

CAA50334.1	X71016	Nicotiana tabacum	polygalacturonase. NPG. Protein sequence is in conflict with the conceptual translation; G27.X.
CAA50337.1	X71019	Nicotiana tabacum	polygalacturonase. NPG. Protein sequence is in conflict with the conceptual translation; G27W.
CAA65072.1	X95800	Brassica napus	polygalacturonase.
BAA89478.1	AB029459	Salix gilgiana	polygalacturonase. SgPG3.
CAA90272.1	Z49971	Brassica napus	Hydrolytic enzyme. Polygalacturonase. pga.
CAA50335.1	X71017	Nicotiana tabacum	polygalacturonase. Npg1. Protein sequence is in conflict with the conceptual translation.
CAA50338.1	X71020	Nicotiana tabacum	polygalacturonase. Npg1.
BAA89479.1	AB029460	Salix gilgiana	polygalacturonase. SgPG4.
AAC14453.1	L12019	Actinidia deliciosa	polygalacturonase.
BAA89476.1	AB029457	Salix gilgiana	polygalacturonase. SgPG1.
AAC26512.1	AF062467	Cucumis melo	polygalacturonase precursor. MPG3.
CAA72003.1	Y11118	Medicago sativa	polygalacturonase. PG3.
CAB42886.1	AJ238848	Phleum pratense	polygalacturonase. pg.
BAA89477.1	AB029458	Salix gilgiana	polygalacturonase. SgPG2.
CAC05658.1	AJ250919	Brassica napus	endopolygalacturonase. pegaz.
CAC05657.1	AJ250918	Brassica napus	endopolygalacturonase. pgaz.
AAA32914.1	L06094	Persea americana	cell wall degradation. polygalacturonase.
AAF71160.1	AF152758	Actinidia chinensis	polygalacturonase A. PGA.
AAF61444.1	AF138858	Lycopersicon esculentum	hydrolyses polygalacturonic acid. polygalacturonase. XOPG1.
AAA34178.1	M37304	Lycopersicon esculentum	polygalacturonase.

CAA32235.1 X14074 *Lycopersicon esculentum*
polygalacturonase.

CAA29148.1 X05656 *Lycopersicon esculentum*
polygalacturonase (AA 1-457).

AAD46483.1 AF128266 *Glycine max*
polygalacturonase PG1.

BAA88472.1 AB035890 *Cucumis sativus*
polygalacturonase. CUPG1.

AAD46484.1 AF128267 *Glycine max*
polygalacturonase PG2.

CAA54448.1 X77231 *Prunus persica*
polygalacturonase. PG.

CAA47055.1 X66426 *Persea americana*
polygalacturonase.

CAA47052.1 X66422 *Zea mays*
polygalacturonase. PG.

SEQ ID NO: 44

AAC61805.1 U28007 *Lycopersicon esculentum*
serine/threonine protein kinase. Pto kinase interactor 1. Pti1. Pti1 kinase.

BAB21241.1 AP002953 *Oryza sativa*
Putative Pto kinase interactor 1. P0426D06.21. contains ESTs
AU108280(E0721),D48017(S13927).

AAF91337.1 AF249318 *Glycine max*
Pti1 kinase-like protein. Pti1b. protein kinase.

AAF91336.1 AF249317 *Glycine max*
Pti1 kinase-like protein. Pti1a. protein kinase.

BAA87853.1 AP000816 *Oryza sativa*
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative
NAK-like Ser/Thr protein kinase. (AF001308).

BAB16871.1 AP002537 *Oryza sativa*
putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs
C22608(R3192),D25110(R3192).

AAG16628.1 AY007545 *Brassica napus*
protein serine/threonine kinase BNK1.

BAB39409.1 AP002901 *Oryza sativa*
putative protein kinase. P0456F08.9. contains EST C23560(R0290).

BAB39873.1 AP002882 *Oryza sativa*
putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

AAC27894.1 AF023164 *Zea mays*
leucine-rich repeat transmembrane protein kinase 1. ltk1.

BAA94509.1 AB041503 *Populus nigra*
protein kinase 1. PnPK1.

BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAC27895.1	AF023165	Zea mays	leucine-rich repeat transmembrane protein kinase 2. Itk2.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
BAA78764.1	AB023482	Oryza sativa	ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
AAG25966.1	AF302082	Nicotiana tabacum	cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
AAB09771.1	U67422	Zea mays	CRINKLY4 precursor. cr4. receptor kinase homolog.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).
AAB47421.1	U59316	Lycopersicon esculentum	serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
AAF76313.1	AF220603	Lycopersicon esculentum	Pto kinase. LescPth5.

CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
AAB47423.1	U59315	Lycopersicon pimpinellifolium	serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
AAF76306.1	AF220602	Lycopersicon pimpinellifolium	Pto kinase.
AAC48914.1	U02271	Lycopersicon pimpinellifolium	protein kinase.
BAA92221.1	AP001278	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
BAA87852.1	AP000816	Oryza sativa	Similar to putative Ser/Thr protein kinase. (AC004218).
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
AAK11566.1	AF318490	Lycopersicon hirsutum	Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
AAK11567.1	AF318491	Lycopersicon hirsutum	Pto-like protein kinase F. LhirPtoF.
CAB51836.1	AJ243961	Oryza sativa	Putative Ser/Thr protein kinase. 11332.7.
AAD38286.1	AC007789	Oryza sativa	putative protein kinase. OSJNBa0049B20.13.
BAB40081.1	AP003074	Oryza sativa	putative receptor protein kinase. OSJNBa0004G10.30.
BAB18321.1	AP002865	Oryza sativa	putative receptor protein kinase. P0034C11.11.
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
SEQ ID NO: 45			
AAB72110.1	U79958	Pisum sativum	BP-80 vacuolar sorting receptor.
AAF80450.1	AF161719	Triticum aestivum	vacuolar targeting receptor bp-80.
AAG60258.1	AY017377	Physcomitrella patens	EGF receptor-like protein. ELP. PPELP; similar to putative vacuolar sorting receptor.
AAF22842.1	AF209910	Prunus dulcis	vacuolar sorting receptor protein. BP-80 type protein.
AAK31596.1	AY029172	Helianthus annuus	EGF receptor-like protein. ELP.

AAB72113.1 U79961 *Zea mays*
vacuolar sorting receptor homolog. similar to *Pisum sativum* BP-80 vacuolar sorting receptor,
GenBank Accession Number U79958.

BAA92985.1 AP001550 *Oryza sativa*
EST D15617(C0960A) corresponds to a region of the predicted gene.; Similar to *Arabidopsis thaliana* chromosome 4, BAC clone F18F4; vacuolar sorting receptor-like protein (AL021637).

SEQ ID NO: 47

BAA00885.1 D10001 *Pisum sativum*
phenylalanine ammonia-lyase.

AAK15640.1 AF326116 *Agastache rugosa*
phenylalanine ammonia-lyase. PAL.

CAB42794.1 AJ238754 *Citrus clementina* x *Citrus reticulata*
phenylalanine-ammonia lyase. pal2.

BAA00886.1 D10002 *Pisum sativum*
phenylalanine ammonia-lyase. PAL1.

BAA00887.1 D10003 *Pisum sativum*
phenylalanine ammonia-lyase. PAL2.

AAB67733.1 U43338 *Citrus limon*
phenylalanine ammonia-lyase. pal6.

AAF40224.1 AF237955 *Rubus idaeus*
phenylalanine ammonia-lyase 2. PAL2. PAL; phenylpropanoid; multigene; flavonoid.

AAA17993.1 M91192 *Trifolium subterraneum*
phenylalanine ammonia-lyase. PAL1.

CAA57057.1 X81159 *Petroselinum crispum*
phenylalanine ammonia-lyase 3. PAL3. tetramere subunit.

AAF40223.1 AF237954 *Rubus idaeus*
phenylalanine ammonia-lyase 1. PAL1. PAL; phenylpropanoid; multigene; flavonoid.

CAA68938.1 Y07654 *Petroselinum crispum*
PAL1 protein. pal1 gene.

CAA57056.1 X81158 *Petroselinum crispum*
phenylalanine ammonia-lyase 2. PAL2. deaminase subunit.

CAB60719.1 AJ250836 *Cicer arietinum*
phenylpropanoid pathway. phenylalanine ammonia-lyase. pal.

CAA05251.1 AJ002221 *Digitalis lanata*
phenylalanine ammonia lyase.

AAC78457.1 AF036948 *Prunus avium*
phenylalanine ammonia-lyase. PAL1.

BAA23367.1 D85850 *Daucus carota*
phenylalanine ammonia-lyase. gDcPAL1.

CAA68256.1 X99997 *Bromheadia finlaysoniana*
phenylalanine ammonia-lyase. pal.

AAA33805.1	L11747	Populus x generosa
phenylalanine ammonia lyase. PAL.		
BAA24928.1	D83075	Lithospermum erythrorhizon
phenylalanine ammonia-lyase.		
CAA34226.1	X16099	Oryza sativa subsp. japonica
phenylalanine ammonia-lyase.		
CAA41169.1	X58180	Medicago sativa
phenylalanine ammonia-lyase. PAL.		
AAA34176.1	M90692	Lycopersicon esculentum
phenylalanine ammonia-lyase. PAL5.		
BAA07860.1	D43802	Populus kitakamiensis
phenylalanine ammonia-lyase.		
AAA84889.1	U39792	Pinus taeda
phenylalanine ammonia-lyase. lpPAL.		
CAA73065.1	Y12461	Helianthus annuus
phenylalanine ammonia lyase. PAL.		
BAA95629.1	AB042520	Catharanthus roseus
phenylalanine ammonia lyase.		
BAA05643.1	D26596	Camellia sinensis
phenylalanine ammonia-lyase.		
BAA24929.1	D83076	Lithospermum erythrorhizon
phenylalanine ammonia-lyase.		
BAA21643.1	D30656	Populus kitakamiensis
phenylalanine ammonia-lyase.		
CAA37129.1	X52953	Glycine max
phenylalanine ammonia-lyase. PAL1.		
AAA34122.1	M84466	Nicotiana tabacum
phenylalanine ammonia lyase. tpa1.		
BAA22948.1	AB008200	Nicotiana tabacum
phenylalanine ammonia-lyase. palB.		
AAA99500.1	L36822	Stylosanthes humilis
phenylalanine ammonia lyase. PAL17.1.		
CAB42793.1	AJ238753	Citrus clementina x Citrus reticulata
phenylalanine-ammonia lyase. pal1.		
AAG49585.1	AF325496	Ipomoea nil
phenylalanine ammonia-lyase.		
CAA55075.1	X78269	Nicotiana tabacum
phenylalanine ammonia-lyase.		
BAA22963.1	D17467	Nicotiana tabacum
phenylalanine ammonia-lyase. TOBPAL1.		
BAA22947.1	AB008199	Nicotiana tabacum
phenylalanine ammonia-lyase. palA.		

AAA34179.2 M83314 *Lycopersicon esculentum*
deamination of phenylalanine to coumarate. phenylalanine ammonia lyase. pal.

BAA11459.1 D78640 *Ipomoea batatas*
Phenylalanine Ammonia-Lyase.

AAA33389.1 M29232 *Ipomoea batatas*
phenylalanine ammonia-lyase.

CAA68036.1 X99705 *Triticum aestivum*
phenylalanine ammonia-lyase. PAL.

CAA61198.1 X87946 *Oryza sativa*
phenylalanine ammonia-lyase. ZB8.

BAA06337.1 D30657 *Populus kitakamiensis*
phenylalanine ammonia-lyase.

AAD45384.1 AF165998 *Vigna unguiculata*
phenylalanine ammonia-lyase.

CAA53733.1 X76130 *Cucumis melo*
phenylalanine ammonia-lyase. pal.

AAA51873.1 U16130 *Persea americana*
phenylalanine ammonia lyase. PAL.

BAB19128.1 AB041361 *Dianthus caryophyllus*
phenylalanine ammonia-lyase. Dcpal1.

CAA34715.1 X16772 *Petroselinum crispum*
phenylalanine ammonia-lyase (AA 137 - 716) (1 is 3rd base in codon).

BAA07861.1 D43803 *Populus kitakamiensis*
phenylalanine ammonia-lyase.

SEQ ID NO: 48

CAB94692.1 AJ242742 *Ipomoea batatas*
Removal of H₂O₂, oxidation of toxic reductants, defence response toward wounding.
peroxidase. pod.

AAD37430.1 AF149280 *Phaseolus vulgaris*
peroxidase 5 precursor. FBP5. secretory peroxidase.

CAA66037.1 X97351 *Populus balsamifera* subsp. *trichocarpa*
signal for ER. peroxidase.

BAA06335.1 D30653 *Populus kitakamiensis*
peroxidase.

AAA34108.1 J02979 *Nicotiana tabacum*
lignin-forming peroxidase precursor (EC 1.11.1.7).

BAA01992.1 D11396 *Nicotiana tabacum*
'peroxidase'.

CAA50597.1 X71593 *Lycopersicon esculentum*
peroxidase. CEVI-1.

CAB67121.1 Y19023 *Lycopersicon esculentum*
peroxidase. cevi-1.

BAA11853.1	D83225	Populus nigra peroxidase.
CAA66034.1	X97348	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA01877.1	D11102	Populus kitakamiensis peroxidase. prxA1.
BAA11852.1	D83224	Populus nigra peroxidase.
CAA66035.1	X97349	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
AAB47602.1	L07554	Linum usitatissimum peroxidase. FLXPER1.
AAD37427.1	AF149277	Phaseolus vulgaris peroxidase 1 precursor. FBP1. secretory peroxidase.
CAA66036.1	X97350	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
AAB97734.1	AF014502	Glycine max seed coat peroxidase precursor. Ep. H2O2 oxidoreductase; class III plant peroxidase.
BAA06334.1	D30652	Populus kitakamiensis peroxidase.
BAA07241.1	D38051	Populus kitakamiensis peroxidase. prxA4a.
CAA62226.1	X90693	Medicago sativa peroxidase1B. prx1B.
CAA62225.1	X90692	Medicago sativa peroxidase1A. prx1A.
CAA62227.1	X90694	Medicago sativa peroxidase1C. prx1C.
AAB41811.1	L36157	Medicago sativa peroxidase. pxdC. amino acid feature: conserved domains, aa 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 .. 73.
AAB41810.1	L36156	Medicago sativa peroxidase. pxdA. amino acid feature: conserved motifs, aa 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
AAC98519.1	AF007211	Glycine max peroxidase precursor. GMIPER1. pathogen-induced.
BAA02840.1	D13683	Populus kitakamiensis peroxidase. HPOX14.
BAA14144.1	D90116	Armoracia rusticana peroxidase isozyme.
AAA33129.1	M91372	Cucumis sativus peroxidase. pre-peroxidase.

BAA14143.1	D90115	Armoracia rusticana	peroxidase isozyme.
BAA08499.1	D49551	Oryza sativa	peroxidase. poxN.
BAA03373.1	D14482	Oryza sativa	putative peroxidase.
AAA34101.1	L02124	Nicotiana tabacum	peroxidase.
BAA82306.1	AB027752	Nicotiana tabacum	peroxidase.
CAA40796.1	X57564	Armoracia rusticana	peroxidase. peroxidase precursor.
AAA33121.1	M32742	Cucumis sativus	peroxidase (CuPer2).
CAA76680.1	Y17192	Cucurbita pepo	peroxidase. aprx. type III peroxidase.
BAA92500.1	AP001383	Oryza sativa	ESTs D39300(R3292),AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).
BAA77388.1	AB024438	Scutellaria baicalensis	peroxidase 2.
AAA33127.1	M91373	Cucumis sativus	peroxidase. pre-peroxidase. putative.
AAD43561.1	AF155124	Gossypium hirsutum	bacterial-induced peroxidase precursor. Perx_Goshiko.
AAB06183.1	M37636	Arachis hypogaea	cationic peroxidase. PNC1.
AAF63027.1	AF244924	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
CAA71492.1	Y10466	Spinacia oleracea	peroxidase. prxr5.
AAB02554.1	L37790	Stylosanthes humilis	cationic peroxidase.
BAA94962.1	AB042103	Asparagus officinalis	peroxidase. AspPOX1.
BAA77389.1	AB024439	Scutellaria baicalensis	peroxidase 3.
SEQ ID NO: 50			
CAA40796.1	X57564	Armoracia rusticana	peroxidase. peroxidase precursor.
BAA03373.1	D14482	Oryza sativa	putative peroxidase.

BAA08499.1	D49551	Oryza sativa	peroxidase. poxN.
CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa	signal for ER. peroxidase.
BAA84764.1	D84400	Oryza sativa	peroxidase. poxA.
BAA03372.1	D14481	Oryza sativa	putative peroxidase.
CAB94692.1	AJ242742	Ipomoea batatas	Removal of H ₂ O ₂ , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
BAA06335.1	D30653	Populus kitakamiensis	peroxidase.
BAA11853.1	D83225	Populus nigra	peroxidase.
AAD37427.1	AF149277	Phaseolus vulgaris	peroxidase 1 precursor. FBP1. secretory peroxidase.
AAD37430.1	AF149280	Phaseolus vulgaris	peroxidase 5 precursor. FBP5. secretory peroxidase.
BAA11852.1	D83224	Populus nigra	peroxidase.
CAA66035.1	X97349	Populus balsamifera subsp. trichocarpa	signal for ER. peroxidase.
CAA66034.1	X97348	Populus balsamifera subsp. trichocarpa	signal for ER. peroxidase.
BAA07241.1	D38051	Populus kitakamiensis	peroxidase. prxA4a.
BAA92500.1	AP001383	Oryza sativa	ESTs D39300(R3292), AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).
CAA50597.1	X71593	Lycopersicon esculentum	peroxidase. CEVI-1.
CAB67121.1	Y19023	Lycopersicon esculentum	peroxidase. cevi-1.
CAA66036.1	X97350	Populus balsamifera subsp. trichocarpa	signal for ER. peroxidase.
AAB47602.1	L07554	Linum usitatissimum	peroxidase. FLXPER1.
CAA62226.1	X90693	Medicago sativa	peroxidase1B. prx1B.
AAA34108.1	J02979	Nicotiana tabacum	lignin-forming peroxidase precursor (EC 1.11.1.7).

CAA62227.1	X90694	Medicago sativa peroxidase1C. prx1C.
BAA06334.1	D30652	Populus kitakamiensis peroxidase.
BAA01992.1	D11396	Nicotiana tabacum 'peroxidase'.
AAD43561.1	AF155124	Gossypium hirsutum bacterial-induced peroxidase precursor. Perx_Goshiko.
BAA82306.1	AB027752	Nicotiana tabacum peroxidase.
AAC98519.1	AF007211	Glycine max peroxidase precursor. GMIPER1. pathogen-induced.
BAA14143.1	D90115	Armoracia rusticana peroxidase isozyme.
AAB97734.1	AF014502	Glycine max seed coat peroxidase precursor. Ep. H2O2 oxidoreductase; class III plant peroxidase.
AAF63027.1	AF244924	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
CAA62225.1	X90692	Medicago sativa peroxidase1A. prx1A.
BAA01877.1	D11102	Populus kitakamiensis peroxidase. prxA1.
AAF63026.1	AF244923	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx14 precursor. type III peroxidase.
BAA14144.1	D90116	Armoracia rusticana peroxidase isozyme.
AAB41810.1	L36156	Medicago sativa peroxidase. pxdA. amino acid feature: conserved motifs, aa 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
AAA34050.1	M74103	Nicotiana sylvestris anionic peroxidase.
CAA62597.1	X91172	Raphanus sativus korean-radish isoperoxidase. prxk1.
AAB02554.1	L37790	Stylosanthes humilis cationic peroxidase.
CAA76680.1	Y17192	Cucurbita pepo peroxidase. aprx. type III peroxidase.
CAA71492.1	Y10466	Spinacia oleracea peroxidase. prxr5.
BAA94962.1	AB042103	Asparagus officinalis peroxidase. AspPOX1.
BAA77389.1	AB024439	Scutellaria baicalensis peroxidase 3.

AAD37428.1 AF149278 Phaseolus vulgaris
peroxidase 3 precursor. FBP3. secretory peroxidase.

AAB41811.1 L36157 Medicago sativa
peroxidase. pxdC. amino acid feature: conserved domains, aa 123 .. 129, 191 .. 198; amino
acid feature: heme-binding domain, aa 68 .. 73.

AAB06183.1 M37636 Arachis hypogaea
cationic peroxidase. PNC1.

SEQ ID NO: 52

BAA02112.1 D12544 Pisum sativum
GTP-binding protein.

CAA98184.1 Z73956 Lotus japonicus
GTP-binding protein. RAB11H. rab11H.

AAK15703.1 AF327517 Oryza sativa
GTP-binding protein.

BAA02904.1 D13758 Oryza sativa
ras-related GTP binding protein. ss230.

BAA02111.1 D12543 Pisum sativum
GTP-binding protein.

BAA02113.1 D12545 Pisum sativum
GTP-binding protein.

CAA98180.1 Z73952 Lotus japonicus
GTP-binding protein. RAB11D. rab11D.

CAB65172.1 AJ245570 Lycopersicon esculentum
putative role in secretion of cell wall modifying enzymes. Rab11 GTPase. Rab11a.

BAA02114.1 D12546 Pisum sativum
GTP-binding protein.

CAA98181.1 Z73953 Lotus japonicus
GTP-binding protein. RAB11E. rab11E.

CAA95859.1 Z71276 Mangifera indica
small GTPase. rabX. homologous to Rab11.

CAA55865.1 X79278 Medicago sativa
GTP binding protein. Rab.

CAA89049.1 Z49190 Beta vulgaris
GTP-binding. small G protein.

CAA98179.1 Z73951 Lotus japonicus
GTP-binding protein. RAB11C. rab11C.

BAA02437.1 D13152 Oryza sativa
GTP binding protein. rgp2.

BAA06701.1 D31905 Zea mays
mgp1 GTP-binding protein. mgp1.

BAA06702.1 D31906 Zea mays
mgp2 GTP-binding protein. mgp2.

BAA02110.1	D12542	Pisum sativum	GTP-binding protein.
CAA98177.1	Z73949	Lotus japonicus	GTP-binding protein. RAB11A. rab11A.
CAA41966.1	X59276	Oryza sativa	GTP-binding protein. rgp1.
AAB97114.1	U58853	Glycine max	small GTP-binding protein. sra1.
CAA98185.1	Z73957	Lotus japonicus	GTP-binding protein. RAB11I. rab11I.
CAA67153.1	X98540	Fagus sylvatica	FSGTP1.
CAA98183.1	Z73955	Lotus japonicus	GTP-binding protein. RAB11G. rab11G.
CAA98182.1	Z73954	Lotus japonicus	GTP-binding protein. RAB11F. rab11F.
CAA54506.1	X77301	Glycine max	GTPase. gmr2.
BAA02108.1	D12540	Pisum sativum	GTP-binding protein.
AAA68983.1	L12395	Brassica napus	signal transduction, membrane vehicle traffic. small GTP-binding protein. bra. putative.
AAD48018.1	AF165095	Gossypium hirsutum	Rab GTP-binding protein Rab11a.
BAA02109.1	D12541	Pisum sativum	GTP-binding protein.
CAA98186.1	Z73958	Lotus japonicus	GTP-binding protein. RAB11J. rab11J.
BAA84640.1	AB007911	Pisum sativum	PRA2. pra2. light-repressible GTP binding protein.
AAD48019.1	AF165096	Gossypium hirsutum	Rab GTP-binding protein Rab11b.
CAA98178.1	Z73950	Lotus japonicus	GTP-binding protein. RAB11B. rab11B.
AAA63901.1	U22432	Zea mays	GTP binding protein. rab2.
CAA98165.1	Z73937	Lotus japonicus	GTP-binding protein. RAB2A. rab2A.
AAA34253.1	L08130	Volvox carteri	GTP-binding protein. yptV4.
AAA90955.1	U32185	Glycine max	vesicular transport. guanine nucleotide regulatory protein. rab2. GTP-binding protein; soyrab.

AAA63902.1 U22433 Zea mays
GTP binding protein. rab2.

SEQ ID NO: 53

CAA64327.1 X94624 Brassica napus
acyl-CoA synthetase.

CAA96523.1 Z72153 Brassica napus
acyl CoA synthetase.

CAC19877.1 AJ401089 Brassica napus
activation of free fatty acids. long chain acyl-CoA synthetase. acs6. activity confirmed by
expression in E. coli.

CAA06820.1 AJ006025 Cicer arietinum
acyl-coA synthetase.

BAA08365.1 D49366 Lithospermum erythrorhizon
4-coumarate:CoA ligase.

CAA36850.1 X52623 Oryza sativa
4-coumarate-CoA ligase.

AAF37734.1 AF052223 Lolium perenne
4-coumarate--CoA ligase 4CL3.

AAF91309.1 AF239686 Rubus idaeus
4-coumarate:coA ligase 2. adenylate-forming enzyme; 4CL2.

AAC24503.1 AF041049 Populus tremuloides
4-coumarate:CoA ligase.

BAA08366.2 D49367 Lithospermum erythrorhizon
4-coumarate:CoA ligase.

AAF91308.1 AF239685 Rubus idaeus
4-coumarate:coA ligase 3. adenylate-forming enzyme; 4CL3.

AAC39366.1 AF008184 Populus x generosa
4-coumarate:CoA ligase 1. 4CL1.

CAA31696.1 X13324 Petroselinum crispum
4-coumarate:CoA ligase Pc4Cl-1 (AA 1-544).

AAC39365.1 AF008183 Populus x generosa
4-coumarate:CoA ligase 2. 4CL2.

AAA33842.1 M62755 Solanum tuberosum
4-coumarate--CoA ligase. St4C1-1.

CAA31697.1 X13325 Petroselinum crispum
4-coumarate:CoA ligase Pc4Cl-2 (AA 1-544).

AAB42383.1 U39405 Pinus taeda
4-coumarate:CoA ligase. lp4CL-1.

AAB42382.1 U39404 Pinus taeda
4-coumarate:CoA ligase. lp4CL-2.

AAA92669.1 U12013 Pinus taeda
4-coumarate-CoA ligase enzyme.

AAF91310.1 AF239687 *Rubus idaeus*
4-coumarate:coA ligase 1. adenylate-forming enzyme; 4CL1.

AAA92668.1 U12012 *Pinus taeda*
4-coumarate-CoA ligase enzyme.

AAF37732.1 AF052221 *Lolium perenne*
4-coumarate--CoA ligase 4CL1.

CAA49575.1 X69954 *Glycine max*
4-coumarate--CoA ligase.

AAC24504.1 AF041050 *Populus tremuloides*
4-coumarate:CoA ligase.

AAF37733.1 AF052222 *Lolium perenne*
4-coumarate--CoA ligase 4CL2.

CAB97359.1 AJ278455 *Juglans nigra*
4-coumarate-CoA ligase. 4CL.

AAA69580.1 L43362 *Oryza sativa*
4-coumarate:CoA ligase isoform 2. 4cl.2. putative.

AAG46175.1 AC018727 *Oryza sativa*
putative 4-coumarate CoA ligase. OSJNBa0056G17.30.

AAF73997.2 AF144504 *Picea smithiana*
4-coumarate:CoA ligase. 4CL.

AAF73995.2 AF144502 *Pinus armandii*
4-coumarate:CoA ligase. 4CL.

AAF73998.2 AF144505 *Cathaya argyrophylla*
4-coumarate:CoA ligase. 4CL.

AAF73994.2 AF144501 *Pinus armandii*
4-coumarate:CoA ligase. 4CL.

AAF73996.2 AF144503 *Pinus armandii*
4-coumarate:CoA ligase. 4CL.

SEQ ID NO: 55

CAA87068.1 Z46944 *Citrus sinensis*
non-photosynthetic ferredoxin.

AAK15005.1 AF233452 *Impatiens balsamina*
ferredoxin. plastidal protein.

AAA33461.1 M73831 *Zea mays*
ferredoxin.

CAB65696.1 AJ270962 *Lycopersicon esculentum*
electron transfer. putative ferredoxin. ferredoxin.

BAA90760.1 AB038037 *Ipomoea nil*
non-photosynthetic ferredoxin.

BAA06456.1 D30794 *Oryza sativa*
ferredoxin.

AAB61593.1	AF003125	Mesembryanthemum crystallinum	ferredoxin I precursor.
AAA33665.1	M31713	Pisum sativum	ferredoxin I precursor.
AAD02175.1	AF039662	Capsicum annuum	delays the harpin-mediated hypersensitive response. ferredoxin-like protein. ap1.
CAA73265.1	Y12734	Physcomitrella patens	ferredoxin.
CAA52980.1	X75089	Triticum aestivum	ferredoxin. petF.
BAA06436.1	D30763	Oryza sativa	ferredoxin.
CAA99756.1	Z75520	Lycopersicon esculentum	transfer of electrons in a wide variety of metabolic reactions. ferredoxin-I. precursor.
AAA33462.1	M73828	Zea mays	ferredoxin.
AAA34028.1	M35660	Spinacia oleracea	ferredoxin I precursor.
CAA26281.1	X02432	Silene latifolia subsp. alba	ferredoxin precursor.
AAA33459.1	M73829	Zea mays	ferredoxin.
AAA33460.1	M73830	Zea mays	ferredoxin.
BAA32348.1	AB016810	Zea mays	ferredoxin. pFD2.
BAA19865.1	D83660	Oryza sativa	root ferredoxin.
AAA33085.1	L10349	Chlamydomonas reinhardtii	ferredoxin. precursor.
AAC49171.1	U29516	Chlamydomonas reinhardtii	ferredoxin precursor. Method: conceptual translation supplied by author.
AAB65699.1	AF010320	Oryza sativa	ferredoxin.
AAK14422.1	AC087851	Oryza sativa	putative ferredoxin. OSJNBb0072E24.16.
SEQ ID NO: 57			
CAB94692.1	AJ242742	Ipomoea batatas	Removal of H ₂ O ₂ , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
AAD37430.1	AF149280	Phaseolus vulgaris	peroxidase 5 precursor. FBP5. secretory peroxidase.

CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA06335.1	D30653	Populus kitakamiensis peroxidase.
AAA34108.1	J02979	Nicotiana tabacum lignin-forming peroxidase precursor (EC 1.11.1.7).
BAA01992.1	D11396	Nicotiana tabacum 'peroxidase'.
CAA66034.1	X97348	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
AAB47602.1	L07554	Linum usitatissimum peroxidase. FLXPER1.
BAA11853.1	D83225	Populus nigra peroxidase.
CAA50597.1	X71593	Lycopersicon esculentum peroxidase. CEVI-1.
CAB67121.1	Y19023	Lycopersicon esculentum peroxidase. cevi-1.
BAA11852.1	D83224	Populus nigra peroxidase.
CAA66035.1	X97349	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
AAD37427.1	AF149277	Phaseolus vulgaris peroxidase 1 precursor. FBP1. secretory peroxidase.
BAA01877.1	D11102	Populus kitakamiensis peroxidase. prxA1.
CAA66036.1	X97350	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
CAA62225.1	X90692	Medicago sativa peroxidase1A. prx1A.
AAB97734.1	AF014502	Glycine max seed coat peroxidase precursor. Ep. H2O2 oxidoreductase; class III plant peroxidase.
CAA62226.1	X90693	Medicago sativa peroxidase1B. prx1B.
CAA62227.1	X90694	Medicago sativa peroxidase1C. prx1C.
BAA06334.1	D30652	Populus kitakamiensis peroxidase.
BAA07241.1	D38051	Populus kitakamiensis peroxidase. prxA4a.
AAB41810.1	L36156	Medicago sativa peroxidase. pxdA. amino acid feature: conserved motifs, aa 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.

AAB41811.1	L36157	Medicago sativa	peroxidase. pxdC. amino acid feature: conserved domains, aa 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 .. 73.
BAA14144.1	D90116	Armoracia rusticana	peroxidase isozyme.
AAC98519.1	AF007211	Glycine max	peroxidase precursor. GMIPER1. pathogen-induced.
BAA02840.1	D13683	Populus kitakamiensis	peroxidase. HPOX14.
BAA14143.1	D90115	Armoracia rusticana	peroxidase isozyme.
AAA33129.1	M91372	Cucumis sativus	peroxidase. pre-peroxidase.
BAA08499.1	D49551	Oryza sativa	peroxidase. poxN.
BAA03373.1	D14482	Oryza sativa	putative peroxidase.
AAA34101.1	L02124	Nicotiana tabacum	peroxidase.
CAA76680.1	Y17192	Cucurbita pepo	peroxidase. aprx. type III peroxidase.
CAA40796.1	X57564	Armoracia rusticana	peroxidase. peroxidase precursor.
AAA33121.1	M32742	Cucumis sativus	peroxidase (CuPer2).
BAA82306.1	AB027752	Nicotiana tabacum	peroxidase.
AAD43561.1	AF155124	Gossypium hirsutum	bacterial-induced peroxidase precursor. Perx_Goshiko.
AAB06183.1	M37636	Arachis hypogaea	cationic peroxidase. PNC1.
AAA33127.1	M91373	Cucumis sativus	peroxidase. pre-peroxidase. putative.
CAA71492.1	Y10466	Spinacia oleracea	peroxidase. prxr5.
AAF63027.1	AF244924	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
AAA33128.1	M91374	Cucumis sativus	peroxidase. putative.
BAA77389.1	AB024439	Scutellaria baicalensis	peroxidase 3.
BAA77388.1	AB024438	Scutellaria baicalensis	peroxidase 2.

AAB02554.1	L37790	<i>Stylosanthes humilis</i> cationic peroxidase.
AAF63026.1	AF244923	<i>Spinacia oleracea</i> hydrogen peroxide catabolism. peroxidase prx14 precursor. type III peroxidase.
SEQ ID NO: 58		
AAG49002.1	AY013246	<i>Hordeum vulgare</i> putative ABC transporter. 635P2.4a; GC splice donor confirmed by cDNA and comparative sequencing.
AAG45492.1	AY013245	<i>Oryza sativa</i> 36I5.4. putative ABC transporter; GC splice donor confirmed by cDNA alignment and comparative sequence.
AAG49003.1	AY013246	<i>Hordeum vulgare</i> putative ABC transporter. 635P2.4b; GC splice donor confirmed by cDNA alignment and comparative sequence.
BAA83352.1	AP000391	<i>Oryza sativa</i> ESTs AU067992(C11433),AU077424(C11433) correspond to a region of the predicted gene.; Similar to ABC transporter-7 (U43892).
BAB17113.1	AP002866	<i>Oryza sativa</i> putative white protein; ATP-binding cassette transporter. P0410E01.34.
BAA90508.1	AP001111	<i>Oryza sativa</i> similar to ABC transporter of <i>Arabidopsis thaliana</i> (AC004697).
BAA90507.1	AP001111	<i>Oryza sativa</i> similar to ABC transporter of <i>Arabidopsis thaliana</i> (AC004697).
BAB40032.1	AP003046	<i>Oryza sativa</i> putative ABC transporter. P0445D12.3.
BAB16495.1	AP002861	<i>Oryza sativa</i> putative ABC transporter ATP-binding protein. P0665D10.21.
BAA94511.1	AB041505	<i>Populus nigra</i> ABC transporter homolog. PnATH.
BAB21275.1	AP002844	<i>Oryza sativa</i> putative ABC transporter protein. P0410E03.6.
BAB21276.1	AP002844	<i>Oryza sativa</i> putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
BAB21279.1	AP002844	<i>Oryza sativa</i> putative ABC transporter protein. P0410E03.10. contains ESTs AU065360(R3463),AU101680(R3463).
CAA94437.1	Z70524	<i>Spirodela polyrrhiza</i> multidrug resistance protein. PDR5-like ABC transporter.
BAB21273.1	AP002844	<i>Oryza sativa</i> putative ABC transporter protein. P0410E03.4.
SEQ ID NO: 59		
CAA71369.1	Y10338	<i>Solanum tuberosum</i> chloride channel Stcl1. putative.

AAD29679.1	AF133209	Nicotiana tabacum	CLC-Nt2 protein. putative chloride channel.
SEQ ID NO: 60			
BAB40094.1	AP003210	Oryza sativa	putative receptor protein kinase. OSJNBa0010K01.7.
AAG52992.1	U77888	Ipomoea nil	receptor-like protein kinase INRPK1a. inrpk1.
AAF59906.1	AF197947	Glycine max	receptor protein kinase-like protein. CLV1B.
AAC36318.1	AF053127	Malus x domestica	leucine-rich receptor-like protein kinase. LRPKml.
AAF91323.1	AF244889	Glycine max	receptor-like protein kinase 2. RLK2. GmRLK2.
AAF91324.1	AF244890	Glycine max	receptor-like protein kinase 3. RLK3. GmRLK3.
AAB36558.1	U77888	Ipomoea nil	receptor-like protein kinase INRPK1. inrpk1. leucine-rich repeat.
BAA83373.1	AP000391	Oryza sativa	ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
BAA84787.1	AP000559	Oryza sativa	ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
AAF91322.1	AF244888	Glycine max	receptor-like protein kinase 1. RLK1. GmRLK1.
AAF59905.1	AF197946	Glycine max	receptor protein kinase-like protein. CLV1A.
AAB61708.1	U93048	Daucus carota	somatic embryogenesis receptor-like kinase. SERK.
CAB51480.1	Y14600	Sorghum bicolor	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
CAC20842.1	AJ250467	Pinus sylvestris	receptor protein kinase. upk.
CAA61510.1	X89226	Oryza sativa	leucine-rich repeat/receptor protein kinase. lrk2.
BAB19337.1	AP003044	Oryza sativa	putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
AAG52994.1	U77888	Ipomoea nil	receptor-like protein kinase INRPK1c. inrpk1.
BAB40081.1	AP003074	Oryza sativa	putative receptor protein kinase. OSJNBa0004G10.30.

BAB18321.1	AP002865	Oryza sativa	putative receptor protein kinase. P0034C11.11.
AAD38286.1	AC007789	Oryza sativa	putative protein kinase. OSJNBa0049B20.13.
BAB07903.1	AP002835	Oryza sativa	putative receptor kinase. P0417G05.10. contains ESTs AU032341(R3918),AU071016(R10613).
AAF34426.1	AF172282	Oryza sativa	leucine rich repeat containing protein kinase. DUPR11.16.
BAA94519.1	AP001800	Oryza sativa	ESTs AU032341(R3918),AU071016(R10613) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4, BAC F9D16; putative receptor kinase (AL035394).
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAA82393.1	AP000367	Oryza sativa	EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative receptor protein kinase. (AC002334).
BAB03631.1	AP002522	Oryza sativa	putative protein kinase Xa21. P0009G03.32.
AAB82755.1	U72725	Oryza longistaminata	receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
AAK27817.1	AC022457	Oryza sativa	putative protein kinase. OSJNBa0006L06.16.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB03621.1	AP002522	Oryza sativa	putative protein kinase Xa21. P0009G03.21.
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).

AAK21965.1 AY028699 Brassica napus
receptor protein kinase PERK1.

AAG16628.1 AY007545 Brassica napus
protein serine/threonine kinase BNK1.

BAA94509.1 AB041503 Populus nigra
protein kinase 1. PnPK1.

BAB39421.1 AP002901 Oryza sativa
putative receptor kinase. P0456F08.21.

BAA94510.1 AB041504 Populus nigra
protein kinase 2. PnPK2.

CAB51836.1 AJ243961 Oryza sativa
Putitive Ser/Thr protein kinase. I1332.7.

BAB17139.1 AP002867 Oryza sativa
putative receptor kinase. P0463F06.31.

BAB07904.1 AP002835 Oryza sativa
putative S-receptor kinase. P0417G05.12.

BAB39409.1 AP002901 Oryza sativa
putative protein kinase. P0456F08.9. contains EST C23560(R0290).

SEQ ID NO: 62

BAA25753.1 AB012932 Vigna radiata
Ca²⁺/H⁺ exchanger. VCAX1.

AAF91350.1 AF256229 Zea mays
calcium/proton exchanger CAX1-like protein.

BAA75232.1 AB018526 Ipomoea nil
H⁺/Ca²⁺ exchanger 2. CAX2.

SEQ ID NO: 63

BAA85655.1 AB026297 Pisum sativum
elicitor-responsive Dof protein ERDP.

AAB70119.1 U82230 Zea mays
transcription factor. prolamin box binding factor. PBF. endosperm-specific DOF protein;
DNA binding.

CAB89831.1 AJ242853 Solanum tuberosum
DNA binding protein. Dof zinc finger protein. dof1.

CAA08755.1 AJ009594 Nicotiana tabacum
Dof zinc finger protein. BBF1.

CAA66601.1 X97942 Nicotiana tabacum
Zn finger protein. NtBBF1.1.

CAA66604.1 X97945 Nicotiana tabacum
Zn finger protein. NtBBF2a.

BAA78575.1 AB028132 Oryza sativa
Dof zinc finger protein.

BAA78572.1 AB028129 Oryza sativa
Dof zinc finger protein.

BAA78573.1	AB028130	Oryza sativa	Dof zinc finger protein.
CAA66606.1	X97947	Nicotiana tabacum	Zn finger protein. NtBBF3.
CAA66605.1	X97946	Nicotiana tabacum	Zn finger protein. NtBBF2b.
BAA78574.1	AB028131	Oryza sativa	Dof zinc finger protein. Rice cDNA for protein that binds to AT-rich sequence of rice carboxypeptidase-3 promoter.
CAA56287.1	X79934	Zea mays	Dof2. No start codon.
CAA56288.1	X79935	Zea mays	Dof3 gene. no start codon.
BAA78576.1	AB028133	Oryza sativa	Dof zinc finger protein.

SEQ ID NO: 64

CAA11219.1	AJ223281	Manihot esculenta	alpha-hydroxynitrile lyase. HNL4.
BAB19413.1	AP002870	Oryza sativa	putative acetone-cyanohydrin lyase. P0458A05.22.
AAC49184.1	U40402	Hevea brasiliensis	hydroxynitrile lyase. hnl.
CAA82334.1	Z29091	Manihot esculenta	alpha-hydroxynitrile lyase.
CAA11428.1	AJ223506	Manihot esculenta	alpha-hydroxynitrile lyase. HNL24.

SEQ ID NO: 67

CAB89831.1	AJ242853	Solanum tuberosum	DNA binding protein. Dof zinc finger protein. dof1.
CAA56288.1	X79935	Zea mays	Dof3 gene. no start codon.
BAA85655.1	AB026297	Pisum sativum	elicitor-responsive Dof protein ERDP.
BAA78575.1	AB028132	Oryza sativa	Dof zinc finger protein.
AAB70119.1	U82230	Zea mays	transcription factor. prolamin box binding factor. PBF. endosperm-specific DOF protein; DNA binding.
CAA08755.1	AJ009594	Nicotiana tabacum	Dof zinc finger protein. BBF1.
CAA66601.1	X97942	Nicotiana tabacum	Zn finger protein. NtBBF1.1.

CAA66606.1 X97947 *Nicotiana tabacum*
Zn finger protein. NtBBF3.

BAA78573.1 AB028130 *Oryza sativa*
Dof zinc finger protein.

BAA78572.1 AB028129 *Oryza sativa*
Dof zinc finger protein.

CAA56287.1 X79934 *Zea mays*
Dof2. No start codon.

CAA66604.1 X97945 *Nicotiana tabacum*
Zn finger protein. NtBBF2a.

CAA66605.1 X97946 *Nicotiana tabacum*
Zn finger protein. NtBBF2b.

BAA78574.1 AB028131 *Oryza sativa*
Dof zinc finger protein. Rice cDNA for protein that binds to AT-rich sequence of rice carboxypeptidase-3 promoter.

BAA78576.1 AB028133 *Oryza sativa*
Dof zinc finger protein.

SEQ ID NO: 68

CAA83453.1 Z31581 *Pisum sativum*
chloroplast outer envelope protein 86.

AAA53276.1 L36857 *Pisum sativum*
component of chloroplast outer membrane protein import apparatus. GTP-binding protein. IAP86.

AAF75761.1 AF262939 *Pisum sativum*
chloroplast protein import component Toc159. major receptor of the chloroplast outer envelope membrane protein import apparatus.

AAG48839.1 AC084218 *Oryza sativa*
similar to *Arabidopsis thaliana* putative chloroplast outer envelope 86-like protein (AC002330).

AAC25785.1 L36856 *Pisum sativum*
component of chloroplast outer membrane protein import apparatus. GTP-binding protein. IAP34.

CAB77551.1 AJ271049 *Zea mays*
a component of the protein translocon at the outer envelope of chloroplast. Toc34-2 protein. toc34B.

CAB65537.1 AJ245968 *Zea mays*
a component of the protein translocon at the outer envelope of chloroplast. Toc34-1 protein. toc34A.

SEQ ID NO: 70

AAB71887.1 AF020791 *Hordeum vulgare*
inserts Fe²⁺ into protoporphyrin IX. ferrochelatase. hemH. protoheme IX ferro-lyase.

BAA05101.1 D26105 *Hordeum vulgare*
ferrochelatase. hemH.

BAA05102.1	D26106	Cucumis sativus	ferrochelatase. hemH.
BAB20760.1	AB037113	Cucumis sativus	ferrochelatase. hemH.
BAA22284.1	AB007120	Oryza sativa	ferrochelatase. hemH.
CAA06705.1	AJ005802	Solanum tuberosum	tetrapyrrole biosynthesis. ferrochelatase.
AAK16728.1	AF332962	Chlamydomonas reinhardtii	ferrochelatase.
AAK16729.1	AF332963	Polytomella sp. 'Pringsheim 198.80'	ferrochelatase.
AAC84139.1	AF101426	Cichorium intybus	ferrochelatase.
SEQ ID NO: 71			
CAA64442.1	X94986	Manihot esculenta	beta glucosidase. bglA.
AAB22162.1	S35175	Manihot esculenta	linamarase. linamarase. beta-glucosidase; Method: conceptual translation with partial peptide sequencing; This sequence comes from Fig. 4.
AAA93032.1	U50201	Prunus serotina	hydrolysis of the cyanogenic glucoside (R)-prunasin. prunasin hydrolase precursor. located in protein bodies of Prunus seeds; encodes 8 putative N-glycosylation sites (N-X-S/T); encodes NEP and ITENG motifs characteristic of the BGA family of beta-glucosidases.
AAA91166.1	U39228	Prunus avium	beta-glucosidase.
AAF34650.1	AF221526	Prunus serotina	hydrolysis of the cyanogenic glucoside (R)-prunasin. prunasin hydrolase isoform PHA precursor. beta-glucosidase; contains 6 potential N-glycosylation sites (N-X-S/T); glycosyl hydrolase family 1 member.
AAF03675.1	AF149311	Rauvolfia serpentina	hydrolyses the glucoalkaloid raucaffricine. raucaffricine-O-beta-D-glucosidase. beta glucosidase; RG; part of the Ajmaline biosynthesis pathway; belongs to family 1 of the glucosyl hydrolases.
CAA57913.1	X82577	Brassica napus	beta-glucosidase. bgl.
BAA78708.1	AB003089	Polygonum tinctorium	beta-glucosidase.
BAA11831.1	D83177	Costus speciosus	saponin metabolite. furostanol glycoside 26-O-beta-glucosidase (F26G). functional expression in E. coli; one of the F26G isozymes.
AAG25897.1	AF170087	Cucurbita pepo	silverleaf whitefly-induced protein 3. SLW3. similar to beta-glucosidase.

AAF04007.1	AF163097	<i>Dalbergia cochinchinensis</i>	beta-fucosidase beta-glucosidase. dalcochinin 8'-O-beta-glucoside beta-glucosidase precursor. BGLU1. rotenoid beta-glucosidase.
AAC69619.1	AF072736	<i>Pinus contorta</i>	beta-glucosidase.
AAB38784.1	U72154	<i>Brassica nigra</i>	beta-glucosidase. psr3.1. PSR3.1; phosphate-starvation responsive enzyme.
AAD02839.1	AF082991	<i>Avena sativa</i>	beta-D-glucosidase beta subunit precursor. P60b. avenacosidase.
AAA87339.1	L41869	<i>Hordeum vulgare</i>	beta-glucosidase. BGQ60. expression specific to starchy endosperm of seed.
AAB71381.1	U95298	<i>Manihot esculenta</i>	linamarase. pLIN-GEN. beta-glucosidase.
CAA55196.1	X78433	<i>Avena sativa</i>	beta-D-glucosidase.
AAC49177.1	U33817	<i>Sorghum bicolor</i>	beta-glucosidase, catalyzes the hydrolysis of the cyanogenic beta-glucoside dhurrin. dhurrinase.
AAD09850.1	U44087	<i>Zea mays</i>	beta-D-glucosidase precursor. glu2. product subunit structure: autodimer of 58.4 kDa monomers Allele: glu2-B73.
AAG00614.1	AF293849	<i>Secale cereale</i>	beta-glucosidase.
AAF28800.1	AF112888	<i>Catharanthus roseus</i>	plays a role in secondary metabolism by hydrolyzing strictosidine to cathenamine during indole alkaloid biosynthesis. strictosidine beta-glucosidase. localized in the endoplasmic reticulum.
CAA40058.1	X56734	<i>Trifolium repens</i>	beta-glucosidase. non-cyanogenic.
CAA40057.1	X56733	<i>Trifolium repens</i>	beta-glucosidase. Li.
AAD10503.1	U33816	<i>Zea mays</i>	functions in defense of young plant parts against pests via the production of hydroxamic acids from hydroxamic acid glucosides. beta-D-glucosidase.
AAA65946.1	U25157	<i>Zea mays</i>	functions in defense of young plant parts against pests via the production of hydroxamic acids from hydroxamic acid glucosides. beta-D-glucosidase.
CAA52293.1	X74217	<i>Zea mays</i>	beta-glucosidase. p60.1.
AAB03266.1	U44773	<i>Zea mays</i>	beta-D-glucosidase. glu1. autodimer of 58.4 kD monomers.
AAK07429.1	AF321287	<i>Musa acuminata</i>	beta-glucosidase.

CAA79989.2	Z21977	Brassica napus	beta thioglucosidase. myrosinase, thioglucoside glucohydrolase. Myr1.Bn1.
AAF34651.1	AF221527	Prunus serotina	putative prunasin hydrolase precursor. beta-glucosidase; glycosyl hydrolase family 1 member.
AAA84906.1	U28047	Oryza sativa	catalyzes the release of either giberellin or cyanogenic substances from their glucoconjugates. beta glucosidase. beta-D-glucoside glucohydrolase; dimer of 60 kDa monomers; localized in the plastid.
CAC08209.1	AJ005950	Cicer arietinum	beta-glucosidase.
SEQ ID NO: 72			
CAA56570.1	X80301	Nicotiana tabacum	axi 1.
AAB72114.1	U81288	Pisum sativum	PsRT17-1. similar to the Nicotiana tabacum axi 1 gene product encoded by the sequence presented in GenBank Accession Number X80301.
SEQ ID NO: 74			
AAG23130.1	AF198260	Lycopersicon esculentum	diacylglycerol kinase variant A. Dgk1. DGK-1; alternatively spliced.
AAG23129.1	AF198259	Lycopersicon esculentum	phosphorylates diacylglycerol to yield phosphatidic acid. diacylglycerol kinase. DGK1. LeDGK1; lipid kinase; non-calmodulin-binding isoform; alternatively spliced product.
AAG23131.1	AF198260	Lycopersicon esculentum	diacylglycerol kinase variant B. Dgk1. CBDGK; calmodulin-binding; alternatively spliced.
AAG23128.1	AF198258	Lycopersicon esculentum	phosphorylates diacylglycerol to yield phosphatidic acid. calmodulin-binding diacylglycerol kinase. DGK1. LeCBDGK; lipid kinase; alternatively spliced product.
SEQ ID NO: 75			
CAC09580.1	AJ298992	Fagus sylvatica	Abscisic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.
AAA34002.1	M67449	Glycine max	protein kinase. PK6.
AAG31141.1	AF305911	Oryza sativa	EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAG31142.1	AF305912	Hordeum vulgare	EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
CAA73722.1	Y13273	Lycopersicon esculentum	putative protein kinase.
AAD46406.1	AF096250	Lycopersicon esculentum	ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.

AAD10056.1	AF110518	Lycopersicon esculentum	ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.
AAD10057.1	AF110519	Lycopersicon esculentum	ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.
CAA06334.1	AJ005077	Lycopersicon esculentum	protein kinase. TCTR2 protein. TCTR2.
AAK30005.1	AY029067	Rosa hybrid cultivar	CTR2 protein kinase.
AAK11734.1	AY027437	Arachis hypogaea	serine/threonine/tyrosine kinase.
CAA73067.1	Y12464	Sorghum bicolor	serine/threonine kinase. SNFL1.
CAA73068.1	Y12465	Sorghum bicolor	serine/threonine kinase. SNFL2.
AAK31267.1	AC079890	Oryza sativa	putative protein kinase. OSJNBb0089A17.2.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
BAB39451.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.24.
BAB17126.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.16.
BAB17321.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.1.
AAF68398.1	AF237568	Oryza sativa	receptor-like protein kinase. RLG2.
BAB17129.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.20.
BAB17348.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.32.
CAA57898.1	X82548	Hordeum vulgare	SNF1-related protein kinase. BKIN2.
BAB17345.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.29.
BAB17116.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.3.
BAB39441.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.11.
CAC20842.1	AJ250467	Pinus sylvestris	receptor protein kinase. upk.

AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrkl.
BAB16918.1	AP002863	Oryza sativa	putative protein kinase. P0005A05.22.
AAF91322.1	AF244888	Glycine max	receptor-like protein kinase 1. RLK1. GmRLK1.
BAB17342.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.26.
AAF78044.1	AF248493	Oryza sativa	receptor-like kinase. RLG18. protein kinase.
AAF91324.1	AF244890	Glycine max	receptor-like protein kinase 3. RLK3. GmRLK3.
AAF59905.1	AF197946	Glycine max	receptor protein kinase-like protein. CLV1A.
AAF91323.1	AF244889	Glycine max	receptor-like protein kinase 2. RLK2. GmRLK2.
AAD46917.1	AF164021	Oryza sativa	receptor kinase.
AAF59906.1	AF197947	Glycine max	receptor protein kinase-like protein. CLV1B.
AAF78018.1	AF238474	Oryza sativa	receptor-like kinase. RLG16. protein kinase.
BAB39438.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.7.
BAA05649.1	D26602	Nicotiana tabacum	protein kinase.
AAC01746.1	AF044489	Oryza sativa	receptor-like protein kinase. drpk1.
CAA71142.1	Y10036	Cucumis sativus	SNF1-related protein kinase.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
CAA61510.1	X89226	Oryza sativa	leucine-rich repeat/receptor protein kinase. lrk2.
SEQ ID NO: 77			
AAD03693.1	AF084554	Brassica napus	fibrillin.
CAA10372.1	AJ131455	Plastid Solanum demissum	carotenoid-associated. fibrillin. c40.4.
CAA50750.1	X71952	Capsicum annuum	fibrillin.
SEQ ID NO: 79			

AAB53155.1	U43629	Beta vulgaris	putative sugar transporter. integral membrane protein. member of major facilitator superfamily.
AAF74566.1	AF215852	Nicotiana tabacum	transport of hexoses across the plastid inner envelope membrane. hexose transporter. pGlcT.
AAG00995.1	AF286906	Mesembryanthemum crystallinum	putative glucose translocator. metabolite transporter; targeted to plastid inner envelope membrane.
AAF74565.1	AF215851	Spinacia oleracea	transport of hexoses across the plastid inner envelope membrane. hexose transporter. pGlcT.
AAF74567.1	AF215853	Solanum tuberosum	transport of hexoses across the plastid inner envelope membrane. hexose transporter. pGlcT.
AAF74568.1	AF215854	Zea mays	transport of hexoses across the plastid inner envelope membrane. hexose transporter. pGlcT.
AAG46179.1	AC018727	Oryza sativa	putative sugar transporter protein. OSJNBa0056G17.3.
AAB88879.1	AF000952	Prunus armeniaca	putative sugar transporter.
AAG43998.1	AF215837	Apium graveolens var. dulce	mannitol transporter. Mat1.
CAA68813.1	Y07520	Chlorella kessleri	H(+)/hexose cotransporter (AA 1-533).
CAA53192.1	X75440	Chlorella kessleri	hexose transporter like protein. HUP3.
CAB52689.1	AJ132224	Lycopersicon esculentum	hexose transporter. ht2.
CAA39036.1	X55349	Chlorella kessleri	H(+)/hexose-cotransporter. HUP1.
CAA47324.1	X66856	Nicotiana tabacum	monosaccharid transporter. MST1.
AAB68028.1	U64902	Beta vulgaris	BvcDNA-205. putative sugar transporter; member of major facilitative superfamily; integral membrane protein.
AAB68029.1	U64903	Beta vulgaris	BvcDNA-397. putative sugar transporter; member of major facilitative superfamily; integral membrane protein.
CAA09419.1	AJ010942	Lycopersicon esculentum	hexose transporter protein.
CAB07812.1	Z93775	Vicia faba	sugar transport. monosaccharid transport protein. hexT.
BAB19864.1	AB052885	Oryza sativa	monosaccharide transporter 3. OsMST3.

AAA79761.1	L08196	<i>Ricinus communis</i> hexose transport. sugar carrier protein. RCSTC.
AAK13147.1	AC083945	<i>Oryza sativa</i> Putative sugar transporter. OSJNBa0058E19.22.
AAB06594.1	U38651	<i>Medicago truncatula</i> sugar transporter.
CAA04511.1	AJ001061	<i>Vitis vinifera</i> hexose uptake. hexose transporter.
AAC61852.1	AF061106	<i>Petunia x hybrida</i> putative monosaccharide transporter 1. pmt1. similar to hexose transporter protein; PMT1.
CAA70777.1	Y09590	<i>Vitis vinifera</i> hexose transporter.
AAA79769.1	L08197	<i>Ricinus communis</i> sugar transport. sugar carrier protein. RCSTA. putative.
CAB06079.1	Z83829	<i>Picea abies</i> monosaccharide transporter. PaMst-1. PaMst-1.
AAA18534.1	L21753	<i>Saccharum hybrid cultivar H65-7052</i> glucose transporter. putative.
CAC00697.1	AJ278765	<i>Lycopersicon esculentum</i> putative sugar transporter. st3.
AAA79857.1	L08188	<i>Ricinus communis</i> hexose transport. hexose carrier protein. HEX6.
BAB19863.1	AB052884	<i>Oryza sativa</i> monosaccharide transporter 2. OsMST2.
BAB19862.1	AB052883	<i>Oryza sativa</i> monosaccharide transporter 1. OsMST1.
AAF91432.1	AF280432	<i>Mesembryanthemum crystallinum</i> putative Na ⁺ /myo-inositol symporter. Itr2. membrane transport protein.
CAB52688.1	AJ132223	<i>Lycopersicon esculentum</i> hexose transporter. ht1.
BAA85398.1	AP000615	<i>Oryza sativa</i> similar to sugar transporter protein. (AL022604).
AAG46115.1	AC073166	<i>Oryza sativa</i> putative sugar transporter. OSJNBb0064P21.3.
CAB52690.1	AJ132225	<i>Lycopersicon esculentum</i> hexose transporter. ht3.
AAA18533.1	L21752	<i>Saccharum hybrid cultivar H65-7052</i> glucose transporter. putative.
AAD55054.1	AF173655	<i>Beta vulgaris</i> glucose transporter. Gt.
BAB39246.1	AP002869	<i>Oryza sativa</i> putative transport protein homolog. P0554D10.30.

AAA79764.1 L08191 *Ricinus communis*
sugar transport. sugar carrier protein. RCSTC. Nucleotides 1 to 23 and 226 to 246 are
originated from degenerated primers; putative.

AAA79762.1 L08189 *Ricinus communis*
sugar transport. sugar carrier protein. RCSTA. Nucleotides 1 to 23 and 226 to 246 are
originated from degenerated primers; putative.

AAA79767.1 L08194 *Ricinus communis*
sugar transport. sugar carrier protein. RCSTG. Nucleotides 1 to 23 and 226 to 246 are
originated from degenerated primers; putative.

AAA79766.1 L08193 *Ricinus communis*
sugar transport. sugar carrier protein. RCSTF. Nucleotides 1 to 23 and 226 to 246 are
originated from degenerated primers; putative.

SEQ ID NO: 82

CAA78386.1 Z13996 *Petunia x hybrida*
DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal
myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has
been obtained by PCR amplification of cDNA.

CAB43399.1 AJ006292 *Antirrhinum majus*
Myb-related transcription factor mixta-like 1. mybml1.

CAA67600.1 X99210 *Lycopersicon esculentum*
myb-related transcription factor. THM16.

BAA93038.1 AP001552 *Oryza sativa*
EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to
Arabidopsis thaliana putative transcription factor (AF062916).

BAA23337.1 D88617 *Oryza sativa*
transfactor. OSMYB1. Osmyb1.

CAA64614.1 X95296 *Lycopersicon esculentum*
transcription factor. THM27. myb-related.

CAA72186.1 Y11351 *Oryza sativa*
myb factor. myb.

AAF22256.1 AF161711 *Pimpinella brachycarpa*
myb-related transcription factor.

AAC04720.1 AF034134 *Gossypium hirsutum*
putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-O.
similar to MYB A encoded by GenBank Accession Number L04497.

AAA82943.1 U39448 *Picea mariana*
MYB-like transcriptional factor MBF1. putative DNA binding region highly similar to the
maize C1.

BAB39987.1 AP003020 *Oryza sativa*
putative transcription factor (myb). P0498A12.16. contains ESTs
AU097474(S5087),D40175(S1959).

BAB39972.1 AP003018 *Oryza sativa*
putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs
AU097474(S5087),D40175(S1959).

BAA23338.1	D88618	Oryza sativa	transfactor. OSMYB2. Osmyb2.
CAA67575.1	X99134	Lycopersicon esculentum	transcription factor. THM6. myb-related.
CAA78387.1	Z13997	Petunia x hybrida	DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
AAA19821.1	L19495	Zea mays	transcriptional activator for anthocyanin synthesis. transcriptional activator.
AAC49394.1	U57002	Zea mays	P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the C-terminal.
AAA33500.1	M73028	Zea mays	myb-like transcription factor. P.
AAG36774.1	AF210616	Zea mays	P2 protein. P2. myb-like transcriptional factor; similar to Zea mays P gene.
BAA88222.1	AB028650	Nicotiana tabacum	myb-related transcription factor LBM2. lbm2.
CAA72185.1	Y11350	Oryza sativa	myb factor. myb.
AAG13574.1	AC037425	Oryza sativa	myb factor. OSJNBa0055P24.4.
AAB41101.1	U72762	Nicotiana tabacum	transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.
BAA88223.1	AB028651	Nicotiana tabacum	myb-related transcription factor LBM3. lbm3.
AAA19819.1	L19496	Zea mays	transcriptional activator for anthocyanin synthesis. transcriptional activator.
BAA88224.1	AB028652	Nicotiana tabacum	myb-related transcription factor LBM4. lbm4.
AAB67720.1	AF015268	Zea mays	activator of anthocyanin structural genes. PL transcription factor. PL.
AAA33492.1	L13454	Zea mays	transcriptional activator for anthocyanin biosynthesis. PI-Bh (Blotched1).
SEQ ID NO: 83			
CAA78387.1	Z13997	Petunia x hybrida	DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
BAA81736.1	AB029165	Glycine max	GmMYB29B2.
BAA81732.1	AB029161	Glycine max	GmMYB29A2.

BAA81731.1	AB029160	Glycine max GmMYB29A1.
BAA81730.1	AB029159	Glycine max GmMYB29A1.
BAA88221.1	AB028649	Nicotiana tabacum myb-related transcription factor LBM1. lbm1.
BAA88224.1	AB028652	Nicotiana tabacum myb-related transcription factor LBM4. lbm4.
CAA66952.1	X98308	Lycopersicon esculentum THM18. myb-related transcription factor.
BAA81733.2	AB029162	Glycine max GmMYB29A2.
CAA72217.1	Y11414	Oryza sativa myb.
BAA88222.1	AB028650	Nicotiana tabacum myb-related transcription factor LBM2. lbm2.
AAB41101.1	U72762	Nicotiana tabacum transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.
BAA88223.1	AB028651	Nicotiana tabacum myb-related transcription factor LBM3. lbm3.
CAA72185.1	Y11350	Oryza sativa myb factor. myb.
AAG13574.1	AC037425	Oryza sativa myb factor. OSJNBa0055P24.4.
AAK19616.1	AF336283	Gossypium hirsutum GHMYB25. ghmyb25. similar to myb; contains an unspliced intron.
CAA78386.1	Z13996	Petunia x hybrida DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
CAA72218.1	Y11415	Oryza sativa myb.
AAA33067.1	L04497	Gossypium hirsutum MYB A; putative.
CAA68235.1	X99973	Hordeum vulgare myb4 transcription factor. myb4.
AAC49394.1	U57002	Zea mays P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the C-terminal.
AAA33500.1	M73028	Zea mays myb-like transcription factor. P.

CAA67600.1	X99210	Lycopersicon esculentum	myb-related transcription factor. THM16.
AAG36774.1	AF210616	Zea mays	P2 protein. P2. myb-like transcriptional factor; similar to Zea mays P gene.
AAF22256.1	AF161711	Pimpinella brachycarpa	myb-related transcription factor.
CAA72187.1	Y11352	Oryza sativa	myb factor. myb.
AAC04718.1	AF034132	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-J. similar to MYB A encoded by GenBank Accession Number L04497.
CAB43399.1	AJ006292	Antirrhinum majus	Myb-related transcription factor mixta-like 1. mybm11.
AAK19615.1	AF336282	Gossypium hirsutum	GHMYB10. ghmyb10. similar to myb.
AAK19618.1	AF336285	Gossypium hirsutum	GHMYB38. ghmyb38. similar to myb.
CAA72186.1	Y11351	Oryza sativa	myb factor. myb.
CAA64614.1	X95296	Lycopersicon esculentum	transcription factor. THM27. myb-related.
CAA50221.1	X70876	Hordeum vulgare	MybHv5. myb2.
BAA23338.1	D88618	Oryza sativa	transfactor. OSMYB2. OsmYb2.
AAK19619.1	AF336286	Gossypium hirsutum	GHMYB9. ghmyb9. similar to myb.
AAA82943.1	U39448	Picea mariana	MYB-like transcriptional factor MBF1. putative DNA binding region highly similar to the maize C1.
AAC04720.1	AF034134	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-O. similar to MYB A encoded by GenBank Accession Number L04497.
AAK19611.1	AF336278	Gossypium hirsutum	BNLGH1233. bnlghi6233. similar to myb.
BAA23337.1	D88617	Oryza sativa	transfactor. OSMYB1. OsmYb1.
BAB39987.1	AP003020	Oryza sativa	putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).
BAB39972.1	AP003018	Oryza sativa	putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).

CAA65525.1 X96749 *Oryza sativa*
myb7.

AAK19617.1 AF336284 *Gossypium hirsutum*
GHMYB36. ghmyb36. similar to myb.

CAA67575.1 X99134 *Lycopersicon esculentum*
transcription factor. THM6. myb-related.

CAA50224.1 X70879 *Hordeum vulgare*
MybHv1. myb1.

SEQ ID NO: 84

BAA88222.1 AB028650 *Nicotiana tabacum*
myb-related transcription factor LBM2. lbm2.

BAA88221.1 AB028649 *Nicotiana tabacum*
myb-related transcription factor LBM1. lbm1.

BAA88224.1 AB028652 *Nicotiana tabacum*
myb-related transcription factor LBM4. lbm4.

CAA78387.1 Z13997 *Petunia x hybrida*
DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb
proto-oncoproteins.

CAA66952.1 X98308 *Lycopersicon esculentum*
THM18. myb-related transcription factor.

AAB41101.1 U72762 *Nicotiana tabacum*
transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix
motif; contains redox-sensitive cysteine.

BAA88223.1 AB028651 *Nicotiana tabacum*
myb-related transcription factor LBM3. lbm3.

BAA81733.2 AB029162 *Glycine max*
GmMYB29A2.

BAA81731.1 AB029160 *Glycine max*
GmMYB29A1.

BAA81730.1 AB029159 *Glycine max*
GmMYB29A1.

BAA81736.1 AB029165 *Glycine max*
GmMYB29B2.

CAA72217.1 Y11414 *Oryza sativa*
myb.

BAA81732.1 AB029161 *Glycine max*
GmMYB29A2.

CAA72185.1 Y11350 *Oryza sativa*
myb factor. myb.

AAG13574.1 AC037425 *Oryza sativa*
myb factor. OSJNBa0055P24.4.

CAA72218.1 Y11415 *Oryza sativa*
myb.

CAA78386.1	Z13996	Petunia x hybrida	DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
AAC49394.1	U57002	Zea mays	P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the C-terminal.
CAB43399.1	AJ006292	Antirrhinum majus	Myb-related transcription factor mixta-like 1. mybml1.
AAK19616.1	AF336283	Gossypium hirsutum	GHMYB25. ghmyb25. similar to myb; contains an unspliced intron.
AAG36774.1	AF210616	Zea mays	P2 protein. P2. myb-like transcriptional factor; similar to Zea mays P gene.
AAA33500.1	M73028	Zea mays	myb-like transcription factor. P.
CAA68235.1	X99973	Hordeum vulgare	myb4 transcription factor. myb4.
CAA72187.1	Y11352	Oryza sativa	myb factor. myb.
AAA33067.1	L04497	Gossypium hirsutum	MYB A; putative.
CAA72186.1	Y11351	Oryza sativa	myb factor. myb.
CAA67600.1	X99210	Lycopersicon esculentum	myb-related transcription factor. THM16.
AAK19618.1	AF336285	Gossypium hirsutum	GHMYB38. ghmyb38. similar to myb.
AAK19611.1	AF336278	Gossypium hirsutum	BNLGHi233. bnlghi6233. similar to myb.
AAC04718.1	AF034132	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-J. similar to MYB A encoded by GenBank Accession Number L04497.
AAK19619.1	AF336286	Gossypium hirsutum	GHMYB9. ghmyb9. similar to myb.
AAK19615.1	AF336282	Gossypium hirsutum	GHMYB10. ghmyb10. similar to myb.
CAA64614.1	X95296	Lycopersicon esculentum	transcription factor. THM27. myb-related.
BAA23338.1	D88618	Oryza sativa	transfactor. OSMYB2. Osmyb2.
BAA23337.1	D88617	Oryza sativa	transfactor. OSMYB1. Osmyb1.

CAA67575.1	X99134	Lycopersicon esculentum	transcription factor. THM6. myb-related.
CAA65525.1	X96749	Oryza sativa	myb7.
BAB39987.1	AP003020	Oryza sativa	putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).
BAB39972.1	AP003018	Oryza sativa	putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).
CAA50221.1	X70876	Hordeum vulgare	MybHv5. myb2.
AAA82943.1	U39448	Picea mariana	MYB-like transcriptional factor MBF1. putative DNA binding region highly similar to the maize C1.
AAF22256.1	AF161711	Pimpinella brachycarpa	myb-related transcription factor.
AAK19617.1	AF336284	Gossypium hirsutum	GHMYB36. ghmyb36. similar to myb.
CAA50222.1	X70877	Hordeum vulgare	MybHv1. myb1.
CAA50224.1	X70879	Hordeum vulgare	MybHv1. myb1.
SEQ ID NO: 85			
AAD11575.1	AF064029	Helianthus tuberosus	lectin 1. LECHeltubal; agglutinin.
AAD11578.1	AF064030	Helianthus tuberosus	lectin 2. LECHeltuba2; agglutinin.
AAD11577.1	AF064032	Helianthus tuberosus	lectin HE17.
AAG10403.1	AF233284	Convolvulus arvensis	mannose-binding lectin. cr8. Conarva.
AAD11576.1	AF064031	Helianthus tuberosus	lectin 3.
AAB82776.2	AF001527	Musa acuminata	ripening-associated protein. similar to lectin.
AAC49564.1	U56820	Calystegia sepium	lectin.
CAB40792.1	AJ237754	Hordeum vulgare	putative lectin. hl#2.
SEQ ID NO: 88			
AAB65163.1	AF002692	Solanum commersonii	glutathione S-transferase, class-phi. GST1. low temperature induced.

CAA55039.1	X78203	Hyoscyamus muticus	glutathione transferase.
AAA33930.1	M84968	Silene vulgaris	glutathione-S-transferase.
AAA33931.1	M84969	Silene vulgaris	glutathione-S-transferase.
AAF65767.1	AF242309	Euphorbia esula	glutathione S-transferase. putative auxin-binding GST.
BAA01394.1	D10524	Nicotiana tabacum	glutathione S-transferase. parB.
CAA96431.1	Z71749	Nicotiana plumbaginifolia	glutathione S-transferase.
AAF61392.1	AF133894	Persea americana	glutathione S-transferase. GTH.
CAB38119.1	AJ010296	Zea mays	Glutathione transferase III(b). gst3b.
CAB38118.1	AJ010295	Zea mays	Glutathione transferase III(a). gst3a.
BAB39935.1	AP002914	Oryza sativa	putative glutathione S-transferase. P0493G01.17.
CAA09190.1	AJ010451	Alopecurus myosuroides	glutathione transferase. GST2a.
CAA09192.1	AJ010453	Alopecurus myosuroides	glutathione transferase. GST2c.
CAA09193.1	AJ010454	Alopecurus myosuroides	glutathione transferase. GST2d.
CAA09191.1	AJ010452	Alopecurus myosuroides	glutathione transferase. GST2b.
BAB39941.1	AP002914	Oryza sativa	putative glutathione S-transferase. P0493G01.23.
AAG34811.1	AF243376	Glycine max	glutathione S-transferase GST 21.
BAB39939.1	AP002914	Oryza sativa	putative glutathione S-transferase. P0493G01.21.
AAG32476.1	AF309383	Oryza sativa subsp. japonica	putative glutathione S-transferase OsGSTF4.
AAG34814.1	AF243379	Glycine max	glutathione S-transferase GST 24.
AAG34812.1	AF243377	Glycine max	glutathione S-transferase GST 22.
BAB39929.1	AP002914	Oryza sativa	putative glutathione transferase. P0493G01.7.

CAA39487.1	X56012	Triticum aestivum	glutathione transferase. gstA1.
AAD56395.1	AF184059	Triticum aestivum	glutathione S-transferase. GST1.
BAB39927.1	AP002914	Oryza sativa	putative glutathione S-transferase. P0493G01.1. contains ESTs AU031696(R0596), C97559(C60386), C28218(C60386), D28287(R0596).
AAA20585.1	U12679	Zea mays	glutathione S-transferase IV. GSTIV.
CAA56047.1	X79515	Zea mays	glutathione transferase. GST27.
CAA39480.1	X56004	Triticum aestivum	glutathione transferase. gstA2.
AAA33469.1	M16902	Zea mays	glutathione S-transferase I.
AAG32475.1	AF309382	Oryza sativa subsp. japonica	putative glutathione S-transferase OsGSTF5.
AAA33470.1	M16901	Zea mays	glutathione S-transferase I.
AAG32477.1	AF309384	Oryza sativa subsp. japonica	putative glutathione S-transferase OsGSTF3.
CAA68993.1	Y07721	Petunia x hybrida	conjugates glutathione to anthocyanin to facilitate transport to the vacuole. glutathione S-transferase. an9 locus.
BAB39940.1	AP002914	Oryza sativa	putative glutathione S-transferase. P0493G01.22.
AAC64007.1	AF062403	Oryza sativa	glutathione S-transferase II.
AAG34823.1	AF244680	Zea mays	glutathione S-transferase GST 15.
AAG34817.1	AF244674	Zea mays	glutathione S-transferase GST 9.
CAB66333.1	AJ279691	Betula pendula	glutathione-S-transferase. gst.
AAG34820.1	AF244677	Zea mays	glutathione S-transferase GST 11.
AAG34821.1	AF244678	Zea mays	glutathione S-transferase GST 13.
CAA05354.1	AJ002380	Oryza sativa	glutathione S-transferase. Rgst I.
AAG34816.1	AF244673	Zea mays	glutathione S-transferase GST 8.

AAG34818.1	AF244675	Zea mays	glutathione S-transferase GST 10.
CAA05355.1	AJ002381	Oryza sativa	glutathione S-transferase. Rgst II.
AAG34824.1	AF244681	Zea mays	glutathione S-transferase GST 16.
SEQ ID NO: 91			
AAG34695.1	AF313492	Matthiola incana	putative cytochrome P450.
CAA71516.1	Y10492	Glycine max	putative cytochrome P450.
BAA12159.1	D83968.	Glycine max	Cytochrome P-450 (CYP93A1).
AAC32274.1	AF081575	Petunia x hybrida	flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.
AAA32913.1	M32885	Persea americana	cytochrome P-450LXXIA1 (cyp71A1).
BAA13076.1	D86351	Glycine max	cytochrome P-450 (CYP93A2).
CAA64635.1	X95342	Nicotiana tabacum	cytochrome P450. hsr515. hypersensitivity-related gene.
CAA65580.1	X96784	Nicotiana tabacum	cytochrome P450. hsr515.
AAD56282.1	AF155332	Petunia x hybrida	flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
BAB12433.1	AB025030	Coptis japonica	p450.
AAG44132.1	AF218296	Pisum sativum	cytochrome P450. P450 isolog.
CAA50155.1	X70824	Solanum melongena	flavonoid hydroxylase (P450). CYP75.
AAB17562.1	U72654	Eustoma grandiflorum	flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
AAF05621.1	AF191772	Papaver somniferum	hydroxylase involved in benzylisoquinoline alkaloid biosynthesis. (S)-N-methylcoclaurine 3'-hydroxylase. CYP80B1. cytochrome P450-dependent monooxygenase.
CAB56503.1	AJ238612	Catharanthus roseus	cytochrome P450.
CAA70575.1	Y09423	Nepeta racemosa	cytochrome P450. CYP71A5.
BAA74466.1	AB022733	Glycyrrhiza echinata	cytochrome P450. CYP Ge-51.

CAA50648.1	X71657	<i>Solanum melongena</i> P450 hydroxylase.
BAA22423.1	AB001380	<i>Glycyrrhiza echinata</i> cytochrome P450. CYP93B1.
BAB40324.1	AB037245	<i>Asparagus officinalis</i> cytochrome P450. ASPI-2.
AAB94588.1	AF022459	<i>Glycine max</i> CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
AAG14961.1	AF214007	<i>Brassica napus</i> cytochrome p450-dependent monooxygenase. BNF5H1.
BAB40323.1	AB037244	<i>Asparagus officinalis</i> cytochrome P450. ASPI-1.
AAB61965.1	U48435	<i>Solanum chacoense</i> putative cytochrome P450.
AAC39452.1	AF014800	<i>Eschscholzia californica</i> hydroxylase involved in the biosynthesis of tetrahydrobenzylisoquinoline alkaloids in plants. (S)-N-methylcoclaurine 3'-hydroxylase. CYP80B1. cytochrome P-450-dependent monooxygenase; CYP80B1v1.
AAG14962.1	AF214008	<i>Brassica napus</i> cytochrome p450-dependent monooxygenase. BNF5H2.
BAA84072.1	AB028152	<i>Torenia hybrida</i> flavone synthase II. cytochrome P450. TFNS5.
AAC39453.1	AF014801	<i>Eschscholzia californica</i> hydroxylase involved in the biosynthesis of tetrahydrobenzylisoquinoline alkaloids in plants. (S)-N-methylcoclaurine 3'-hydroxylase. CYP80B1. cytochrome P-450-dependent monooxygenase; CYP80B1v2.
AAD47832.1	AF166332	<i>Nicotiana tabacum</i> cytochrome P450.
SEQ ID NO: 92		
AAG42490.1	AF321001	<i>Suaeda maritima</i> subsp. <i>salsa</i> S-adenosylmethionine synthetase 2.
AAG17666.1	AF271220	<i>Brassica juncea</i> S-adenosylmethionine synthetase. MSAMS2.
BAA96637.1	AP002482	<i>Oryza sativa</i> Similar to <i>Oryza sativa</i> S-adenosylmethionine synthetase 1 (P46611).
AAG17036.1	AF187821	<i>Pinus contorta</i> catalyzes the reaction between methionine and ATP to S-adenosylmethionine. S- adenosylmethionine synthetase. sams2.
BAA94605.1	AB041534	<i>Camellia sinensis</i> s-adenosylmethionine synthetase. SAM.
AAA81377.1	U17239	<i>Actinidia chinensis</i> S-adenosylmethionine synthetase.

AAB38500.1	U79767	Mesembryanthemum crystallinum	S-adenosylmethionine synthetase. methionine adenosyltransferase.
AAA81378.1	U17240	Actinidia chinensis	S-adenosylmethionine synthetase.
BAA09895.1	D63835	Hordeum vulgare	S-adenosylmethionine synthetase.
AAA33274.1	M61882	Dianthus caryophyllus	S-adenosylmethionine synthetase. CARSAM2.
AAA58773.1	L36681	Pisum sativum	S-adenosylmethionine synthase. precursor for ethylene and polyamine biosynthesis.
AAA58772.1	L36680	Pisum sativum	precursor for ethylene and polyamine biosynthesis. S-adenosylmethionine synthase.
AAA81379.1	U17241	Actinidia chinensis	S-adenosylmethionine synthetase.
AAA33857.1	M62758	Petroselinum crispum	S-adenosylmethionine synthetase. SMS-1.
AAG17035.1	AF187820	Pinus contorta	catalyzes the reaction between methionine and ATP to S-adenosylmethionine. S-adenosylmethionine synthetase. sams1.
AAB71833.1	AF008568	Chlamydomonas reinhardtii	S-adenosylmethionine synthetase. CHRSAMS.
AAA33858.1	M62757	Petroselinum crispum	S-adenosylmethionine synthetase. SMS-2.
BAA21726.1	AB006187	Nicotiana tabacum	S-adenosylmethionine synthase. BYJ90.
AAF78525.1	AF195233	Pyrus pyrifolia	S-adenosylmethionine synthase. SAMS.

SEQ ID NO: 94

AAB36543.1	U77935	Phaseolus vulgaris	DnaJ-like protein. synthesis and expression are regulated by heavy metal stress, virus infection and wounding treatment, suggesting that DnaJ-like protein plays a role in plant defense.
------------	--------	--------------------	---

SEQ ID NO: 95

AAB36546.1	U77940	Phaseolus vulgaris	polyubiquitin. expression is regulated by heavy metal stress, UV, virus infection, heat shock and wounding treatment, this suggests that ubiquitin plays a role in plant defense.
------------	--------	--------------------	---

SEQ ID NO: 98

AAF22109.1	AF119411	Lupinus albus	ethylene biosynthesis enzyme. 1-aminocyclopropane-1-carboxylate synthase 1. ACS1. ACC synthase; S-adenosyl-L-methionine methylthioadenosine-lyase.
AAC83146.1	AF057562	Nicotiana glutinosa	1-aminocyclopropane-1-carboxylate synthase. ACS1. ACC synthase.

AAB06724.1	U64804	Petunia x hybrida	ethylene biosynthesis enzyme. 1-aminocyclopropane-1-carboxylate synthase. PH-ACS1.
CAA79478.1	Z18953	Petunia x hybrida	1-aminocyclopropane-1-carboxylate synthase.
AAB17279.1	U72390	Lycopersicon esculentum	converts S-adenosylmethionine to 1-aminocyclopropane-1-carboxylate hormone biosynthesis. 1-aminocyclopropane-1-carboxylate synthase. LE-ACS1B.
BAA94600.1	AB033503	Populus euramericana	1-aminocyclopropane-1-carboxylate synthase. peacs-2.
BAA96743.1	AB044662	Prunus persica	1-aminocyclopropane-1-carboxylate synthase. PP-ACS1.
CAB60831.1	AJ012696	Citrus sinensis	ACC synthase. acs2.
CAA09477.1	AJ011095	Citrus sinensis	ACC synthase. acs-1.
CAA41855.1	X59139	Lycopersicon esculentum	1-aminocyclopropane 1-carboxylate synthase. LE-Acc2.
BAA90549.1	AB031026	Prunus mume	ACC synthase. PM-ACS1. 1-aminocyclopropane-1-carboxylic acid synthase.
AAA81580.1	M34289	Lycopersicon esculentum	1-aminocyclopropane-1-carboxylate synthase.
CAA44397.1	X62536	Lycopersicon esculentum	1-aminocyclopropane 1-carboxylate synthase.
CAA46797.1	X65982	Nicotiana tabacum	1-aminocyclopropane 1-carboxylate synthase.
BAA78333.1	AB015625	Pyrus pyrifolia	1-aminocyclopropane-1-carboxylic acid synthase. pPPACS3.
CAA41856.1	X59145	Lycopersicon esculentum	1-aminocyclopropane 1-carboxylate synthase. LE-ACC2.
AAB17278.1	U72389	Lycopersicon esculentum	converts S-adenosylmethionine to 1-aminocyclopropane-1-carboxylate hormone biosynthesis. 1-aminocyclopropane-1-carboxylate synthase. LE-ACS1A.
AAF97614.1	U18056	Lycopersicon esculentum	converts SAM to ACC; plant hormone biosynthesis. 1-amino-cyclopropane-1-carboxylate synthase. LE-ACS1A. ACC synthase; direct precursor of ethylene; one member of a multigene family.
BAB16433.1	AB041521	Solanum tuberosum	ACC synthase. ppACS1.
BAA34923.1	AB013100	Lycopersicon esculentum	1-aminocyclopropane-1-carboxylate synthase. LE-ACS6. ACC synthase.
BAA25916.1	AB013346	Lycopersicon esculentum	1-aminocyclopropane-1-carboxylate synthase.

AAF97615.1	U18057	<i>Lycopersicon esculentum</i>	converts SAM to ACC; plant hormone biosynthesis. 1-amino-cyclopropane-1-carboxylate synthase. LE-ACS1B. ACC synthase; direct precursor of ethylene; one member of a multigene family.
BAA92350.1	AB034992	<i>Malus x domestica</i>	1-aminocyclopropane-1-carboxylate synthase. MdACS-5A.
BAA92351.1	AB034993	<i>Malus x domestica</i>	1-aminocyclopropane-1-carboxylate synthase. MdACS-5B.
BAA93712.1	AB032935	<i>Cucumis melo</i>	1-aminocyclopropane-1-carboxylate synthase. CMe-ACS1.
BAA94599.1	AB033502	<i>Populus euphratica</i>	1-aminocyclopropane-1-carboxylate synthase. peacs-1.
BAA33374.1	AB006803	<i>Cucumis sativus</i>	ACC synthase. CS-ACS1.
BAA93714.1	AB032937	<i>Cucumis sativus</i>	1-aminocyclopropane-1-carboxylate synthase. CS-ACS1.
AAC49153.1	U17229	<i>Pelargonium x hortorum</i>	1-aminocyclopropane 1-carboxylate synthase. ACC synthase.
CAA06288.1	AJ005002	<i>Nicotiana tabacum</i>	1-cyclopropane-1-carboxylate synthase. acs2.
CAB65314.1	AJ131836	<i>Nicotiana tabacum</i>	1-aminocyclopropane-1-carboxylate synthase. acs2.
AAC15777.1	AF061605	<i>Nicotiana glutinosa</i>	ACC synthase. ACS3.
AAC83147.1	AF057563	<i>Nicotiana glutinosa</i>	1-aminocyclopropane-1-carboxylate synthase. ACS2. ACC synthase.
BAA06464.1	D30805	<i>Cucumis melo</i>	1-aminocyclopropane-1-carboxylate synthase.
BAA83618.1	AB025906	<i>Cucumis melo</i>	1-aminocyclopropane-1-carboxylate synthase. CMe-ACS1 (ME-ACS1).
AAB70885.1	U88971	<i>Pelargonium x hortorum</i>	1-aminocyclopropane-1-carboxylate synthase. GACS2. similar to <i>Pelargonium hortorum</i> clone pGAC-2, Genbank Accession Number U17231.
AAA33113.1	M58323	<i>Cucurbita pepo</i>	1-aminocyclopropane-1-carboxylate synthase.
AAA33111.1	M61195	<i>Cucurbita pepo</i>	1-aminocyclopropane-1-carboxylate synthase. CP-ACC1A.
CAA57724.1	X82273	<i>Brassica oleracea</i>	1-aminocyclopropane-1-carboxylate synthase.
CAA47474.1	X67100	<i>Glycine max</i>	1-aminocyclopropane 1-carboxylate synthase.
AAA33112.1	M61195	<i>Cucurbita pepo</i>	1-aminocyclopropane-1-carboxylate synthase. CP-ACC1B.

AAC98809.1	U68216	<i>Carica papaya</i>	ACC synthase. fruit specific; ripening related.
CAA51227.1	X72676	<i>Brassica juncea</i>	1-aminocyclopropane-1-carboxylate synthase. MACC.
BAA00838.1	D01032	<i>Cucurbita maxima</i>	1-aminocyclopropane-1-carboxylate synthase. accW.
AAA34131.1	M63490	<i>Lycopersicon esculentum</i>	enzyme. 1-aminocyclopropane-1-carboxylate synthase.
AAA03164.1	M88487	<i>Lycopersicon esculentum</i>	1-aminocyclopropane-1-carboxylate synthase. ACC4.
CAA41857.1	X59146	<i>Lycopersicon esculentum</i>	1-aminocyclopropane 1-carboxylate synthase. LE-ACC4.
CAA77688.1	Z11613	<i>Vigna radiata</i>	1-aminocyclopropane 1-carboxylate synthase.
CAA67118.1	X98492	<i>Nicotiana tabacum</i>	ACC synthase. ACCS2.

SEQ ID NO: 99

BAA22976.1	D63457	<i>Arabis gemmifera</i>	alcohol dehydrogenase. Adh. ADH.
BAA22973.1	D63454	<i>Arabis gemmifera</i>	alcohol dehydrogenase. Adh. ADH.
AAF23537.1	AF110439	<i>Arabis glabra</i>	alcohol dehydrogenase.
BAA22978.1	D63459	<i>Arabis gemmifera</i>	alcohol dehydrogenase. Adh. ADH.
BAA22974.1	D63455	<i>Arabis gemmifera</i>	alcohol dehydrogenase. Adh. ADH.
AAF23540.1	AF110442	<i>Arabidopsis halleri</i>	alcohol dehydrogenase.
AAF23551.1	AF110453	<i>Arabidopsis lyrata</i> subsp. <i>petraea</i>	alcohol dehydrogenase.
AAF23539.1	AF110441	<i>Halimolobos perplexa</i> var. <i>lemhiensis</i>	alcohol dehydrogenase.
BAA22975.1	D63456	<i>Arabis gemmifera</i>	alcohol dehydrogenase. Adh. ADH.
AAF23546.1	AF110448	<i>Arabis lyallii</i>	alcohol dehydrogenase.
AAF23548.1	AF110450	<i>Arabis parishii</i>	alcohol dehydrogenase.
AAF23550.1	AF110452	<i>Arabidopsis lyrata</i> subsp. <i>petraea</i>	alcohol dehydrogenase.

BAA22972.1	D63453	<i>Arabis gemmifera</i> alcohol dehydrogenase. Adh. ADH.
BAA22971.1	D63452	<i>Arabis gemmifera</i> alcohol dehydrogenase. Adh. ADH.
BAA22977.1	D63458	<i>Arabis gemmifera</i> alcohol dehydrogenase. Adh. ADH.
AAF23549.1	AF110451	<i>Arabis pauciflora</i> alcohol dehydrogenase.
AAF23545.1	AF110447	<i>Arabis lignifera</i> alcohol dehydrogenase.
AAF23536.1	AF110438	<i>Arabis fendleri</i> alcohol dehydrogenase.
AAF23541.1	AF110443	<i>Arabis hirsuta</i> alcohol dehydrogenase.
AAF23531.1	AF110433	<i>Arabis blepharophylla</i> alcohol dehydrogenase.
AAF23530.1	AF110432	<i>Arabis blepharophylla</i> alcohol dehydrogenase.
AAF23523.1	AF110425	<i>Aubrieta deltoidea</i> alcohol dehydrogenase.
AAF23529.1	AF110431	<i>Arabis blepharophylla</i> alcohol dehydrogenase.
AAF23547.1	AF110449	<i>Arabidopsis lyrata</i> subsp. <i>lyrata</i> alcohol dehydrogenase.
AAF23533.1	AF110435	<i>Capsella rubella</i> alcohol dehydrogenase.
AAF23534.1	AF110436	<i>Arabis drummondii</i> alcohol dehydrogenase.
AAF23532.1	AF110434	<i>Brassica oleracea</i> alcohol dehydrogenase.
AAF23556.1	AF110458	<i>Barbarea vulgaris</i> alcohol dehydrogenase.
AAF23555.1	AF110457	<i>Arabis turrita</i> alcohol dehydrogenase.
AAF23538.1	AF110440	<i>Arabidopsis griffithiana</i> alcohol dehydrogenase.
AAF23524.1	AF110426	<i>Arabis alpina</i> alcohol dehydrogenase.
AAF23543.1	AF110445	<i>Arabis hirsuta</i> alcohol dehydrogenase.
AAF23525.1	AF110427	<i>Arabis alpina</i> alcohol dehydrogenase.

AAF23527.1	AF110429	<i>Arabis alpina</i> alcohol dehydrogenase.
AAF23535.1	AF110437	<i>Arabis drummondii</i> alcohol dehydrogenase.
AAF23553.1	AF110455	<i>Arabis procurrens</i> alcohol dehydrogenase.
AAF23544.1	AF110446	<i>Arabis jacquinii</i> alcohol dehydrogenase.
AAF23526.1	AF110428	<i>Arabis alpina</i> alcohol dehydrogenase.
AAF23528.1	AF110430	<i>Cardamine amara</i> alcohol dehydrogenase.
AAF23552.1	AF110454	<i>Arabis procurrens</i> alcohol dehydrogenase.
AAF23542.1	AF110444	<i>Arabis hirsuta</i> alcohol dehydrogenase.
AAC79418.1	AF037560	<i>Leavenworthia stylosa</i> alcohol dehydrogenase 3. Adh3.
BAA34682.1	AB015504	<i>Arabidopsis griffithiana</i> alcohol dehydrogenase. Adh.
BAA34685.1	AB015507	<i>Arabidopsis suecica</i> alcohol dehydrogenase. Adh.
BAA34683.1	AB015505	<i>Arabidopsis korshinskyi</i> alcohol dehydrogenase. Adh.
CAB72921.1	AJ251281	<i>Arabidopsis lyrata</i> subsp. <i>petraea</i> alcohol dehydrogenase. adh.
CAB72920.1	AJ251280	<i>Arabidopsis lyrata</i> subsp. <i>petraea</i> alcohol dehydrogenase. adh.
CAB72919.1	AJ251279	<i>Arabidopsis lyrata</i> subsp. <i>petraea</i> alcohol dehydrogenase. adh.
CAB72918.1	AJ251278	<i>Arabidopsis lyrata</i> subsp. <i>petraea</i> alcohol dehydrogenase. adh.
CAB72917.1	AJ251277	<i>Arabidopsis lyrata</i> subsp. <i>petraea</i> alcohol dehydrogenase. adh.

SEQ ID NO: 100

AAD09518.1 U64925 *Nicotiana tabacum*
NTGP4. similar to AIG1; geranylgeranylated protein.

SEQ ID NO: 102

BAA12039.1 D83669 *Spinacia oleracea*
stromal ascorbate peroxidase.
BAA19611.1 D77997 *Spinacia oleracea*
thylakoid-bound ascorbate peroxidase.

BAA24610.1	AB002467	Spinacia oleracea stromal ascorbate peroxidase. APX2.
BAA24609.1	AB002467	Spinacia oleracea thylakoid-bound ascorbate peroxidase. APX2.
AAC19394.1	AF069316	Mesembryanthemum crystallinum stromal L-ascorbate peroxidase precursor.
AAC19393.1	AF069315	Mesembryanthemum crystallinum thylakoid-bound L-ascorbate peroxidase precursor.
BAA78553.1	AB022274	Chloroplast Nicotiana tabacum stromal ascorbate peroxidase.
BAA78552.1	AB022273	Chloroplast Nicotiana tabacum thylakoid-bound ascorbate peroxidase.
BAA22196.1	D88420	Cucurbita sp. a hydrogen peroxide-scavenging enzyme. stromal ascorbate peroxidase.
BAA12029.1	D83656	Cucurbita sp. 2AsA+H2O2 ---> 2MDA+2H2O. thylakoid-bound ascorbate peroxidase.
CAA11265.1	AJ223325	Chlamydomonas reinhardtii ascorbate peroxidase. apx1.
BAA83595.1	AB009084	Chlamydomonas sp. W80 chloroplast ascorbate peroxidase.
AAD30294.1	AF139190	Mesembryanthemum crystallinum cytosolic ascorbate peroxidase. similar to L0-328, R6-3, L72-2.
AAB52954.1	U37060	Gossypium hirsutum ascorbate peroxidase. glyoxysomal membrane-bound protein.
AAD43334.1	AF159254	Zantedeschia aethiopica ascorbate peroxidase. apx2. putative glyoxysomal membrane-bound protein.
AAC08576.1	AF053474	Zantedeschia aethiopica cytosolic ascorbate peroxidase. apx.
AAD43338.1	AF158654	Fragaria x ananassa cytosolic ascorbate peroxidase APX26.
AAD43336.1	AF158652	Fragaria x ananassa cytosolic ascorbate peroxidase. ApxSC. corresponds to mRNA sequence deposited in GenBank Accession Number AF039953.
AAB95222.1	AF039953	Fragaria x ananassa cytosolic ascorbate peroxidase. ApxSC.
AAD41408.1	AF159633	Fragaria x ananassa cytosolic ascorbate peroxidase. APX.
AAD41407.1	AF159632	Fragaria x ananassa cytosolic ascorbate peroxidase. APX.
AAD41403.1	AF159628	Fragaria x ananassa cytosolic ascorbate peroxidase. APX.
AAD41402.1	AF159627	Fragaria x ananassa cytosolic ascorbate peroxidase. APX.

AAD43337.1	AF158653	Fragaria x ananassa	cytosolic ascorbate peroxidase APX19.
AAD41406.1	AF159631	Fragaria x ananassa	cytosolic ascorbate peroxidase. APX.
AAD41404.1	AF159629	Fragaria x ananassa	cytosolic ascorbate peroxidase. APX.
AAB94574.1	AF022213	Fragaria x ananassa	cytosolic ascorbate peroxidase. APX-c.
AAD41405.1	AF159630	Fragaria x ananassa	cytosolic ascorbate peroxidase. APX.
BAA08264.1	D45423	Oryza sativa	ascorbate peroxidase.
BAA13671.1	D88649	Cucumis sativus	cytosolic ascorbate peroxidase.
CAA55209.1	X78452	Raphanus sativus	L-ascorbate peroxidase. APX.
BAA12890.1	D85864	Spinacia oleracea	cytosolic ascorbate peroxidase.
AAA99518.1	L20864	Spinacia oleracea	ascorbate peroxidase.
BAA12918.1	D85912	Nicotiana tabacum	cytosolic ascorbate peroxidase.
AAB03844.1	U61379	Vigna unguiculata	ascorbate peroxidase.
CAB58361.1	Y16773	Lycopersicon esculentum	ascorbate peroxidase. Apx. H2O2 scavenger, cytosolic protein.
CAA57140.1	X81376	Capsicum annuum	L-ascorbate peroxidase.
CAA06996.1	AJ006358	Hordeum vulgare	ascorbate peroxidase. apx.
AAF22246.1	AF159380	Pimpinella brachycarpa	ascorbate peroxidase. APX.
AAA86689.1	U15933	Nicotiana tabacum	reduction of hydrogen peroxide. ascorbate peroxidase. APX.
CAA84406.1	Z34934	Zea mays	cytosolic ascorbate peroxidase. apx.
CAA43992.1	X62077	Pisum sativum	L-ascorbate peroxidase. AppxI.
AAA33645.1	M93051	Pisum sativum	hydrogen peroxide removal; oxidative stress. ascorbate peroxidase. ApxI.
AAB01221.1	U56634	Glycine max	ascorbate peroxidase 2. APx2.

AAA61779.1 L10292 Glycine max
ascorbate peroxidase. Automated Edman sequencing of the N-terminal amino acids confirmed that the protein was authentic ascorbate peroxidase; putative.

BAB20889.1 AB053297 Oryza sativa
L-ascorbate peroxidase. APXb.

CAA72247.1 Y11461 Brassica napus
L-ascorbate peroxidase. APX.

BAB17666.1 AB050724 Oryza sativa subsp. japonica
ascorbate peroxidase. APXb.

AAD20022.1 AF127804 Glycine max
ascorbate peroxidase. apx1. AsPOX; cytosolic.

AAB94927.1 AF038839 Brassica juncea
ascorbate peroxidase.

SEQ ID NO: 103

AAA74900.1 L34343 Ruta graveolens
anthranilate synthase alpha subunit.

AAA74901.1 L34344 Ruta graveolens
anthranilate synthase alpha subunit.

AAC27795.1 AF079168 Nicotiana tabacum
feedback-insensitive anthranilate synthase alpha-2 chain. ASA2.

BAA82095.1 AB022603 Oryza sativa
anthranilate synthase alpha 2 subunit. OsASA2.

BAA82094.1 AB022602 Oryza sativa
anthranilate synthase alpha 1 subunit. OsASA1.

CAC29060.1 AJ250008 Catharanthus roseus
enzyme in tryptophan biosynthesis. anthranilate synthase alpha subunit. asa.

CAA06837.1 AJ006065 Catharanthus roseus
isochorismate synthase.

SEQ ID NO: 104

CAA57724.1 X82273 Brassica oleracea
1-aminocyclopropane-1-carboxylate synthase.

CAA51227.1 X72676 Brassica juncea
1-aminocyclopropane-1-carboxylate synthase. MACC.

AAC83147.1 AF057563 Nicotiana glutinosa
1-aminocyclopropane-1-carboxylate synthase. ACS2. ACC synthase.

CAB60722.1 AJ012551 Citrus sinensis
ACC synthase. acs1.

CAB60721.1 AJ012550 Citrus sinensis
ACC synthase. acs1.

CAA06288.1 AJ005002 Nicotiana tabacum
1-cyclopropane-1-carboxylate synthase. acs2.

CAB65314.1 AJ131836 Nicotiana tabacum
1-aminocyclopropane-1-carboxylate synthase. acs2.

BAA78333.1	AB015625	<i>Pyrus pyrifolia</i>	1-aminocyclopropane-1-carboxylic acid synthase. pPPACS3.
AAB17279.1	U72390	<i>Lycopersicon esculentum</i>	converts S-adenosylmethionine to 1-aminocyclopropane-1-carboxylate hormone biosynthesis. 1-aminocyclopropane-1-carboxylate synthase. LE-ACS1B.
AAF97614.1	U18056	<i>Lycopersicon esculentum</i>	converts SAM to ACC; plant hormone biosynthesis. 1-amino-cyclopropane-1-carboxylate synthase. LE-ACS1A. ACC synthase; direct precursor of ethylene; one member of a multigene family.
AAF97615.1	U18057	<i>Lycopersicon esculentum</i>	converts SAM to ACC; plant hormone biosynthesis. 1-amino-cyclopropane-1-carboxylate synthase. LE-ACS1B. ACC synthase; direct precursor of ethylene; one member of a multigene family.
AAB17278.1	U72389	<i>Lycopersicon esculentum</i>	converts S-adenosylmethionine to 1-aminocyclopropane-1-carboxylate hormone biosynthesis. 1-aminocyclopropane-1-carboxylate synthase. LE-ACS1A.
CAA46797.1	X65982	<i>Nicotiana tabacum</i>	1-aminocyclopropane 1-carboxylate synthase.
BAA06464.1	D30805	<i>Cucumis melo</i>	1-aminocyclopropane-1-carboxylate synthase.
AAB06724.1	U64804	<i>Petunia x hybrida</i>	ethylene biosynthesis enzyme. 1-aminocyclopropane-1-carboxylate synthase. PH-ACS1.
CAA79478.1	Z18953	<i>Petunia x hybrida</i>	1-aminocyclopropane-1-carboxylate synthase.
BAA94599.1	AB033502	<i>Populus euphratica</i>	1-aminocyclopropane-1-carboxylate synthase. peacs-1.
CAA67118.1	X98492	<i>Nicotiana tabacum</i>	ACC synthase. ACCS2.
CAA79477.1	Z18952	<i>Dianthus caryophyllus</i>	1-aminocyclopropane 1-carboxylate synthase.
AAA33275.1	M66619	<i>Dianthus caryophyllus</i>	1-aminocyclopropane-1-carboxylate synthase. CARACC.
BAA83618.1	AB025906	<i>Cucumis melo</i>	1-aminocyclopropane-1-carboxylate synthase. CMe-ACS1 (ME-ACS1).
BAA34923.1	AB013100	<i>Lycopersicon esculentum</i>	1-aminocyclopropane-1-carboxylate synthase. LE-ACS6. ACC synthase.
BAA25916.1	AB013346	<i>Lycopersicon esculentum</i>	1-aminocyclopropane-1-carboxylate synthase.
CAB60831.1	AJ012696	<i>Citrus sinensis</i>	ACC synthase. acs2.
CAA41855.1	X59139	<i>Lycopersicon esculentum</i>	1-aminocyclopropane 1-carboxylate synthase. LE-Acc2.

CAA44397.1	X62536	Lycopersicon esculentum	1-aminocyclopropane 1-carboxylate synthase.
CAA41856.1	X59145	Lycopersicon esculentum	1-aminocyclopropane 1-carboxylate synthase. LE-ACC2.
AAA81580.1	M34289	Lycopersicon esculentum	1-aminocyclopropane-1-carboxylate synthase.
AAC98809.1	U68216	Carica papaya	ACC synthase. fruit specific; ripening related.
BAA92350.1	AB034992	Malus x domestica	1-aminocyclopropane-1-carboxylate synthase. MdACS-5A.
BAA92351.1	AB034993	Malus x domestica	1-aminocyclopropane-1-carboxylate synthase. MdACS-5B.
BAA94600.1	AB033503	Populus euramericana	1-aminocyclopropane-1-carboxylate synthase. peacs-2.
CAA77688.1	Z11613	Vigna radiata	1-aminocyclopropane 1-carboxylate synthase.
CAA47474.1	X67100	Glycine max	1-aminocyclopropane 1-carboxylate synthase.
AAB70885.1	U88971	Pelargonium x hortorum	1-aminocyclopropane-1-carboxylate synthase. GACS2. similar to Pelargonium hortorum clone pGAC-2, Genbank Accession Number U17231.
AAD04199.1	AF016459	Pisum sativum	1-aminocyclopropane-1-carboxylate synthase. ACS2. ACC synthase.
BAB18464.1	D86242	Cucumis melo	1-aminocyclopropane-1-carboxylate synthase. CMe-ACS2 (ME-ACS2).
BAA93713.1	AB032936	Cucumis melo	1-aminocyclopropane-1-carboxylate synthase. CMe-ACS2.
BAA93715.1	AB032938	Cucumis sativus	1-aminocyclopropane-1-carboxylate synthase. CS-ACS2.
BAA33375.1	AB006804	Cucumis sativus	ACC synthase. CS-ACS2.
BAB16433.1	AB041521	Solanum tuberosum	ACC synthase. ppACS1.
AAC15777.1	AF061605	Nicotiana glutinosa	ACC synthase. ACS3.
CAA72191.1	Y11357	Carica papaya	1-aminocyclopropane-1-carboxylate synthase.
BAA96743.1	AB044662	Prunus persica	1-aminocyclopropane-1-carboxylate synthase. PP-ACS1.
BAA90549.1	AB031026	Prunus mume	ACC synthase. PM-ACS1. 1-aminocyclopropane-1-carboxylic acid synthase.
BAA93712.1	AB032935	Cucumis melo	1-aminocyclopropane-1-carboxylate synthase. CMe-ACS1.

AAF22109.1 AF119411 *Lupinus albus*
ethylene biosynthesis enzyme. 1-aminocyclopropane-1-carboxylate synthase 1. ACS1. ACC
synthase; S-adenosyl-L-methionine methylthioadenosine-lyase.

AAC83146.1 AF057562 *Nicotiana glutinosa*
1-aminocyclopropane-1-carboxylate synthase. ACS1. ACC synthase.

CAA09477.1 AJ011095 *Citrus sinensis*
ACC synthase. acs-1.

BAA93714.1 AB032937 *Cucumis sativus*
1-aminocyclopropane-1-carboxylate synthase. CS-ACS1.

SEQ ID NO: 106

AAF63205.1 AF245119 *Mesembryanthemum crystallinum*
AP2-related transcription factor. CDBP. stress induced transcription factor.

BAA97122.1 AB016264 *Nicotiana sylvestris*
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-
related) gene of higher plant. ethylene-responsive element binding factor. nserf2.

AAC50047.1 U89255 *Lycopersicon esculentum*
binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti4.

BAA07321.1 D38123 *Nicotiana tabacum*
ERF1. ethylene-responsive transcription factor.

AAC62619.1 AF057373 *Nicotiana tabacum*
transcription factor. ethylene response element binding protein 1. EREBP1.

BAA87068.1 AB035270 *Matricaria chamomilla*
ethylene-responsive element binding protein1 homolog. McEREBP1.

AAC49740.1 U89256 *Lycopersicon esculentum*
binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti5.

AAG43545.1 AF211527 *Nicotiana tabacum*
Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.

BAA97124.1 AB016266 *Nicotiana sylvestris*
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-
related) gene of higher plant. ethylene-responsive element binding factor. nserf4.

CAB96900.1 AJ251250 *Catharanthus roseus*
transcription factor. AP2-domain DNA-binding protein. orca3.

CAB96899.1 AJ251249 *Catharanthus roseus*
transcription factor. AP2-domain DNA-binding protein. orca3.

AAB38748.1 U81157 *Nicotiana tabacum*
S25-XPI DNA binding protein.

AAG60182.1 AC084763 *Oryza sativa*
putative ethylene-responsive element binding protein. OSJNBa0027P10.12.

AAK31279.1 AC079890 *Oryza sativa*
putative ethylene-responsive element binding protein. OSJNBb0089A17.16.

CAB93940.1 AJ238740 *Catharanthus roseus*
putative transcription factor. AP2-domain DNA-binding protein. orca2.

AAC49741.1	U89257	Lycopersicon esculentum	DNA-binding protein binds the GCC box pathogenesis-related promoter element. Pti6.
CAC12822.1	AJ299252	Nicotiana tabacum	AP2 domain-containing transcription factor. ap2.
BAB03248.1	AB037183	Oryza sativa	ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
AAC14323.1	AF058827	Nicotiana tabacum	TSI1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pti6.
BAA97123.1	AB016265	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
AAD00708.1	U91857	Stylosanthes hamata	ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.
AAF05606.1	AF190770	Oryza sativa	EREBP-like protein. tsh1. TSH1; induced by ethylene.
BAA76734.1	AB024575	Nicotiana tabacum	ethylene responsive element binding factor.
AAC29516.1	U77655	Solanum tuberosum	DNA binding protein homolog. STWAAEIRD.
AAF23899.1	AF193803	Oryza sativa	transcription factor EREBP1. EREBP/AP2-like transcription factor.
CAB93939.1	AJ238739	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca1.
AAD45623.1	AF084185	Brassica napus	dehydration responsive element binding protein. DNA binding protein; DRE binding protein.
AAK31271.1	AC079890	Oryza sativa	putative transcriptional factor. OSJNBb0089A17.22.
AAG43548.1	AF211530	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
BAB21218.1	AP002913	Oryza sativa	putative DNA binding protein RAV2. P0480E02.24.
AAG43549.1	AF211531	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
BAB21211.1	AP002913	Oryza sativa	putative DNA binding protein RAV2. P0480E02.17.
AAK01088.1	AF298230	Hordeum vulgare	CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
AAK01089.1	AF298231	Hordeum vulgare	CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.

SEQ ID NO: 107

AAF63205.1	AF245119	Mesembryanthemum crystallinum	AP2-related transcription factor. CDBP. stress induced transcription factor.
AAC50047.1	U89255	Lycopersicon esculentum	binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti4.
BAA97122.1	AB016264	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.
BAA07321.1	D38123	Nicotiana tabacum	ERF1. ethylene-responsive transcription factor.
AAC62619.1	AF057373	Nicotiana tabacum	transcription factor. ethylene response element binding protein 1. EREBP1.
BAA87068.1	AB035270	Matricaria chamomilla	ethylene-responsive element binding protein1 homolog. McEREBP1.
CAB96899.1	AJ251249	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
CAB96900.1	AJ251250	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
AAB38748.1	U81157	Nicotiana tabacum	S25-XP1 DNA binding protein.
AAC49740.1	U89256	Lycopersicon esculentum	binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti5.
CAB93940.1	AJ238740	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca2.
AAG43545.1	AF211527	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.
BAA97124.1	AB016266	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
AAG60182.1	AC084763	Oryza sativa	putative ethylene-responsive element binding protein. OSJNBa0027P10.12.
AAK31279.1	AC079890	Oryza sativa	putative ethylene-responsive element binding protein. OSJNBb0089A17.16.
BAA97123.1	AB016265	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
AAD00708.1	U91857	Stylosanthes hamata	ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.
AAC14323.1	AF058827	Nicotiana tabacum	TSI1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pti6.
CAC12822.1	AJ299252	Nicotiana tabacum	AP2 domain-containing transcription factor. ap2.

BAB03248.1	AB037183	Oryza sativa	ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
AAF05606.1	AF190770	Oryza sativa	EREBP-like protein. tsh1. TSH1; induced by ethylene.
BAA76734.1	AB024575	Nicotiana tabacum	ethylene responsive element binding factor.
AAC49741.1	U89257	Lycopersicon esculentum	DNA-binding protein binds the GCC box pathogenesis-related promoter element. Pti6.
AAF23899.1	AF193803	Oryza sativa	transcription factor EREBP1. EREBP/AP2-like transcription factor.
AAC29516.1	U77655	Solanum tuberosum	DNA binding protein homolog. STWAAEIRD.
CAB93939.1	AJ238739	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca1.
BAA78738.1	AB023482	Oryza sativa	EST AU055776(S20048) corresponds to a region of the predicted gene.; Similar to Arabidopsis thaliana AP2 domain containing protein RAP2.10 mRNA, partial cds.(AF003103).
AAD45623.1	AF084185	Brassica napus	dehydration responsive element binding protein. DNA binding protein; DRE binding protein.
AAG43548.1	AF211530	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
AAG43549.1	AF211531	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
BAA99376.1	AP002526	Oryza sativa	ESTs AU093391(E60370),AU091593(C60458), AU093392(E60370) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana BAC F21J9; AP2 domain protein. (AC000103).
BAB21218.1	AP002913	Oryza sativa	putative DNA binding protein RAV2. P0480E02.24.
AAK31271.1	AC079890	Oryza sativa	putative transcriptional factor. OSJNBb0089A17.22.
BAB21211.1	AP002913	Oryza sativa	putative DNA binding protein RAV2. P0480E02.17.
AAK01088.1	AF298230	Hordeum vulgare	CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
AAG59618.1	AF239616	Hordeum vulgare	CRT/DRE-binding factor. CBF.
AAK01089.1	AF298231	Hordeum vulgare	CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.
SEQ ID NO: 109			

BAA97124.1	AB016266	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
AAG43545.1	AF211527	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.
AAK31279.1	AC079890	Oryza sativa	putative ethylene-responsive element binding protein. OSJNBb0089A17.16.
AAG60182.1	AC084763	Oryza sativa	putative ethylene-responsive element binding protein. OSJNBa0027P10.12.
BAA87068.1	AB035270	Matricaria chamomilla	ethylene-responsive element binding protein1 homolog. McEREBP1.
AAF63205.1	AF245119	Mesembryanthemum crystallinum	AP2-related transcription factor. CDBP. stress induced transcription factor.
AAC50047.1	U89255	Lycopersicon esculentum	binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti4.
BAA97122.1	AB016264	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.
BAA07321.1	D38123	Nicotiana tabacum	ERF1. ethylene-responsive transcription factor.
CAB93940.1	AJ238740	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca2.
AAC49740.1	U89256	Lycopersicon esculentum	binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti5.
AAC62619.1	AF057373	Nicotiana tabacum	transcription factor. ethylene response element binding protein 1. EREBP1.
AAB38748.1	U81157	Nicotiana tabacum	S25-XP1 DNA binding protein.
CAC12822.1	AJ299252	Nicotiana tabacum	AP2 domain-containing transcription factor. ap2.
CAB96900.1	AJ251250	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
CAB96899.1	AJ251249	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
BAA97123.1	AB016265	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
BAB03248.1	AB037183	Oryza sativa	ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
AAD00708.1	U91857	Stylosanthes hamata	ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.

AAC14323.1	AF058827	Nicotiana tabacum	Ts11. Ts11. contains putative AP2 DNA-binding domain; similar to Pti6.
AAC49741.1	U89257	Lycopersicon esculentum	DNA-binding protein binds the GCC box pathogenesis-related promoter element. Pti6.
AAC29516.1	U77655	Solanum tuberosum	DNA binding protein homolog. STWAAEIRD.
AAF05606.1	AF190770	Oryza sativa	EREBP-like protein. tsh1. TSH1; induced by ethylene.
BAA76734.1	AB024575	Nicotiana tabacum	ethylene responsive element binding factor.
AAF23899.1	AF193803	Oryza sativa	transcription factor EREBP1. EREBP/AP2-like transcription factor.
BAA78738.1	AB023482	Oryza sativa	EST AU055776(S20048) corresponds to a region of the predicted gene.; Similar to Arabidopsis thaliana AP2 domain containing protein RAP2.10 mRNA, partial cds.(AF003103).
CAB93939.1	AJ238739	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca1.
AAD45623.1	AF084185	Brassica napus	dehydration responsive element binding protein. DNA binding protein; DRE binding protein.
AAG43549.1	AF211531	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
AAG43548.1	AF211530	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
AAK31271.1	AC079890	Oryza sativa	putative transcriptional factor. OSJNBb0089A17.22.
AAK01088.1	AF298230	Hordeum vulgare	CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
BAA99376.1	AP002526	Oryza sativa	ESTs AU093391(E60370), AU091593(C60458), AU093392(E60370) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana BAC F21J9; AP2 domain protein. (AC000103).
AAG59619.1	AF243384	Oryza sativa	CRT/DRE binding factor. CBF. DREB.
BAB21218.1	AP002913	Oryza sativa	putative DNA binding protein RAV2. P0480E02.24.
AAG32659.1	AF253971	Picea abies	APETALA2-related transcription factor 2. AP2L2. PaAP2L2.
AAC49567.1	U41466	Zea mays	Glossy15. Glossy15. AP2 DNA-binding domain protein; similar to the Arabidopsis floral homeotic gene APETALA2; maize AP2-domain regulator of leaf epidermal traits; homeotic regulator of leaf epidermal cell identity; allele: W64A; putative transcription factor.

SEQ ID NO: 110

AAG43545.1	AF211527	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.
BAA97124.1	AB016266	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
AAK31279.1	AC079890	Oryza sativa	putative ethylene-responsive element binding protein. OSJNBb0089A17.16.
AAG60182.1	AC084763	Oryza sativa	putative ethylene-responsive element binding protein. OSJNBa0027P10.12.
AAF63205.1	AF245119	Mesembryanthemum crystallinum	AP2-related transcription factor. CDBP. stress induced transcription factor.
BAA97122.1	AB016264	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.
BAA87068.1	AB035270	Matricaria chamomilla	ethylene-responsive element binding protein1 homolog. McEREBP1.
AAC50047.1	U89255	Lycopersicon esculentum	binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti4.
BAA07321.1	D38123	Nicotiana tabacum	ERF1. ethylene-responsive transcription factor.
AAC49740.1	U89256	Lycopersicon esculentum	binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti5.
CAB93940.1	AJ238740	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca2.
AAC62619.1	AF057373	Nicotiana tabacum	transcription factor. ethylene response element binding protein 1. EREBP1.
CAB96899.1	AJ251249	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
CAB96900.1	AJ251250	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
AAB38748.1	U81157	Nicotiana tabacum	S25-XP1 DNA binding protein.
CAC12822.1	AJ299252	Nicotiana tabacum	AP2 domain-containing transcription factor. ap2.
AAF05606.1	AF190770	Oryza sativa	EREBP-like protein. tsh1. TSH1; induced by ethylene.
AAC29516.1	U77655	Solanum tuberosum	DNA binding protein homolog. STWAAEIRD.
AAF23899.1	AF193803	Oryza sativa	transcription factor EREBP1. EREBP/AP2-like transcription factor.
BAB03248.1	AB037183	Oryza sativa	ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.

BAA97123.1	AB016265	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
BAA76734.1	AB024575	Nicotiana tabacum	ethylene responsive element binding factor.
AAD00708.1	U91857	Stylosanthes hamata	ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.
AAC49741.1	U89257	Lycopersicon esculentum	DNA-binding protein binds the GCC box pathogenesis-related promoter element. Pti6.
AAC14323.1	AF058827	Nicotiana tabacum	TSI1. Tsil. contains putative AP2 DNA-binding domain; similar to Pti6.
CAB93939.1	AJ238739	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca1.
AAD45623.1	AF084185	Brassica napus	dehydration responsive element binding protein. DNA binding protein; DRE binding protein.
AAG43548.1	AF211530	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
AAG43549.1	AF211531	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
AAK31271.1	AC079890	Oryza sativa	putative transcriptional factor. OSJNBb0089A17.22.
BAB21218.1	AP002913	Oryza sativa	putative DNA binding protein RAV2. P0480E02.24.
AAK01088.1	AF298230	Hordeum vulgare	CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
AAG59619.1	AF243384	Oryza sativa	CRT/DRE binding factor. CBF. DREB.
BAB21211.1	AP002913	Oryza sativa	putative DNA binding protein RAV2. P0480E02.17.
AAK01089.1	AF298231	Hordeum vulgare	CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.
SEQ ID NO: 111			
AAF87216.1	AF231351	Nicotiana tabacum	plastidic glucose 6-phosphate dehydrogenase. G6PDHP2.
CAA67782.1	X99405	Nicotiana tabacum	glucose-6-phosphate dehydrogenase. G6PD.
AAB69317.1	AF012861	Petroselinum crispum	plastidic glucose-6-phosphate dehydrogenase. pG6PDH.
CAB52708.1	AJ010712	Solanum tuberosum	glucose-6-phosphate 1-dehydrogenase. g6pd.

CAB52685.1	AJ132346	Dunaliella bioculata	plastidic glucose-6-phosphate dehydrogenase. g6PD.
CAA04994.1	AJ001772	Nicotiana tabacum	glucose-6-phosphate dehydrogenase. TCG18.
CAA58775.1	X83923	Solanum tuberosum	glucose-6-phosphate dehydrogenase.
CAA03941.1	AJ000184	Spinacia oleracea	Glucose-6-phosphate dehydrogenase. G6PD.
CAA03939.1	AJ000182	Spinacia oleracea	Glucose-6-phosphate dehydrogenase. G6PD.
CAA03940.1	AJ000183	Spinacia oleracea	Glucose-6-phosphate dehydrogenase. G6PD.
AAB41552.1	U18238	Medicago sativa subsp. sativa	glucose-6-phosphate dehydrogenase.
AAD11426.1	AF097663	Mesembryanthemum crystallinum	cytoplasmic glucose-6-phosphate 1-dehydrogenase. G6PD.
AAB69319.1	AF012863	Petroselinum crispum	cytosolic glucose-6-phosphate dehydrogenase 2. cG6PDH2.
CAA52442.1	X74421	Solanum tuberosum	glucose-6-phosphate 1-dehydrogenase. g6pdh. homotetramer.
AAB69318.1	AF012862	Petroselinum crispum	cytosolic glucose-6-phosphate dehydrogenase 1. cG6PDH1.
BAA97662.1	AB029454	Triticum aestivum	glucose-6-phosphate dehydrogenase. g6pdh.
BAA97663.1	AB029455	Triticum aestivum	glucose-6-phosphate dehydrogenase. g6pdh.
CAA04993.1	AJ001770	Nicotiana tabacum	glucose-6-phosphate dehydrogenase. TCG9.
CAA04992.1	AJ001769	Nicotiana tabacum	glucose-6-phosphate dehydrogenase. TCG6.
BAA97664.1	AB029456	Triticum aestivum	glucose-6-phosphate dehydrogenase. g6pdh.
AAG23802.1	AF260736	Cucurbita pepo	plastidic glucose-6-phosphate dehydrogenase.
CAB66330.1	AJ279688	Betula pendula	glucose-6-phosphate dehydrogenase. g6pd.
BAA82155.1	AB011441	Triticum aestivum	glucose-6-phosphate dehydrogenase. WESR5. salt-stress responding gene.
CAA06200.1	AJ004900	Glycine max	pentose phosphate pathway oxidoreductase generating NADPH. glucose-6-phosphate-dehydrogenase.

SEQ ID NO: 112

CAA48611.1	X68652	Raphanus sativus	hydroxymethylglutaryl-CoA reductase (NADPH). HMG2.
CAA48610.1	X68651	Raphanus sativus	hydroxymethylglutaryl-CoA reductase (NADPH). HMG1.
AAC05089.1	AF038046	Gossypium hirsutum	catalyzes the synthesis of mevalonate from hmg-coA. 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2. hmg2. hmg-coA reductase 2; HMGR2.
AAA33108.1	M96068	Catharanthus roseus	hydroxymethylglutaryl-CoA reductase. HMGR.
BAA36291.1	AB021862	Cucumis melo	HMG-CoA reductase. Cm-HMGR. putative.
AAB52551.1	U51985	Solanum tuberosum	HMG-CoA reductase.
AAA93498.1	L01400	Solanum tuberosum	convert HMG-CoA into mevalonate. hydroxymethylglutaryl coenzyme A reductase. hmgr. putative.
AAB87727.1	U60452	Nicotiana tabacum	hydroxy-methylglutaryl-coenzyme A reductase. HMGR1.
CAA70440.1	Y09238	Zea mays	3-hydroxy-3-methylglutaryl coenzyme A reductase.
CAA45181.1	X63649	Nicotiana glauca	catalyzes synthesis of mevalonate. 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR. endoplasmic reticulum location.
AAD28179.1	AF110383	Capsicum annuum	3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR2M. HMGR.
AAB52552.1	U51986	Solanum tuberosum	HMG-CoA reductase.
BAA93631.1	AB022690	Solanum tuberosum	3-hydroxy-3-methylglutaryl coenzyme A reductase. HMG3.
AAB62581.1	U68072	Lycopersicon esculentum	3-hydroxy-3-methylglutaryl CoA reductase 2. HMG2.
AAB69726.1	U72145	Camptotheca acuminata	converts HMGC CoA to mevalonate. 3-hydroxy-3-methylglutaryl coenzyme a reductase. hmg3. HMGR.
AAB53748.1	U95816	Oryza sativa	3-hydroxy-3-methylglutaryl-CoA reductase. HMGR.
BAB20771.1	AB041031	Solanum tuberosum	3-hydroxy-3-methylglutaryl coenzyme A reductase. HMG2.
AAB69727.1	U72146	Camptotheca acuminata	3-hydroxy-3-methylglutaryl coenzyme A reductase. converts HMGC CoA in mevalonate precursor for isoprenoid compounds; HMGR; hmg2; similar to protein encoded by GenBank Accession Number L10390.

AAD47596.1	AF142473	Artemisia annua	HMG-CoA reductase. HMGR1.
AAA34169.1	M63642	Lycopersicon esculentum	3-hydroxy-3-methylglutaryl coenzyme A reductase. hmg2.
AAA68966.1	U14625	Artemisia annua	3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM4.
AAA33358.1	M74798	Hevea brasiliensis	3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
AAA68965.1	U14624	Artemisia annua	3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM1.
AAD08820.1	U43961	Oryza sativa	3-hydroxy-3-methylglutaryl-CoA reductase. HMGR.
AAA33360.1	M74800	Hevea brasiliensis	3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
CAA92821.1	Z68504	Oryza sativa	3-hydroxy-3-methylglutaryl-CoA reductase.
AAC05088.1	AF038045	Gossypium hirsutum	catalyzes the synthesis of mevalonate from hmg-coA. 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1. hmg1. hmg-coA reductase 1; HMGR1.
AAC15475.1	AF034760	Tagetes erecta	3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAC15476.1	AF034761	Tagetes erecta	3-hydroxy-3-methylglutaryl coenzyme A reductase.
CAA38469.1	X54659	Hevea brasiliensis	hydroxymethylglutaryl-CoA reductase. HMGR1.
CAA38467.1	X54657	Hevea brasiliensis	hydroxymethylglutaryl-CoA reductase. HMGR1.
AAD38873.1	AF110382	Oryza sativa	3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR3G. HMG-CoA reductase.
AAA33040.1	L10390	Camptotheca acuminata	3-hydroxy-3-methylglutaryl coA reductase.
AAD03789.1	U43711	Morus alba	catalyzes the final step in mevalonate pathway. 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR.
AAA21720.1	L28995	Oryza sativa	conversion of hydroxymethylglutaryl coenzyme A to mevalonate. 3-hydroxy-3-methylglutaryl coenzyme A reductase. putative.
AAC72378.1	AF096838	Solanum tuberosum	3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAB04043.1	L40938	Lycopersicon esculentum	HMGR CoA reductase. HMGR1.
CAA38468.1	X54658	Hevea brasiliensis	hydroxymethylglutaryl-CoA reductase. HMGR2.

CAA52787.1 X74783 *Lithospermum erythrorhizon*
3-hydroxy-3-methyl glutaryl coenzyme A reductase. Lehmgr1.

AAD09278.1 U97683 *Glycine max*
catalyzes the synthesis of mevalonate, the specific precursor of all isoprenoid compounds present in plants. 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMG-CoA reductase.

AAG43469.1 AF196964 *Bixa orellana*
catalyzes mevalonate synthesis from hmg-CoA. 3-hydroxy-3-methylglutaryl-coenzyme A reductase.

BAA09705.1 D63389 *Cucumis sativus*
3-hydroxy-3-methylglutaryl CoA reductase.

AAB47161.1 S82272 *Gossypium barbadense*
3-hydroxy-3-methylglutaryl coenzyme A reductase. /gene="3-hydroxy-3-methylglutaryl coenzyme A reductase,. This sequence comes from Fig. 2; 3-hydroxy-3-methylglutaryl CoA reductase; HMGR.

AAA33359.1 M74799 *Hevea brasiliensis*
3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmg3.

AAC37432.1 L34825 *Solanum tuberosum*
HMG-CoA reductase. hmg1 gene family.

AAC37434.1 L34827 *Solanum tuberosum*
HMG-CoA reductase. hmg1 gene family.

AAC37431.1 L34823 *Solanum tuberosum*
HMG-CoA reductase. hmg1 gene family.

AAC37433.1 L34826 *Solanum tuberosum*
HMG-CoA reductase. hmg1 gene family.

AAC37435.1 L34828 *Solanum tuberosum*
HMG-CoA reductase. hmg1 gene family.

AAC37436.1 L34829 *Solanum tuberosum*
HMG-CoA reductase. hmg1 gene family.

SEQ ID NO: 113

AAC49676.1 U77345 *Zea mays*
lethal leaf-spot 1. lls1. Allele: wild-type; LLS1; similar to bacterial ring-hydroxylating dioxygenase.

AAG03051.1 AF284781 *Oryza sativa*
LLS1 protein. Lls1.

SEQ ID NO: 115

BAA82379.1 AP000367 *Oryza sativa*
Similar to putative receptor kinase. (AC002332).

BAA87853.1 AP000816 *Oryza sativa*
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

AAG25966.1 AF302082 *Nicotiana tabacum*
cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.

BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAC27894.1	AF023164	Zea mays	leucine-rich repeat transmembrane protein kinase 1. ltk1.
AAC27895.1	AF023165	Zea mays	leucine-rich repeat transmembrane protein kinase 2. ltk2.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.

BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
CAA47962.1	X67733	Zea mays	receptor-like protein kinase. PK1.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
AAB09771.1	U67422	Zea mays	CRINKLY4 precursor. cr4. receptor kinase homolog.
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
BAA06538.1	D31737	Nicotiana tabacum	protein-serine/threonine kinase.
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
CAB51480.1	Y14600	Sorghum bicolor	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
BAA87852.1	AP000816	Oryza sativa	Similar to putative Ser/Thr protein kinase. (AC004218).
BAA92221.1	AP001278	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
BAA78764.1	AB023482	Oryza sativa	ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.

AAB47422.1 U59318 *Lycopersicon esculentum*
serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.

BAA21132.1 D88193 *Brassica rapa*
S-receptor kinase. SRK9 (B.c).

SEQ ID NO: 117

AAA34002.1 M67449 *Glycine max*
protein kinase. PK6.

AAG31141.1 AF305911 *Oryza sativa*
EDR1. EDR1. MAP kinase kinase kinase; similar to *Arabidopsis thaliana* EDR1.

AAG31142.1 AF305912 *Hordeum vulgare*
EDR1. EDR1. MAP kinase kinase kinase; similar to *Arabidopsis thaliana* EDR1.

CAC09580.1 AJ298992 *Fagus sylvatica*
Absciscic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.

CAA06334.1 AJ005077 *Lycopersicon esculentum*
protein kinase. TCTR2 protein. TCTR2.

AAD10057.1 AF110519 *Lycopersicon esculentum*
ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.

AAD10056.1 AF110518 *Lycopersicon esculentum*
ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.

AAD46406.1 AF096250 *Lycopersicon esculentum*
ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to *Arabidopsis thaliana* negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.

CAA73722.1 Y13273 *Lycopersicon esculentum*
putative protein kinase.

AAK11734.1 AY027437 *Arachis hypogaea*
serine/threonine/tyrosine kinase.

AAK30005.1 AY029067 *Rosa hybrid cultivar*
CTR2 protein kinase.

AAF66615.1 AF142596 *Nicotiana tabacum*
LRR receptor-like protein kinase.

CAA73068.1 Y12465 *Sorghum bicolor*
serine/threonine kinase. SNFL2.

CAA61510.1 X89226 *Oryza sativa*
leucine-rich repeat/receptor protein kinase. lrk2.

BAA83688.1 AB011967 *Oryza sativa*
OsPK4. OsPK4. protein kinase.

AAF34436.1 AF172282 *Oryza sativa*
similar to mitogen-activated protein kinases. DUPR11.32.

AAF22219.1 AF141378 *Zea mays*
protein kinase PK4. ZmPK4.

BAA87852.1	AP000816	Oryza sativa	Similar to putative Ser/Thr protein kinase. (AC004218).
BAA92221.1	AP001278	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
AAF91323.1	AF244889	Glycine max	receptor-like protein kinase 2. RLK2. GmRLK2.
BAB40094.1	AP003210	Oryza sativa	putative receptor protein kinase. OSJNBa0010K01.7.
AAF91324.1	AF244890	Glycine max	receptor-like protein kinase 3. RLK3. GmRLK3.
BAA34675.1	AB011670	Triticum aestivum	wpk4 protein kinase. wpk4.
BAA92970.1	AP001551	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4 BAC clone F28A21 ; putative protein kinase. (AL035526).
AAF91322.1	AF244888	Glycine max	receptor-like protein kinase 1. RLK1. GmRLK1.
BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
CAA73067.1	Y12464	Sorghum bicolor	serine/threonine kinase. SNFL1.
AAF59906.1	AF197947	Glycine max	receptor protein kinase-like protein. CLV1B.
AAF59905.1	AF197946	Glycine max	receptor protein kinase-like protein. CLV1A.
BAB16918.1	AP002863	Oryza sativa	putative protein kinase. P0005A05.22.
AAC36318.1	AF053127	Malus x domestica	leucine-rich receptor-like protein kinase. LRPKml.
BAA83689.1	AB011968	Oryza sativa	OsPK7. OsPK7. protein kinase.
CAA74646.1	Y14274	Sorghum bicolor	putative serine/threonine protein kinase. SNFL3.
BAA95893.1	AP002071	Oryza sativa	Similar to Arabidopsis thaliana wak4 gene; wall-associated kinase 4. (AJ009695).
BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
AAC83393.1	U83625	Zea mays	protein kinase ZmMEK1. mitogen-activated; ERK-activating protein kinase (MEK) homolog.

BAA92972.1 AP001551 *Oryza sativa*
ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene.
Similar to *Arabidopsis thaliana* chromosome 4 BAC clone F6I18 ; putative protein kinase.
(AL022198).

BAB18292.1 AP002860 *Oryza sativa*
putative receptor-like protein kinase. P0409B08.19.

BAB40015.1 AP003021 *Oryza sativa*
putative wall-associated kinase 1. P0503E05.18.

BAA05648.1 D26601 *Nicotiana tabacum*
protein kinase.

AAC27489.1 AF077130 *Oryza sativa*
receptor-like protein kinase.

AAC02535.1 AF044260 *Oryza sativa*
receptor serine/threonine kinase. protein kinase.

AAG40578.1 AF216314 *Oryza sativa*
MAP kinase kinase 1. protein kinase; MEK1.

CAA08997.1 AJ010093 *Brassica napus*
MAP3K beta 1 protein kinase. MAP3K beta 1.

SEQ ID NO: 118

AAD21199.1 AF127797 *Capsicum chinense*
putative bZIP DNA-binding protein.

CAC00658.1 AJ292745 *Petroselinum crispum*
bZIP type transcription factor. common plant regulatory factor 7. cprf7.

CAC00657.1 AJ292744 *Petroselinum crispum*
bZIP type transcription factor. common plant regulatory factor 6. cprf6.

CAA74023.1 Y13676 *Antirrhinum majus*
bZIP DNA-binding protein.

CAA74022.1 Y13675 *Antirrhinum majus*
bZIP DNA-binding protein.

BAA22204.1 D63951 *Nicotiana tabacum*
TBZ17. tbz17. bZIP protein.

AAD55394.1 AF176641 *Lycopersicon esculentum*
bZIP DNA-binding protein.

CAA44607.1 X62745 *Zea mays*
ocs-binding factor 1. OBF1.

AAK25822.1 AF350505 *Phaseolus vulgaris*
bZip transcription factor.

AAK01953.1 AY026054 *Phaseolus acutifolius*
bZIP. transcription factor.

CAA71687.1 Y10685 *Glycine max*
bZIP DNA-binding protein. G/HBF-1. G/HBF-1.

AAC37418.1 L34551 *Oryza sativa*
transcriptional activator protein. RITA-1.

BAA36492.1	AB021736	Oryza sativa	bZIP protein.
BAA11431.1	D78609	Oryza sativa	bZIP protein.
CAA41453.1	X58577	Petroselinum crispum	DNA-binding protein; bZIP type. CPRF2.
CAA71768.1	Y10809	Petroselinum crispum	bZIP DNA-binding protein. CPRF4a.
AAD42938.1	AF084972	Catharanthus roseus	G-Box binding protein 2. GBF2. basic leucine zipper; trans-regulatory factor.
AAC49556.1	U04295	Oryza sativa	DNA-binding factor of bZIP class. osZIP-1a.
BAA07289.1	D38111	Triticum aestivum	transcription factor HBP-1a(17).
CAA71795.1	Y10834	Hordeum vulgare	bZIP transcription factor 2. Blz2.
CAA70216.1	Y09013	Triticum aestivum	transcriptional activator. SPA.
CAA40101.1	X56781	Triticum aestivum	transcription factor. HBP-1a. la-17.
AAA80169.1	U10270	Zea mays	G-box binding factor 1. GBF1.
CAA11499.1	AJ223624	Spinacia oleracea	basic leucine zipper protein. bZIP.
AAC49474.1	U41817	Phaseolus vulgaris	regulator of MAT2. ROM2. Repressor of seed-specific lectin (phytohemagglutinin) gene; bZIP transcriptional repressor.
AAB40291.1	U42208	Oryza sativa	OSBZ8. G-box binding protein; GBF type bZIP protein.
BAA02304.1	D12920	Triticum aestivum	transcription factor HBP-1a(c14).
SEQ ID NO: 119			
BAA96200.1	AP002093	Oryza sativa	EST D40368(S2303) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome II putative cytochrome P450 (AC004077).
BAA96158.1	AP002092	Oryza sativa	EST D40368(S2303) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome II BAC T31E10; putative cytochrome P450 (AC004077).
BAA96196.1	AP002093	Oryza sativa	ESTs AU086027(S2303),D40339(S2251) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome II BAC T31E10; putative cytochrome P450 (AC004077).

BAA96154.1	AP002092	Oryza sativa	ESTs AU086027(S2303),D40339(S2251) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome II BAC T31E10; putative cytochrome P450 (AC004077).
BAA96193.1	AP002093	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC T31E10; putative cytochrome P450 (AC004077).
BAA96151.1	AP002092	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC T31E10; putative cytochrome P450 (AC004077).
BAA96194.1	AP002093	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC T31E10; putative cytochrome P450 (AC004077).
BAA96152.1	AP002092	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC T31E10; putative cytochrome P450 (AC004077).
AAG41777.1	AF212991	Cucurbita maxima	ent-kaurene oxidase. CYP88A2. cytochrome P450; similar to maize Dwarf3 protein.
AAK11616.1	AF326277	Hordeum vulgare	ent-kaurenoic acid oxidase. KAO1. cytochrome P450; CYP88A; HvKAO1.
AAK00946.1	AF318211	Taxus cuspidata	5-alpha-taxadienol-10-beta-hydroxylase. cytochrome P450-like protein.
AAC49659.1	U74319	Sorghum bicolor	obtusifolios 14-alpha demethylase CYP51. CYP51. cytochrome P450 catalyzing the 14-alpha demethylation of obtusifolios in plants.
AAA17746.1	L19075	Catharanthus roseus	cytochrome P450. CYP72C. putative.
AAA33106.1	L10081	Catharanthus roseus	cytochrome P-450 protein. CYP72. putative; CYP72 protein.
AAA17732.1	L19074	Catharanthus roseus	cytochrome P450. CYP72B.
CAB56503.1	AJ238612	Catharanthus roseus	cytochrome P450.
AAB17070.1	U54770	Lycopersicon esculentum	cytochrome P450 homolog. dwarf.
CAB41490.1	AJ238439	Cicer arietinum	cytochrome P450 monooxygenase. cyp81E3v2.
BAB19089.1	AP002744	Oryza sativa	putative cytochrome P450. P0006C01.31. contains ESTs D24685(R2374),AU031882(R2374).
AAD44150.1	AF124815	Mentha spicata	cytochrome p450.
BAB19110.1	AP002839	Oryza sativa	putative cytochrome P450. P0688A04.16. contains ESTs D24685(R2374),AU031882(R2374).

BAA74465.1	AB022732	Glycyrrhiza echinata cytochrome P450. CYP Ge-31.
BAA22422.1	AB001379	Glycyrrhiza echinata cytochrome P450. CYP81E1.
CAA10067.1	AJ012581	Cicer arietinum cytochrome P450. cyp81E3.
BAB40322.1	AB036772	Triticum aestivum cytochrome P450. N-1.
CAB43505.1	AJ239051	Cicer arietinum cytochrome P450. cyp81E2.
CAB56742.1	AJ249800	Cicer arietinum cytochrome P450 monooxygenase. cyp81E5.
AAF89209.1	AF279252	Vigna radiata cytochrome P450. CipCYP.
BAA93634.1	AB025016	Lotus japonicus cytochrome P450.
BAB19107.1	AP002839	Oryza sativa putative cytochrome P450. P0688A04.13. contains ESTs AU100635(C10787),D22354(C10787).
BAB19086.1	AP002744	Oryza sativa putative cytochrome P450. P0006C01.28. contains ESTs AU100635(C10787),D22354(C10787).
CAA04116.1	AJ000477	Helianthus tuberosus fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
CAA04117.1	AJ000478	Helianthus tuberosus fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l. chimeric sequence (from 5'- race).
CAA71517.1	Y10493	Glycine max putative cytochrome P450.
BAB21156.1	AP002899	Oryza sativa putative cytochrome P450. P0456A01.12.
AAG13498.1	AC068924	Oryza sativa putative cytochrome P450. OSJNBa0026L12.20.
AAF34534.1	AF195813	Lupinus albus isoflavone synthase 1. ifsl. cytochrome P450.
CAA83941.1	Z33875	Mentha x piperita cytochrome P-450 oxidase.
AAF34533.1	AF195812	Pisum sativum isoflavone synthase 1. ifsl. cytochrome P450.
AAF45142.1	AF195818	Glycine max isoflavone synthase 1. ifsl. cytochrome P450.

SEQ ID NO: 120

CAB42052.1 AJ242045 *Lycopersicon esculentum*
nicotianamine synthase. chln.

BAA74581.1 AB011264 *Hordeum vulgare*
nicochianamine synthase 3. hvnas3.

AAD32651.1 AF136942 *Hordeum vulgare*
nicotianamine synthase 2. nashor2.

BAA74582.1 AB011265 *Hordeum vulgare*
nicochianamine synthase 2. hvnas2.

BAB17824.1 AB023819 *Oryza sativa*
nicotianamine synthase 3. osnas3.

AAD32650.1 AF136941 *Hordeum vulgare*
nicotianamine synthase 1. nashor1.

BAA74583.1 AB011266 *Hordeum vulgare*
nicotianamine Synthase 4. hvnas4.

BAA74586.1 AB011269 *Hordeum vulgare*
nicotianamine Synthase 6. hvnas6.

BAA74587.1 AB019525 *Hordeum vulgare*
nicotianamine synthase 7. hvnas7.

BAB17826.1 AB046401 *Oryza sativa*
nicotianamine synthase 2. OsNAS2.

BAB17823.1 AB023818 *Oryza sativa*
nicotianamine synthase 2. osnas2.

BAB17825.1 AB046401 *Oryza sativa*
nicotianamine synthase 1. OsNAS1.

BAA74588.2 AB021746 *Oryza sativa*
nicotianamine synthase 1. osnas1.

BAA74580.1 AB010086 *Hordeum vulgare*
nicotianamine synthase 1. hvnas1.

BAA74585.1 AB011268 *Hordeum vulgare*
nicotianamine Synthase 5-2. hvnas5-2.

BAA74584.1 AB011267 *Hordeum vulgare*
nicotianamine synthase 5-1. hvnas5-1.

SEQ ID NO: 122

AAD01804.1 AF026480 *Dianthus caryophyllus*
lipase. lipid-protein-particle associated.

BAB39417.1 AP002901 *Oryza sativa*
putative lipase. P0456F08.17. contains ESTs
C99390(E11001),AU101109(E0858),AU101332(E11001).

AAB07724.1 U55867 *Ipomoea nil*
Pn47p. lipase-like protein.

AAK31273.1 AC079890 *Oryza sativa*
putative lipase. OSJNBb0089A17.13.

SEQ ID NO: 123

BAA21923.1	AB006601	Petunia x hybrida
ZPT2-14.	C2H2 zinc finger protein,	2 finger.
BAA21922.1	AB006600	Petunia x hybrida
ZPT2-13.	C2H2 zinc finger protein,	2finger.
BAA21921.1	AB006599	Petunia x hybrida
ZPT2-12.	C2H2 zinc finger protein,	2 finger.
BAA19110.1	AB000451	Petunia x hybrida
PETHy;ZPT2-5.	Cys(2) His(2) zinc finger protein,	2 fingers.
BAA21926.1	AB006604	Petunia x hybrida
ZPT2-9.	C2H2 zinc finger protein,	2 finger.
BAA21925.1	AB006603	Petunia x hybrida
ZPT2-8.	C2H2 zinc finger protein,	2 finger.
BAA21924.1	AB006602	Petunia x hybrida
ZPT2-7.	C2H2 zinc finger protein,	2finger.
BAA21920.1	AB006598	Petunia x hybrida
ZPT2-11.	C2H2 zinc finger protein,	2finger.
CAA60828.1	X87374	Pisum sativum
putative zinc finger protein.		
BAA19111.1	AB000452	Petunia x hybrida
PETHy;ZPT2-6.	Cys(2) His(2) zinc finger protein,	2 fingers.
CAB77055.1	Y18788	Medicago sativa
putative TFIIIA (or kruppel)-like zinc finger protein.		
BAA96071.1	AB035133	Petunia x hybrida
C2H2 zinc-finger protein ZPT3-3.	ZPT3-3.	
BAA21927.1	AB006605	Petunia x hybrida
ZPT3-3.	C2H2 zinc finger protein,	3 finger.
BAA96070.1	AB035132	Petunia x hybrida
C2H2 zinc-finger protein ZPT2-10.	PETHy;ZPT2-10.	
BAA21919.1	AB006597	Petunia x hybrida
ZPT2-10.	C2H2 zinc finger protein,	2 finger.
AAK01713.1	AF332876	Oryza sativa
zinc finger transcription factor ZF1.		
AAC06243.1	AF053077	Nicotiana tabacum
transcription factor. osmotic stress-induced zinc-finger protein.	zfp.	
BAA05079.1	D26086	Petunia x hybrida
zinc-finger protein.		
BAA05078.1	D26085	Petunia x hybrida
zinc-finger DNA binding protein.		
AAB39638.1	U68763	Glycine max
putative transcription factor. SCOF-1. scof-1. zinc-finger protein.		
BAA05076.1	D26083	Petunia x hybrida
zinc-finger DNA binding protein.		

BAA05077.1	D26084	Petunia x hybrida	zinc-finger DNA binding protein.
BAA21928.1	AB006606	Petunia x hybrida	ZPT4-4. C2H2 zinc finger protein, 4 finger.
BAA19114.1	AB000455	Petunia x hybrida	PETHy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.
AAD26942.1	AF119050	Datisca glomerata	zinc-finger protein 1. zfp1. DgZFP1.
BAA19112.1	AB000453	Petunia x hybrida	PETHy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.
AAB53260.1	U76554	Brassica rapa	transcription factor. zinc-finger protein-1. BR42.
AAB53261.1	U76555	Brassica rapa	zinc-finger protein BcZFP1. BcZFP1(3-2z).
BAA19926.1	AB000456	Petunia x hybrida	PETHy; ZPT4-2. C2H2 zinc finger protein, 4 finger.
SEQ ID NO: 126			
CAA10134.1	AJ012693	Cicer arietinum	basic blue copper protein.
CAB65280.1	AJ248323	Medicago sativa subsp. x varia	basic blue protein. babl.
AAC32448.1	U76296	Spinacia oleracea	plantacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Plantacyanins; non-glycosylated.
AAF66243.1	AF243181	Lycopersicon esculentum	plantacyanin. naturally occurring cupredoxin with a Val residue in the position of the axial ligand Met; member of the plantacyanin subfamily of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins.
AAD10251.1	AF031195	Triticum aestivum	blue copper-binding protein homolog. S85.
AAF66242.1	AF243180	Lycopersicon esculentum	dicyanin. binuclear blue copper protein; contains two stellacyanins linked together.
CAA80963.1	Z25471	Pisum sativum	blue copper protein.
AAC64163.1	AF093537	Zea mays	blue copper protein. similar to pea blue copper protein in GenBank Accession Number Z25471.

AAC32421.1 U65511 *Cucumis sativus*
 putative oxygen activation and/or lignin formation. stellacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Stellacyanins; similar to *Rhus vernicifera* stellacyanin: SwissProt Accession Number P00302; similar to umecyanin: SwissProt Accession Number P42849; similar to mavicyanin; SwissProt Accession Number P80728; similar to BCB encoded by GenBank Accession Number Z15058; similar to F18A8.9, encoded by GenBank Accession Number AC003105; similar to F7F1.27 encoded by GenBank Accession Number AC004669; similar to F9D12.16 encoded by GenBank Accession Number AF077407; glycoprotein.

SEQ ID NO: 127

AAA17000.1 L08632 *Glycine max*
 pyruvate kinase.

CAA37727.1 X53688 *Solanum tuberosum*
 pyruvate kinase.

CAA82628.1 Z29492 *Nicotiana tabacum*
 glycolytic enzyme. pyruvate kinase.

AAF44707.1 AF242871 *Lilium longiflorum*
 cytosolic pyruvate kinase.

BAA88185.1 AP000836 *Oryza sativa*
 ESTs AU081247(C50004), AU068940(C51113) correspond to a region of the predicted gene. Similar to pyruvate kinase (Q42954).

BAA76433.1 AB025005 *Cicer arietinum*
 pyruvate kinase.

CAA49996.1 X70653 *Nicotiana tabacum*
 pyruvate kinase. PKTL7. monomer.

CAA82223.1 Z28374 *Nicotiana tabacum*
 glycolytic enzyme. Pyruvate kinase; plastid isozyme.

CAA82222.1 Z28373 *Nicotiana tabacum*
 Glycolytic enzyme. pyruvate kinase; plastid isozyme.

AAA33871.1 M64737 *Ricinus communis*
 ATP:pyruvate phosphotransferase.

AAA33870.1 M64736 *Ricinus communis*
 ATP:pyruvate phosphotransferase.

SEQ ID NO: 129

BAB12433.1 AB025030 *Coptis japonica*
 p450.

AAF05621.1 AF191772 *Papaver somniferum*
 hydroxylase involved in benzylisoquinoline alkaloid biosynthesis. (S)-N-methylcoclaurine 3'-hydroxylase. CYP80B1. cytochrome P450-dependent monooxygenase.

AAC39452.1	AF014800	<i>Eschscholzia californica</i> hydroxylase involved in the biosynthesis of tetrahydrobenzylisoquinoline alkaloids in plants. (S)-N-methylcoclaaurine 3'-hydroxylase. CYP80B1. cytochrome P-450-dependent monooxygenase; CYP80B1v1.
AAC39453.1	AF014801	<i>Eschscholzia californica</i> hydroxylase involved in the biosynthesis of tetrahydrobenzylisoquinoline alkaloids in plants. (S)-N-methylcoclaaurine 3'-hydroxylase. CYP80B1. cytochrome P-450-dependent monooxygenase; CYP80B1v2.
AAA32913.1	M32885	<i>Persea americana</i> cytochrome P-450LXXIA1 (cyp71A1).
AAA19701.1	L24438	<i>Thlaspi arvense</i> cytochrome P450.
CAA50648.1	X71657	<i>Solanum melongena</i> P450 hydroxylase.
AAG34695.1	AF313492	<i>Matthiola incana</i> putative cytochrome P450.
AAG44132.1	AF218296	<i>Pisum sativum</i> cytochrome P450. P450 isolog.
BAA12159.1	D83968	<i>Glycine max</i> Cytochrome P-450 (CYP93A1).
AAC48987.1	U09610	<i>Berberis stolonifera</i> cytochrome P-450 CYP80.
AAD56282.1	AF155332	<i>Petunia x hybrida</i> flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
AAC32274.1	AF081575	<i>Petunia x hybrida</i> flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.
AAB17562.1	U72654	<i>Eustoma grandiflorum</i> flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
BAA84916.1	AB032833	<i>Cicer arietinum</i> cytochrome P450. CYP76D1.
AAB94588.1	AF022459	<i>Glycine max</i> CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
BAB40324.1	AB037245	<i>Asparagus officinalis</i> cytochrome P450. ASPI-2.
BAB40323.1	AB037244	<i>Asparagus officinalis</i> cytochrome P450. ASPI-1.
CAA50155.1	X70824	<i>Solanum melongena</i> flavonoid hydroxylase (P450). CYP75.
AAC39318.1	AF029858	<i>Sorghum bicolor</i> second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p- hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.

CAB56503.1	AJ238612	Catharanthus roseus cytochrome P450.
CAA71514.1	Y10490	Glycine max putative cytochrome P450.
BAA84071.1	AB028151	Antirrhinum majus flavone synthase II. cytochrome P450. AFNS2.
CAA70575.1	Y09423	Nepeta racemosa cytochrome P450. CYP71A5.
CAA70576.1	Y09424	Nepeta racemosa cytochrome P450. CYP71A6.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
BAA84072.1	AB028152	Torenia hybrida flavone synthase II. cytochrome P450. TFNS5.
CAA71516.1	Y10492	Glycine max putative cytochrome P450.
BAA13076.1	D86351	Glycine max cytochrome P-450 (CYP93A2).
CAA71517.1	Y10493	Glycine max putative cytochrome P450.
SEQ ID NO: 132		
CAB55396.1	AL117264	Oryza sativa zwh12.1. similar to Arabidopsis putative UDP-galactase-4-epimerase (AC007060); Method: conceptual translation with partial peptide sequencing.
SEQ ID NO: 133		
AAG43835.1	AF213455	Zea mays protein phosphatase type-2C. pp2c-1. PP2C-1.
AAG13599.1	AC051633	Oryza sativa putative protein phosphatase-2C. OSJNBb0015I11.26.
AAG46118.1	AC073166	Oryza sativa putative protein phosphatase-2C. OSJNBb0064P21.12. tRNA-Lys.
BAB12036.1	AP002820	Oryza sativa putative protein phosphatase. P0702D12.18.
AAC36698.1	AF075580	Meisembryanthemum crystallinum protein phosphatase-2C. PP2C.
CAC10359.1	AJ277087	Nicotiana tabacum protein phosphatase 2C. PP2C2.
CAB90633.1	AJ277743	Fagus sylvatica protein phosphatase 2C (PP2C). pp2C1. ABA-induced protein.
CAC10358.1	AJ277086	Nicotiana tabacum protein phosphatase 2C. PP2C1.
CAA72341.1	Y11607	Medicago sativa protein phosphatase 2C. MP2C.

AAC36697.1	AF075579	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
CAB61839.1	AJ242803	Sporobolus stapfianus putative serine/threonine phosphatase type 2c.
AAC36700.1	AF075582	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
AAD17804.1	AF092431	Lotus japonicus nodule-enhanced protein phosphatase type 2C. NPP2C1.
AAD17805.1	AF092432	Lotus japonicus protein phosphatase type 2C. PP2C2.
CAC09575.1	AJ298987	Fagus sylvatica protein phosphatase 2C (PP2C). pp2Cf1.
AAC36699.1	AF075581	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
AAD11430.1	AF097667	Mesembryanthemum crystallinum protein phosphatase 2C homolog. PP2C.
CAB90634.1	AJ277744	Fagus sylvatica protein phosphatase 2C (PP2C). pp2C2. ABA and calcium induced protein.
AAC26828.1	AF075603	Oryza sativa kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases. kinase associated protein phosphatase. kapp. type 2C protein phosphatase.
AAC35951.1	AF079355	Mesembryanthemum crystallinum protein phosphatase-2c. PP2C.
AAK20060.1	AC025783	Oryza sativa putative protein phosphatase 2C. OSJNBa0001O14.1.
AAB93832.1	U81960	Zea mays kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases; type 2C protein phosphatase. kinase associated protein phosphatase. KAPP.
CAC09576.1	AJ298988	Fagus sylvatica protein phosphatase 2C (PP2C). pp2Cf2.
SEQ ID NO: 134		
AAD26116.1	AF106954	Brassica napus galactinol synthase. GS. UDP-D-galactose:myo-inositol-D- galactosyltransferase.
CAB51130.1	AJ243815	Pisum sativum role in alpha galactoside synthesis. putative galactinol synthase.
CAB51533.1	AJ237693	Ajuga reptans galactosyl transfer from UDP-galactose to myo-inositol to form galactinol. galactinol synthase, isoform GolS-1. GolS.
CAB51534.1	AJ237694	Ajuga reptans galactosyl transfer from UDP-galactose to myo-inositol. galactinol synthase, isoform GolS-2. GolS.

AAD55726.1 AF178569 *Vitis riparia*
galactinol synthase. WSI76. water stress induced protein.

SEQ ID NO: 135

AAB57734.1 U64818 *Lycopersicon esculentum*
fructokinase. Frk2.

AAB51108.1 U62329 *Lycopersicon esculentum*
fructokinase. FK.

AAA80675.1 U37838 *Beta vulgaris*
fructokinase.

CAA78283.1 Z12823 *Solanum tuberosum*
fructokinase.

AAB57733.1 U64817 *Lycopersicon esculentum*
fructokinase. Frk1.

SEQ ID NO: 138

BAA94601.1 AB033504 *Populus euramericana*
1-aminocyclopropane-1-carboxylate oxidase. peaco-1.

AAA33697.1 L21978 *Petunia x hybrida*
1-aminocyclopropane-1-carboxylate oxidase. ACO3.

AAC48977.1 U07953 *Pelargonium x hortorum*
1-aminocyclopropane-1-carboxylate oxidase.

CAA54449.1 X77232 *Prunus persica*
1-aminocyclopropane-1-carboxylate oxidase. PAO1.

AAF36483.1 AF129073 *Prunus persica*
1-aminocyclopropane-1-carboxylate oxidase. ACO1.

AAC33524.1 AF026793 *Prunus armeniaca*
1-aminocyclopropane-1-carboxylate oxidase. ACC oxidase.

AAB70884.1 U67861 *Pelargonium x hortorum*
1-aminocyclopropane-1-carboxylate oxidase. GACO3.

AAG49361.1 AF321533 *Citrus sinensis*
ACC oxidase.

BAA90550.1 AB031027 *Prunus mume*
ACC oxidase. PM-ACO1. 1-aminocyclopropane-1-carboxylic acid oxidase.

AAA99792.1 U54565 *Nicotiana glutinosa*
oxidation of 1-aminocyclopropane-1-carboxylic acid. 1-aminocyclopropane-1-carboxylic acid
oxidase. NGACO1. ACC oxidase.

AAB05171.1 U62764 *Nicotiana glutinosa*
oxidation of 1-aminocyclopropane-1-carboxylic acid. ACC oxidase. NGACO3.

AAC37381.1 L21976 *Petunia x hybrida*
1-aminocyclopropane-1-carboxylate oxidase. ACO1.

CAA71738.1 Y10749 *Betula pendula*
1-aminocyclopropane-1-carboxylate oxidase. ACO.

CAA86468.1 Z46349 *Nicotiana tabacum*
1-aminocyclopropane-1-carboxylate deaminase.

BAA83466.1	AB012857	Nicotiana tabacum	ACC oxidase.
AAC98808.1	U68215	Carica papaya	ACC oxidase. fruit specific; ripening related.
BAA06526.1	D31727	Cucumis melo	1-aminocyclopropane-1-carboxylate oxidase.
CAA64797.1	X95551	Cucumis melo	ACC oxidase.
CAA58232.1	X83229	Nicotiana tabacum	ethylene forming enzyme. 1-aminocyclopropane-1-carboxylate oxidase.
BAA34924.1	AB013101	Lycopersicon esculentum	1-aminocyclopropane-1-carboxylate oxidase. LE-ACO4. ACC oxidase.
AAF64528.1	AF254125	Carica papaya	1-aminocyclopropane-1-carboxylate oxidase. ACC oxidase.
AAA33698.1	L21979	Petunia x hybrida	1-aminocyclopropane-1-carboxylate oxidase. ACO4.
CAA41212.1	X58273	Lycopersicon esculentum	conversion of ACC to ethylene. 1-Aminocyclopropane-1-carboxylic acid oxidase. LEACO1.
BAA21541.1	AB003514	Actinidia deliciosa	1-aminocyclopropane-1-carboxylic acid oxidase.
AAB71421.1	L29405	Helianthus annuus	1-aminocyclopropapne-1-carboxylic acid oxidase. ACC oxidase.
AAA99793.1	U54566	Nicotiana glutinosa	oxidation of 1-aminocyclopropane-1-carboxylic acid. 1-aminocyclopropane-1-carboxylic acid oxidase. NGACO2. ACC oxidase.
AAF36484.1	AF129074	Prunus persica	1-aminocyclopropane-1-carboxylate oxidase. ACO2.
CAA64799.1	X95553	Cucumis melo	ACC oxidase.
CAA90904.1	Z54199	Lycopersicon esculentum	catalyses the final step in ethylene biosynthesis. 1-aminocyclopropane-1-carboxylic acid oxidase. ACO3.
CAA68538.1	Y00478	Lycopersicon esculentum	conversion of ACC to ethylene. 1-aminocyclopropane-1-carboxylate oxidase. LEACO2.
CAB97173.1	AJ297435	Mangifera indica	ethene biosynthesis. putative 1-aminocyclopropane-1-carboxylic acid oxidase. acol.
CAA82646.1	Z29529	Nicotiana tabacum	oxidation of 1-aminocyclopropane-1-carboxylic acid. ethylene forming enzyme (EFE).
AAC12934.1	AF053354	Phaseolus vulgaris	1-aminocyclopropane-1-carboxylic acid oxidase. ACO1. ACC oxidase.
AAB70883.1	U19856	Pelargonium x hortorum	1-aminocyclopropane-1-carboxylate oxidase.

AAC67233.1	AF033582	Cucumis sativus	ACC oxidase 2. Cs-ACO2.
AAB02051.1	L76283	Carica papaya	formation of ethylene. 1-aminocyclopropane-1-carboxylate oxidase. putative.
BAA33377.1	AB006806	Cucumis sativus	ACC oxidase. CS-ACO1.
BAA33378.1	AB006807	Cucumis sativus	ACC oxidase. CS-ACO2.
CAA71140.1	Y10034	Rumex palustris	1-aminocyclopropane-1-carboxylic acid oxidase.
AAA33644.1	M98357	Pisum sativum	convert ACC to ethylene. 1-aminocyclopropane-1-carboxylate oxidase.
AAC48921.1	U06046	Vigna radiata	1-aminocyclopropane-1-carboxylate oxidase homolog.
AAK07883.1	AF315316	Vigna radiata	ACC oxidase. ACO.
AAA33273.1	L35152	Dianthus caryophyllus	amino-cyclopropane carboxylic acid oxidase.
CAA74328.1	Y14005	Malus x domestica	Converts ACC into ethylene in apple fruit. ACC oxidase.
SEQ ID NO: 139			
AAB65777.1	U97522	Vitis vinifera	class IV endochitinase. VvChi4B.
AAB65776.1	U97521	Vitis vinifera	class IV endochitinase. VvChi4A.
CAC17793.1	AJ301671	Nicotiana sylvestris	hydrolysis of chitin. endochitinase. chnb. class I chitinase.
AAA34070.1	M15173	Nicotiana tabacum	endochitinase precursor (EC 3.2.1.14).
CAA30142.1	X07130	Solanum tuberosum	endochitinase.
CAA53626.1	X76041	Triticum aestivum	endochitinase. CHI.
SEQ ID NO: 140			
AAB94587.1	AF022458	Glycine max	CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
BAA92894.1	AB006790	Petunia x hybrida	cytochrome P450. IMT-2.
AAD56282.1	AF155332	Petunia x hybrida	flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
AAG44132.1	AF218296	Pisum sativum	cytochrome P450. P450 isolog.

CAA65580.1	X96784	Nicotiana tabacum cytochrome P450. hsr515.
AAA32913.1	M32885	Persea americana cytochrome P-450LXXIA1 (cyp71A1).
CAA64635.1	X95342	Nicotiana tabacum cytochrome P450. hsr515. hypersensitivity-related gene.
CAA70575.1	Y09423	Nepeta racemosa cytochrome P450. CYP71A5.
BAB40323.1	AB037244	Asparagus officinalis cytochrome P450. ASPI-1.
BAB40324.1	AB037245	Asparagus officinalis cytochrome P450. ASPI-2.
CAA50312.1	X70981	Solanum melongena P450 hydroxylase. CYPEG2.
CAA50155.1	X70824	Solanum melongena flavonoid hydroxylase (P450). CYP75.
AAB17562.1	U72654	Eustoma grandiflorum flavonoid 3',5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
BAA84071.1	AB028151	Antirrhinum majus flavone synthase II. cytochrome P450. AFNS2.
AAC32274.1	AF081575	Petunia x hybrida flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.
AAG34695.1	AF313492	Matthiola incana putative cytochrome P450.
AAB94588.1	AF022459	Glycine max CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
AAD37433.1	AF150881	Lycopersicon esculentum x Lycopersicon peruvianum catalyzes the hydroxylation of ferulic acid to 5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome P450-dependent monooxygenase; F5H; FAH1.
CAA71517.1	Y10493	Glycine max putative cytochrome P450.
BAA13414.1	D87520	Glycyrrhiza echinata putative trans-cinnamic acid 4-hydroxylase. cytochrome P450 (CYP73A14). CYP Ge-1.
AAA19701.1	L24438	Thlaspi arvense cytochrome P450.
CAA50645.1	X71654	Solanum melongena P450 hydroxylase.
BAA03635.1	D14990	Solanum melongena Cytochrome P-450EG4.
BAA93634.1	AB025016	Lotus japonicus cytochrome P450.
AAC05148.1	AF049067	Pinus radiata cytochrome P450. PRE74.

CAA70576.1 Y09424 *Nepeta racemosa*
cytochrome P450. CYP71A6.

AAG10196.1 AF286647 *Gossypium arboreum*
cinnamate-4-hydroxylase. LP89. P450.

AAB94584.1 AF022157 *Glycine max*
capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10.
cytochrome P450 monooxygenase.

CAA50648.1 X71657 *Solanum melongena*
P450 hydroxylase.

CAB43505.1 AJ239051 *Cicer arietinum*
cytochrome P450. cyp81E2.

SEQ ID NO: 141

AAB97167.1 AF030882 *Zea mays*
SU1 isoamylase. sugary1. starch debranching enzyme.

AAA91298.1 U18908 *Zea mays*
Sulp. Sugary1. similar to *Pseudomonas* sp. isoamylase, Swiss-Prot Accession Number
P26501.

AAD33889.1 AF142589 *Hordeum vulgare*
isoamylase 1.

BAA29041.1 AB015615 *Oryza sativa*
isoamylase.

AAD33891.1 AF142591 *Solanum tuberosum*
isoamylase 1.

AAD33890.1 AF142590 *Triticum aestivum*
isoamylase 1.

AAD53260.1 AF142588 *Hordeum vulgare*
isoamylase 1.

SEQ ID NO: 145

AAG35777.1 AF273844 *Brassica oleracea* var. *alboglabra*
thioredoxin-h-like protein 1. THL1.

AAB53694.1 U59379 *Brassica napus*
thioredoxin-h-like-1. THL-1. thioredoxin-h homolog.

CAA61908.1 X89759 *Brassica oleracea*
pollen coat protein. bopcl7.

BAA25681.1 AB010434 *Brassica rapa*
Thioredoxin. PEC-2.

BAB20886.1 AB053294 *Oryza sativa*
thioredoxin h. RTRXH2.

AAB53695.1 U59380 *Brassica napus*
thioredoxin-h-like-2. THL-2. thioredoxin-h homolog.

AAF88067.1 AF286593 *Triticum aestivum*
thioredoxin H. similar to wheat thioredoxin H.

CAA94534.1	Z70677	Ricinus communis thioredoxin.
CAA05081.1	AJ001903	Triticum turgidum subsp. durum thioredoxin H.
CAA49540.1	X69915	Triticum aestivum unnamed protein product.
BAA13524.1	D87984	Fagopyrum esculentum thioredoxin.
CAA41415.1	X58527	Nicotiana tabacum thioredoxin.
CAA77847.1	Z11803	Nicotiana tabacum THIOREDOXIN.
AAC32111.1	AF051206	Picea mariana probable thioredoxin H. Sb09. similar to Nicotiana tabacum thioredoxin H1 encoded by GenBank Accession Number X58527.
BAA05546.1	D26547	Oryza sativa rice thioredoxin h.
BAA04864.1	D21836	Oryza sativa thioredoxin h. encoding rice phloem sap 13kD protein-1.
AAB51522.1	U92541	Oryza sativa thioredoxin h.
AAD49232.1	AF159387	Lolium perenne thioredoxin-like protein. Trx.
AAD56954.1	AF186240	Secale cereale thioredoxin-like protein. Trx.
AAD49231.1	AF159386	Secale cereale thioredoxin-like protein. Trx.
AAD49230.1	AF159385	Hordeum bulbosum thioredoxin-like protein. Trx.
AAD49234.1	AF159389	Phalaris coerulescens thioredoxin-like protein. Trx.
AAD49233.1	AF159388	Phalaris coerulescens thioredoxin-like protein. Trx.
BAB39913.1	AP002912	Oryza sativa thioredoxin-like protein. P0028E10.17. contains EST C72705(E2091).
CAA55399.1	X78822	Chlamydomonas reinhardtii thioredoxin h. Trx.
CAA56850.1	X80887	Chlamydomonas reinhardtii thioredoxin h. Trx h.
AAD33596.1	AF133127	Hevea brasiliensis thioredoxin h.
CAA35826.1	X51462	Spinacia oleracea thioredoxin M precursor (AA -67 to 114).

CAA35827.1	X51463	Spinacia oleracea thioredoxin M precursor (AA -67 to 114).
CAA45098.1	X63537	Pisum sativum thioredoxin F. isoform.
AAC49357.1	U35830	Pisum sativum thioredoxin f.
AAC19392.1	AF069314	Mesembryanthemum crystallinum thioredoxin F precursor.
AAC04671.1	AF018174	Brassica napus thioredoxin-f. TRXF.
AAB47556.1	U87141	Mesembryanthemum crystallinum thioredoxin h.
CAA53900.1	X76269	Pisum sativum thioredoxin m.
AAC49358.1	U35831	Pisum sativum thioredoxin m. chloroplastic.
CAA33082.1	X14959	Spinacia oleracea pre-thioredoxin f (AA -77 to 113).
CAA06736.1	AJ005841	Oryza sativa thioredoxin M.
CAA55398.1	X78821	Chlamydomonas reinhardtii thioredoxin m. Trx.
CAA56851.1	X80888	Chlamydomonas reinhardtii thioredoxin m. Trx m.
CAA44209.1	X62335	Chlamydomonas reinhardtii thioredoxin Ch2. Trx.
AAA92464.1	L40957	Zea mays regulation of activities of photosynthetic enzymes. thioredoxin M. putative.
CAA06735.1	AJ005840	Triticum aestivum thioredoxin M.
AAB52409.1	U76831	Brassica napus thioredoxin-m.
AAD45358.1	AF160870	Brassica napus thioredoxin-m precursor.
CAA71103.1	Y09987	Solanum tuberosum CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa).
AAA32662.1	M82973	Medicago sativa putative endomembrane protein; putative.
CAA77575.1	Z11499	Medicago sativa protein disulfide isomerase.

SEQ ID NO: 148

AAA33376.1	L36129	Helianthus annuus	NADPH thioredoxin reductase.
SEQ ID NO: 150			
AAA92013.1	U49454	Prunus persica	beta-1,3-glucanase. Gns1.
CAA54952.1	X77990	Brassica rapa	beta-1,3-glucanase. bgl.
AAF33405.1	AF230109	Populus x canescens	beta-1,3 glucanase. BGLUC.
AAA33946.1	M37753	Glycine max	beta-1,3-endoglucanase (EC 3.2.1.39).
CAA03908.1	AJ000081	Citrus sinensis	glucan hydrolase. beta-1,3-glucanase. gns1.
CAB91554.1	AJ277900	Vitis vinifera	beta 1-3 glucanase. gl.
AAB03501.1	U41323	Glycine max	beta-1,3-glucanase. SGN1.
AAA34078.1	M63634	Nicotiana plumbaginifolia	regulator of beta(1,3)-glucanase. beta(1,3)-glucanase regulator.
CAA30261.1	X07280	Nicotiana plumbaginifolia	beta-glucanase.
AAA51643.1	M23120	Nicotiana plumbaginifolia	beta-glucanase precursor.
AAA87456.1	U22147	Hevea brasiliensis	beta-1,3-glucanase. HGN1. hydrolytic enzyme.
CAB38443.1	AJ133470	Hevea brasiliensis	beta-1,3-glucanase. hgn1.
AAA03618.1	M80608	Lycopersicon esculentum	beta-1,3-glucanase.
AAA18928.1	U01901	Solanum tuberosum	catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). glub2. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAC19114.1	AF067863	Solanum tuberosum	1,3-beta-glucan glucanohydrolase. glucanase.
CAA92278.1	Z68154	Gossypium hirsutum	1,3-beta-glucanase.
AAG24921.1	AF311749	Hevea brasiliensis	beta-1,3-glucanase.
AAA63539.1	M60402	Nicotiana tabacum	glucan beta-1,3-glucanase. glucanase GLA.

AAA63540.1	M60403	Nicotiana tabacum	glucan-1,3-beta-glucosidase. glucanase GLB.
AAA88794.1	U01900	Solanum tuberosum	catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). gluB1. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAA63541.1	M59442	Nicotiana tabacum	basic beta-1,3-glucanase. glucanase.
AAB82772.2	AF001523	Musa acuminata	beta-1, 3-glucanase. similar to beta-1, 3-glucanase.
CAA37289.1	X53129	Phaseolus vulgaris	1,3,-beta-D-glucanase.
AAF08679.1	AF004838	Musa acuminata	beta-1,3-glucanase.
AAD33881.1	AF141654	Nicotiana tabacum	beta-1,3-glucanase. GGL4.
AAD33880.1	AF141653	Nicotiana tabacum	beta-1,3-glucanase. GGL1.
AAA33648.1	L02212	Pisum sativum	beta-1,3-glucan hydrolysis. beta-1,3-glucanase. putative.
AAA34082.1	M20620	Nicotiana tabacum	prepro-beta-1,3-glucanase precursor.
AAA19111.1	U01902	Solanum tuberosum	catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). gluB3. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
CAA57255.1	X81560	Nicotiana tabacum	(1-)-beta-glucanase. Sp41a.
AAA34053.1	M60464	Nicotiana tabacum	beta-1,3-glucanase.
AAA63542.1	M59443	Nicotiana tabacum	acidic beta-1,3-glucanase. glucanase.
AAB24398.1	S51479	Pisum sativum	beta-1,3-glucanase. beta-1,3-glucanase. This sequence comes from Fig. 1B.
AAB41551.1	U27179	Medicago sativa subsp. sativa	acidic glucanase.
AAD10384.1	U72253	Oryza sativa	beta-1,3-glucanase precursor. Gns7.
AAA03617.1	M80604	Lycopersicon esculentum	beta-1,3-glucanase.

SEQ ID NO: 151

BAA19102.1	AB000408	Populus kitakamiensis o-methyltransferase. caffeoyl-CoA 3-O-methyltransferase.
AAC28973.1	U20736	Medicago sativa subsp. sativa synthesis of feruloyl-CoA from caffeoyl-CoA and S-adenosyl-L-methionine. S-adenosyl-L-methionine:trans-caffeoyl-CoA 3-O-methyltransferase. CCOMT.
CAA12198.1	AJ224894	Populus balsamifera subsp. trichocarpa methylates lignin precursors. caffeoyl-CoA 3-O-methyltransferase.
CAA11496.1	AJ223621	Populus balsamifera subsp. trichocarpa caffeoyl CoA 3-O-methyltransferase. CCoAOMT1.
AAB80931.1	AF022775	Nicotiana tabacum caffeoyl-CoA 3-O-methyltransferase 5. CCoAOMT-5. implicated in lignification and defense reaction against pathogens.
CAA83943.1	Z33878	Petroselinum crispum caffeoyl-CoA 3-O-methyltransferase.
AAA33851.1	M69184	Petroselinum crispum caffeoyl-CoA 3-O-methyltransferase. CCoAMT.
CAA90894.1	Z54183	Petroselinum crispum trans-caffeoyl-CoA 3-O-methyltransferase. CCoAOMT.
CAA90969.1	Z54233	Vitis vinifera plant defense and lignification. caffeoyl-CoA O-methyltransferase.
AAA59389.1	U13151	Zinnia elegans S-adenosyl-L-methionine:trans-caffeoyl-CoA 3-O-methyltransferase. CCoAOMT.
CAB05369.1	Z82982	Nicotiana tabacum methylation of caffeoyl-CoA in lignin biosynthesis. caffeoyl-CoA O-methyltransferase 5. CCoAOMT-5.
AAA80651.1	U27116	Populus tremuloides caffeoyl-CoA 3-O-methyltransferase. S-adenosyl-L-methionine caffeoyl-CoA 3-O-methyltransferase; similar to Swiss-Prot Accession Number P28034; similar to proteins encoded by GenBank accession Numbers U20736, U13151, and L22203; Mr = 27.9 kDa and pI = 5.16.
AAC08395.1	AF053553	Mesembryanthemum crystallinum caffeoyl-CoA O-methyltransferase.
CAA12200.1	AJ224896	Populus balsamifera subsp. trichocarpa methylates lignin precursors. caffeoyl-CoA 3-O-methyltransferase.
CAA12199.1	AJ224895	Populus balsamifera subsp. trichocarpa methylates lignin precursors. caffeoyl-CoA 3-O-methyltransferase.
CAA11495.1	AJ223620	Populus balsamifera subsp. trichocarpa caffeoyl CoA 3-O-methyltransferase. CCoAOMT2.
AAD50443.1	AF168780	Eucalyptus globulus caffeoyl-CoA O-methyltransferase. CCoAOMT2.
AAF44689.1	AF240466	Populus tomentosa caffeoyl-CoA O-methyltransferase. CCoAOMT.

AAC49913.1	U38612	Nicotiana tabacum	methylation of caffeoyl-CoA in feruloyl-coA in phenylpropanoid pathway. caffeoyl-coenzymeA O-methyltransferase. CCoAOMT-1.
CAA72911.1	Y12228	Eucalyptus gunnii	caffeoyl-CoA O-methyltransferase. COOAMT.
AAC49916.1	U62736	Nicotiana tabacum	methylation of caffeoyl-CoA in feruloyl-CoA in phenylpropanoid pathway (lignin biosynthesis). caffeoyl-CoA O-methyltransferase 4. CCoAOMT-4.
BAA78733.1	AB023482	Oryza sativa	ESTs AU058067(E20733), AAU058070(E20873) correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase mRNA, complete cds.(U27116).
CAA91228.1	Z56282	Nicotiana tabacum	plant defense and lignification. caffeoyl-CoA O-methyltransferase. NTCCOAOMT.
AAC49914.1	U62734	Nicotiana tabacum	methylation of caffeoyl-CoA in feruloyl-CoA in phenylpropanoid pathway (lignin biosynthesis). caffeoyl-CoA O-methyltransferase 2. CCoAOMT-2.
AAC26191.1	AF046122	Eucalyptus globulus	catalyses the methylation of caffeoyl CoA in lignin biosynthesis. caffeoyl-CoA 3-O-methyltransferase. CCOMT. S-adenosyl-L-methionine:caffeoyl-CoA 3-O-methyltransferase.
AAC49915.1	U62735	Nicotiana tabacum	methylation of caffeoyl-CoA in feruloyl-CoA in phenylpropanoid pathway (lignin biosynthesis). caffeoyl-CoA O-methyltransferase 3. CCoAOMT-3.
AAD02050.1	AF036095	Pinus taeda	caffeoyl-CoA O-methyltransferase. CCoAOMT. lignin pathway O-methyltransferase.
AAK16714.1	AF327458	Populus alba x Populus glandulosa	caffeoyl-CoA 3-O-methyltransferase. CCoAOMT.
CAB45150.1	AJ242981	Zea mays	lignin synthesis. Caffeoyl CoA O-methyltransferase. ccoAOMT.
CAB45149.1	AJ242980	Zea mays	lignin synthesis. Caffeoyl CoA O-methyltransferase. ccoAOMT.
AAB61680.1	L22203	Stellaria longipes	S-adenosyl-L-methionine:trans-caffeoyl-CoA 3-O-methyltransferase. 26.7-kDa; pI=5.3.
BAA88234.1	AB035144	Citrus natsudaidai	Methylation of caffeoyl-coA in feruloyl-coA in phenylpropanoid pathway. caffeoyl-CoA 3-O-methyltransferase. CCoAMT.
BAA81776.1	AP000364	Oryza sativa	ESTs C98431(E0144),C71728(E0144) correspond to a region of the predicted gene.; Similar to Medicago sativa S-adenosyl-L-methionine. (U20736).
BAA81774.1	AP000364	Oryza sativa	ESTs AU030740(E60171),AU030739(E60171) correspond to a region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase. (U27116).
BAA81777.1	AP000364	Oryza sativa	Similar to Petroselinum crispum caffeoyl-CoA 3-O-methyltransferase. (S49342).

CAA10217.1	AJ130841	Populus balsamifera subsp. trichocarpa methylates lignin precursors. caffeoyl-CoA 3-O-methyltransferase.
CAA04769.1	AJ001447	Fragaria vesca caffeoyl-CoA 3-O-methyltransferase. putative.
AAD50441.1	AF168778	Eucalyptus globulus caffeoyl-CoA O-methyltransferase. CCoAOMT1.
AAD50442.1	AF168779	Eucalyptus globulus caffeoyl-CoA O-methyltransferase. CCoAOMT2.
AAC15067.1	AF060180	Nicotiana tabacum plant lignification and defense. caffeoyl-coenzyme A trunc2. truncated caffeoyl-coenzyme A.
SEQ ID NO: 152		
AAK11255.1	AF329729	Nicotiana tabacum regulator of gene silencing. rgs-CaM; calmodulin-related protein.
AAD10245.1	AF030033	Phaseolus vulgaris calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
CAA62150.1	X90560	Physcomitrella patens Calmodulin. CaM.
BAA94696.1	AB041711	Chara corallina calmodulin. cccam1.
BAA96536.1	AB044286	Chara corallina calmodulin. ccam.
BAA94697.1	AB041712	Chara corallina calmodulin. cccam2.
BAA87825.1	AP000815	Oryza sativa ESTs AU030013(E50493),AU081341(E50493) correspond to a region of the predicted gene. Similar to O.sativa gene encoding calmodulin. (Z12828).
CAA61980.1	X89890	Bidens pilosa Calmodulin.
AAA19571.1	U10150	Brassica napus calcium binding. calmodulin. bcml.
AAA87347.1	M88307	Brassica juncea calmodulin.
CAA74111.1	Y13784	Mougeotia scalaris Calmodulin.
AAA92677.1	U13736	Pisum sativum binds calcium. calmodulin-like protein.
AAA34015.1	L01433	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-4. putative.
AAA33083.1	M20729	Chlamydomonas reinhardtii calmodulin.
AAK25753.1	AF334833	Castanea sativa calmodulin. CAM2.

AAF73157.1	AF150059	Brassica napus calmodulin. CaM1. involved in seed germination.
CAA74307.1	Y13974	Zea mays calmodulin.
AAA34238.1	L20507	Vigna radiata calmodulin.
AAA34237.1	L20691	Vigna radiata calmodulin.
AAC49587.1	U49105	Triticum aestivum calmodulin TaCaM4-1. calcium-binding protein.
AAC49586.1	U49104	Triticum aestivum calmodulin TaCaM3-3. calcium-binding protein.
AAC49585.1	U49103	Triticum aestivum calmodulin TaCaM3-2. calcium-binding protein.
AAC49584.1	U48693	Triticum aestivum calmodulin TaCaM3-1. calcium-binding protein.
AAC49580.1	U48689	Triticum aestivum calmodulin TaCaM1-3. calcium-binding protein.
AAC49579.1	U48688	Triticum aestivum calmodulin TaCaM1-2. calcium binding protein.
AAC49578.1	U48242	Triticum aestivum calmodulin TaCaM1-1. calcium-binding.
AAA34014.1	L01432	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-3. putative.
AAA03580.1	L01431	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-2. putative.
AAA34013.1	L01430	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-1. putative.
AAB36130.1	S81594	Vigna radiata auxin-regulated calmodulin. auxin-regulated calmodulin, arCaM. This sequence comes from Fig. 1; arCaM.
AAA33901.1	L18913	Oryza sativa calcium binding protein, signal transduction. calmodulin. putative.
AAA92681.1	U13882	Pisum sativum calcium-binding protein. calmodulin.
AAA33706.1	M80836	Petunia x hybrida calmodulin. CAM81.
AAA33705.1	M80831	Petunia x hybrida calmodulin-related protein. CAM53.
CAA78287.1	Z12827	Oryza sativa calcium binding protein, signal transduction. calmodulin.
CAA46150.1	X65016	Oryza sativa calmodulin. cam.

CAA36644.1	X52398	Medicago sativa calmodulin (AA 1-149).
CAA43143.1	X60738	Malus x domestica Calmodulin. CaM.
CAA78301.1	Z12839	Lilium longiflorum calcium binding protein, signal transduction. calmodulin.
AAA33397.1	L18912	Lilium longiflorum calcium binding protein, signal transduction. calmodulin. putative.
AAB68399.1	U79736	Helianthus annuus calmodulin. HaCaM.
CAA42423.1	X59751	Daucus carota calmodulin. Ccam-1.
AAA32938.1	M27303	Hordeum vulgare calmodulin.
BAA88540.1	AP000969	Oryza sativa ESTs AU081349(E61253), D41425(S3918) correspond to a region of the predicted gene. Similar to calmodulin. (AF042840).
AAG27432.1	AF295637	Elaeis guineensis calmodulin.
AAG11418.1	AF292108	Prunus avium calmodulin.
AAC36059.1	AF042840	Oryza sativa calmodulin. CaM1.
SEQ ID NO: 153		
CAA40474.1	X57187	Phaseolus vulgaris chitinase. Chi4.
AAB65776.1	U97521	Vitis vinifera class IV endochitinase. VvChi4A.
CAA61281.1	X88803	Vigna unguiculata chitinase class 4. CHI4.
AAB65777.1	U97522	Vitis vinifera class IV endochitinase. VvChi4B.
BAA22966.1	D45182	Chenopodium amaranticolor chitinase.
BAA22968.1	D45184	Chenopodium amaranticolor chitinase.
BAA22965.1	D45181	Chenopodium amaranticolor chitinase.
CAA43708.1	X61488	Brassica napus chitinase.
BAA22967.1	D45183	Chenopodium amaranticolor chitinase.

CAA53544.1	X75945	Beta vulgaris chitinase. Ch4.
AAC49435.1	U52845	Daucus carota class IV chitinase EP3-1/H5. EP3.
AAB08468.1	U52846	Daucus carota class IV chitinase EP3-2/H1. EP3.
AAB08470.1	U52848	Daucus carota class IV chitinase EP3B/E6. EP3.
AAB08469.1	U52847	Daucus carota class IV chitinase EP3-3/E7. EP3.
AAA33445.1	M84165	Zea mays chitinase B. seed chitinase.
AAA33444.1	M84164	Zea mays chitinase A. seed chitinase.
AAA32916.1	L25826	Beta vulgaris chitinase. SP2.
AAD28733.1	AF112966	Triticum aestivum chitinase IV precursor. Cht4.
BAB21377.1	AB054811	Oryza sativa PR-3 class IV chitinase. Cht4. Catalytic domain.
BAB21374.1	AB054687	Oryza sativa PR-3 class IV chitinase. Cht4. catalytic domain.
BAA19793.1	AB003194	Oryza sativa chitinase IIb.
AAA85364.1	L42467	Picea glauca chitinase. chi.
AAB01665.1	U21848	Brassica napus chitinase class IV. LSC222.
AAC35981.1	AF090336	Citrus sinensis chitin hydrolase. chitinase CHI1. chi1.
AAD28730.1	AF112963	Triticum aestivum chitinase II precursor. Cht2.
AAF04454.1	AF000966	Poa pratensis chitinase. Chi2.
CAC17793.1	AJ301671	Nicotiana sylvestris hydrolysis of chitin. endochitinase. chnb. class I chitinase.
AAF04453.1	AF000964	Poa pratensis chitinase. Chi1.
CAA34812.1	X16938	Nicotiana tabacum chitinase precursor.
CAA34813.1	X16939	Nicotiana tabacum chitinase precursor (AA -23 to 306).

CAA45822.1	X64519	Nicotiana tabacum	chitinase B class I. CHN200.
CAA35945.1	X51599	Nicotiana tabacum	chitinase. CHN50.
AAB23374.1	S44869	Nicotiana tabacum	basic chitinase. basic chitinase. This sequence comes from Fig. 1.
AAA34070.1	M15173	Nicotiana tabacum	endochitinase precursor (EC 3.2.1.14).
CAA30142.1	X07130	Solanum tuberosum	endochitinase.
CAA33517.1	X15494	Solanum tuberosum	pre-chitinase (AA -26 to 302).
AAG53609.1	AF280437	Secale cereale	31.7 kDa class I endochitinase-antifreeze protein precursor. cht9.
CAB01591.1	Z78202	Persea americana	hydrolysis of the 1,4-beta-linkages of chitin. endochitinase. chl1.
CAA53626.1	X76041	Triticum aestivum	endochitinase. CHI.
CAA78845.1	Z15140	Lycopersicon esculentum	chitinase. Encodes 30 kD basic intracellular chitinase.
AAC16010.1	AF061805	Elaeagnus umbellata	acidic chitinase.
AAA32640.1	M94106	Allium sativum	chitinase. chitinase.
AAA32641.1	M94105	Allium sativum	chitinase. chitinase.
AAA56787.1	L34211	Hordeum vulgare	hydrolysis of chitin. chitinase. CHI33.
AAA17409.1	U02607	Solanum tuberosum	catalyzes the random hydrolysis of 1,4-beta-(2-acetamido-2-deoxy-D-glucoside) linkages in chitin; plant defense gene. chitinase. chtB3. induced expression in response to infection, elicitor, ethylene, wounding; preproprotein; gene product subunit is monomer.
AAA18332.1	U02605	Solanum tuberosum	catalyzes the random hydrolysis of 1,4-beta-(2-acetamido-2-deoxy-D-glucoside) linkages in chitin; plant defense gene. chitinase. chtB1. induced expression in response to infection, elicitor, ethylene, wounding; preproprotein; gene product subunit is a monomer.
CAA45821.1	X64518	Nicotiana tabacum	chitinase C class I. CHN14.
SEQ ID NO: 154			
AAB35812.1	S80554	Arabidopsis	chalcone synthase. chalcone synthase, CHS. This sequence comes from Fig. 5; CHS.
AAF23570.1	AF112095	Arabidopsis halleri	chalcone synthase. CHS.

AAF23568.1	AF112093	<i>Arabidopsis griffithiana</i> chalcone synthase. CHS.
AAG43351.1	AF144533	<i>Arabidopsis korshinskyi</i> chalcone synthase. chs.
AAF23581.1	AF112106	<i>Capsella rubella</i> chalcone synthase. CHS.
AAF23569.1	AF112094	<i>Halimolobos perplexa</i> var. <i>perplexa</i> chalcone synthase. CHS.
AAG43349.1	AF144531	<i>Arabidopsis himalaica</i> chalcone synthase. chs.
AAF23575.1	AF112100	<i>Arabidopsis lyrata</i> subsp. <i>lyrata</i> chalcone synthase. CHS.
AAF23567.1	AF112092	<i>Arabidopsis griffithiana</i> chalcone synthase. CHS.
AAF23578.1	AF112103	<i>Arabidopsis lyrata</i> subsp. <i>petraea</i> chalcone synthase. CHS.
AAF23576.1	AF112101	<i>Arabis parishii</i> chalcone synthase. CHS.
AAF23574.1	AF112099	<i>Arabis lyallii</i> chalcone synthase. CHS.
AAF23566.1	AF112091	<i>Arabis glabra</i> chalcone synthase. CHS.
AAF23565.1	AF112090	<i>Arabis fendleri</i> chalcone synthase. CHS.
AAF23563.1	AF112088	<i>Arabis drummondii</i> chalcone synthase. CHS.
AAF23564.1	AF112089	<i>Arabis drummondii</i> chalcone synthase. CHS.
AAF23579.1	AF112104	<i>Arabidopsis lyrata</i> subsp. <i>petraea</i> chalcone synthase. CHS.
AAF23573.1	AF112098	<i>Arabis lignifera</i> chalcone synthase. CHS.
AAF23560.1	AF112085	<i>Cardamine amara</i> chalcone synthase. CHS.
AAG43348.1	AF144530	<i>Rorippa amphibia</i> chalcone synthase. chs.
AAG43356.1	AF144538	<i>Cardamine penzesii</i> chalcone synthase. chs.
AAG43359.1	AF144541	<i>Sisymbrium irio</i> chalcone synthase. chs.
AAG43352.1	AF144534	<i>Lepidium campestre</i> chalcone synthase. chs.

CAA32495.1	X14314	Sinapis alba
chalcone synthase (AA 1-395).		
AAG43357.1	AF144539	Cardamine rivularis
chalcone synthase. chs.		
AAF23583.1	AF112108	Barbarea vulgaris
chalcone synthase. CHS.		
AAC31914.1	AF076336	Brassica napus
chalcone synthase B2. CHSB2.		
AAC31912.1	AF076334	Brassica napus
chalcone synthase A2. CHSA2.		
AAF23577.1	AF112102	Arabis pauciflora
chalcone synthase. CHS.		
AAG43350.1	AF144532	Cochlearia danica
chalcone synthase. chs.		
CAA34460.1	X16437	Sinapis alba
chalcone synthase.		
CAA35600.1	X17577	Matthiola incana
chalcone synthase (AA 1-394).		
AAG43358.1	AF144540	Cardamine pratensis
chalcone synthase. chs.		
AAG43353.1	AF144535	Thlaspi arvense
chalcone synthase. chs.		
AAC31913.1	AF076335	Brassica napus
chalcone synthase B1. CHSB1.		
AAF23571.1	AF112096	Arabis hirsuta
chalcone synthase. CHS.		
AAF23582.1	AF112107	Arabis turrita
chalcone synthase. CHS.		
AAG43406.1	AF174529	Aubrieta deltoidea
chalcone synthase. chs.		
AAG43355.1	AF144537	Alliaria petiolata
chalcone synthase. chs.		
AAF23580.1	AF112105	Arabis procurrens
chalcone synthase. CHS.		
AAF23572.1	AF112097	Arabis jacquinii
chalcone synthase. CHS.		
AAF23562.1	AF112087	Arabis blepharophylla
chalcone synthase. CHS.		
AAF23584.1	AF112109	Aubrieta deltoidea
chalcone synthase. CHS.		
AAG43354.1	AF144536	Microthlaspi perfoliatum
chalcone synthase. chs.		

AAF23557.1	AF112082	Aethionema grandiflora chalcone synthase. CHS.
AAF23558.1	AF112083	Arabis alpina chalcone synthase. CHS.
AAF23559.1	AF112084	Arabis alpina chalcone synthase. CHS.
AAB87072.1	AF031922	Raphanus sativus chalcone synthase. CHS.
AAG43360.1	AF144542	Ionopsidium abulense chalcone synthase. chs.
AAC31911.1	AF076333	Brassica napus chalcone synthase A1. CHSA1.
SEQ ID NO: 156		
AAD10327.1	U63534	Fragaria x ananassa catalyzes the reduction of cinnamylaldehydes leading to monolignols. cinnamyl alcohol dehydrogenase. CAD. involved with lignin biosynthesis.
AAK28509.1	AF320110	Fragaria x ananassa cinnamyl alcohol dehydrogenase.
AAB38503.1	U79770	Mesembryanthemum crystallinum cinnamyl-alcohol dehydrogenase Eli3.
CAA48028.1	X67817	Petroselinum crispum Eli3.
AAC15467.1	U24561	Apium graveolens converts mannitol to mannose. mannitol dehydrogenase. Mtd. 1-oxidoreductase; induced with sodium salicylate; similar to the plant defense gene ELI3 in Arabidopsis thaliana, PIR Accession Number S28044; EC number unassigned; MTD.
AAC35846.1	AF083333	Medicago sativa cinnamyl-alcohol dehydrogenase. MsaCad1.
AAC61854.1	AF067082	Apium graveolens oxidizes mannitol to mannose. mannitol dehydrogenase. Mtd. mannitol 1-oxidoreductase.
AAA74882.1	L36823	Stylosanthes humilis cinnamyl-alcohol dehydrogenase. CAD1.
AAA74883.1	L36456	Stylosanthes humilis cinnamyl-alcohol dehydrogenase. CAD3.
AAF72100.1	AF146691	Lycopersicon esculentum ELI3. Eli3. similar] to cinnamyl alcohol dehydrogenase.
CAA86072.1	Z37991	Pinus taeda cinnamyl alcohol dehydrogenase.
CAA05095.1	AJ001924	Picea abies cinnamyl alcohol dehydrogenase. cad2.
AAB38774.1	U62394	Pinus radiata cinnamyl alcohol dehydrogenase. CAD.

CAA51226.1	X72675	<i>Picea abies</i> cinnamyl-alcohol dehydrogenase.
CAA05097.1	AJ001926	<i>Picea abies</i> cinnamyl alcohol dehydrogenase. cad8.
CAA05096.1	AJ001925	<i>Picea abies</i> cinnamyl alcohol dehydrogenase. cad7.
AAC31166.1	AF060491	<i>Pinus radiata</i> cinnamyl alcohol dehydrogenase. CAD.
CAA86073.1	Z37992	<i>Pinus taeda</i> cinnamyl alcohol dehydrogenase.
CAA44216.1	X62343	<i>Nicotiana tabacum</i> cinnamyl-alcohol dehydrogenase. CAD14.
CAA44217.1	X62344	<i>Nicotiana tabacum</i> cinnamyl-alcohol dehydrogenase. CAD19.
BAA03099.1	D13991	<i>Aralia cordata</i> cinnamyl alcohol dehydrogenase. cadacl.
CAA79625.1	Z19573	<i>Medicago sativa</i> lignin biosynthesis. cinnamyl alcohol dehydrogenase.
AAF43140.1	AF217957	<i>Populus tremuloides</i> cinnamyl alcohol dehydrogenase. CAD.
AAC35845.1	AF083332	<i>Medicago sativa</i> cinnamyl-alcohol dehydrogenase. MsaCad2.
CAC07423.1	AJ295837	<i>Populus balsamifera</i> subsp. <i>trichocarpa</i> lignin monomer biosynthesis. cinnamyl alcohol dehydrogenase. cad.
CAA79622.1	Z19568	<i>Populus deltoides</i> lignin biosynthesis. cinnamyl alcohol dehydrogenase.
AAC07987.1	AF038561	<i>Eucalyptus globulus</i> catalyses the reduction of cinnamaldehydes to the corresponding cinnamyl alcohols as the last step in the production of lignin monomers. cinnamyl alcohol dehydrogenase. CAD.
AAG15553.1	AF294793	<i>Eucalyptus saligna</i> cinnamyl alcohol dehydrogenase. cad. CAD.
AAK00679.1	AF229407	<i>Brassica napus</i> Eli3 product. ELI3-BN-2. protein identity based on similarity to Arabidopsis sequence; intron/exon junctions deduced from alignments to DNA or mRNA sequences already present in the GenBank database.
CAA46585.1	X65631	<i>Eucalyptus gunnii</i> cinnamyl-alcohol dehydrogenase. cad.
CAA53211.1	X75480	<i>Eucalyptus gunnii</i> cinnamyl-alcohol dehydrogenase. CAD.
AAK00681.1	AF229409	<i>Brassica napus</i> Eli3 product. ELI3-BN-4. protein identity based on similarity to Arabidopsis sequence; intron/exon junctions deduced from alignments to DNA or mRNA sequences already present in the GenBank database.

AAB70908.1 AF010290 *Lolium perenne*
cinnamyl alcohol dehydrogenase. CAD.

AAK00682.1 AF229410 *Brassica oleracea*
Eli3 product. ELI3-BO-1. protein identity based on similarity to Arabidopsis sequence;
intron/exon junctions deduced from alignments to DNA or mRNA sequences already present
in the GenBank database.

CAA74070.1 Y13733 *Zea mays*
cinnamyl alcohol dehydrogenase. cad.

CAA06687.1 AJ005702 *Zea mays*
cinnamyl alcohol dehydrogenase. cad.

AAK00678.1 AF229406 *Brassica napus*
Eli3 product. ELI3-BN-1. protein identity based on similarity to Arabidopsis sequence;
intron/exon junctions deduced from alignments to DNA or mRNA sequences already present
in the GenBank database.

CAA13177.1 AJ231135 *Saccharum officinarum*
lignin biosynthesis. cinnamyl alcohol dehydrogenase. cad.

AAK00684.1 AF229412 *Brassica rapa*
Eli3 product. ELI3-BR-2. protein identity based on similarity to Arabidopsis sequence;
intron/exon junctions deduced from alignments to DNA or mRNA sequences already present
in the GenBank database.

AAK00680.1 AF229408 *Brassica napus*
Eli3 product. ELI3-BN-3. protein identity based on similarity to Arabidopsis sequence;
intron/exon junctions deduced from alignments to DNA or mRNA sequences already present
in the GenBank database.

AAK00683.1 AF229411 *Brassica rapa*
Eli3 product. ELI3-BR-1. protein identity based on similarity to Arabidopsis sequence;
intron/exon junctions deduced from alignments to DNA or mRNA sequences already present
in the GenBank database.

BAA19487.1 D86590 *Zinnia elegans*
cinnamyl alcohol dehydrogenase. ZCAD1.

BAA04046.1 D16624 *Eucalyptus botryoides*
cinnamyl alcohol dehydrogenase. Cad1:Eb:1.

AAD18000.1 AF109157 *Eucalyptus globulus*
cinnamyl alcohol dehydrogenase. CAD.

AAF23409.1 AF207552 *Brassica napus*
cinnamyl alcohol dehydrogenase. CADa-1.

AAF23412.1 AF207555 *Brassica rapa*
cinnamyl alcohol dehydrogenase. CADa.

AAF23411.1 AF207554 *Brassica oleracea*
cinnamyl alcohol dehydrogenase. CADa.

AAF23410.1 AF207553 *Brassica napus*
cinnamyl alcohol dehydrogenase. CADa-2.

AAF23416.1 AF207559 *Brassica rapa*
cinnamyl alcohol dehydrogenase. CADb.

AAF23415.1 AF207558 *Brassica oleracea*
cinnamyl alcohol dehydrogenase. CADb.

SEQ ID NO: 158

BAA87853.1 AP000816 *Oryza sativa*
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

BAA78764.1 AB023482 *Oryza sativa*
ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to *Arabidopsis thaliana* APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).

AAF43496.1 AF131222 *Lophopyrum elongatum*
protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.

AAK11674.1 AF339747 *Lophopyrum elongatum*
protein kinase. ESI47.

BAB16871.1 AP002537 *Oryza sativa*
putative protein kinase APK1A*Arabidopsis thaliana*. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

AAG16628.1 AY007545 *Brassica napus*
protein serine/threonine kinase BNK1.

AAC27894.1 AF023164 *Zea mays*
leucine-rich repeat transmembrane protein kinase 1. ltk1.

BAA94509.1 AB041503 *Populus nigra*
protein kinase 1. PnPK1.

BAA94510.1 AB041504 *Populus nigra*
protein kinase 2. PnPK2.

BAB03429.1 AP002817 *Oryza sativa*
EST C22619(S11214) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).

BAB07999.1 AP002525 *Oryza sativa*
putative protein kinase. P0462H08.22. contains EST C22619(S11214).

BAB39409.1 AP002901 *Oryza sativa*
putative protein kinase. P0456F08.9. contains EST C23560(R0290).

AAC27895.1 AF023165 *Zea mays*
leucine-rich repeat transmembrane protein kinase 2. ltk2.

BAB21241.1 AP002953 *Oryza sativa*
Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721),D48017(S13927).

AAG59657.1 AC084319 *Oryza sativa*
putative protein kinase. OSJNBa0004B24.20.

AAF91337.1 AF249318 *Glycine max*
Pti1 kinase-like protein. Pti1b. protein kinase.

AAF91336.1 AF249317 *Glycine max*
Pti1 kinase-like protein. Pti1a. protein kinase.

CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
BAA87852.1	AP000816	Oryza sativa	Similar to putative Ser/Thr protein kinase. (AC004218).
BAA92221.1	AP001278	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
AAB09771.1	U67422	Zea mays	CRINKLY4 precursor. cr4. receptor kinase homolog.
BAB18321.1	AP002865	Oryza sativa	putative receptor protein kinase. P0034C11.11.
BAB40081.1	AP003074	Oryza sativa	putative receptor protein kinase. OSJNBa0004G10.30.
AAC61805.1	U28007	Lycopersicon esculentum	serine/threonine protein kinase. Pto kinase interactor 1. Pti1. Pti1 kinase.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAD38286.1	AC007789	Oryza sativa	putative protein kinase. OSJNBa0049B20.13.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAF34428.1	AF172282	Oryza sativa	receptor-like protein kinase. DUPR11.18.
AAG25966.1	AF302082	Nicotiana tabacum	cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
CAB51836.1	AJ243961	Oryza sativa	Putative Ser/Thr protein kinase. 11332.7.
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).

CAA97692.1 Z73295 *Catharanthus roseus*
receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser.
Mechanism: autophosphorylation in cis.

BAA84787.1 AP000559 *Oryza sativa*
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar
to receptor protein kinase, ERECTA (AC004484).

BAA83373.1 AP000391 *Oryza sativa*
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar
to receptor protein kinase, ERECTA (AC004484).

AAF76313.1 AF220603 *Lycopersicon esculentum*
Pto kinase. LescPth5.

AAB47421.1 U59316 *Lycopersicon esculentum*
serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in
tomato.

CAA79355.1 Z18921 *Brassica oleracea*
S-receptor kinase-like protein.

AAA33915.1 L27821 *Oryza sativa*
receptor type serine/threonine kinase. protein kinase.

BAA95893.1 AP002071 *Oryza sativa*
Similar to *Arabidopsis thaliana* wak4 gene; wall-associated kinase 4. (AJ009695).

AAC36318.1 AF053127 *Malus x domestica*
leucine-rich receptor-like protein kinase. LRPKml.

SEQ ID NO: 159

AAA86687.1 U15777 *Lupinus albus*
farnesyl pyrophosphate synthase. fps1.

AAA87729.1 U20771 *Lupinus albus*
farnesyl pyrophosphate synthase. fps1.

CAA72793.1 Y12072 *Gossypium arboreum*
farnesyl pyrophosphate synthase. fps1.

BAB40665.1 AB053486 *Humulus lupulus*
farnesyl pyrophosphate synthase. fpps.

BAB40666.1 AB053487 *Humulus lupulus*
farnesyl pyrophosphate synthase. fpps.

CAA57893.1 X82543 *Parthenium argentatum*
farnesyl diphosphate synthase. fps2.

AAC78557.1 AF019892 *Helianthus annuus*
farnesyl pyrophosphate synthase. FPS.

CAA57892.1 X82542 *Parthenium argentatum*
farnesyl diphosphate synthase. fps1.

AAC49452.1 U36376 *Artemisia annua*
farnesyl diphosphate synthase. fps1.

CAA59170.1 X84695 *Capsicum annuum*
dimethylallyltransferase. Fps, farnesyl pyrophosphate synthase gene.

AAC73051.1	AF048747	<i>Lycopersicon esculentum</i>	synthesis of farnesyl pyrophosphate. farnesyl pyrophosphate synthase. FPS1. prenyl transferase; farnesyl diphosphate synthetase.
AAD17204.1	AF112881	<i>Artemisia annua</i>	farnesyl diphosphate synthase.
BAA19856.1	D85317	<i>Oryza sativa</i>	farnesyl pyrophosphate synthase. dimethylallyltransferase; geranyltranstransferase.
BAA36276.1	AB021747	<i>Oryza sativa</i>	farnesyl diphosphate synthase. FPPS1.
AAD32648.1	AF136602	<i>Artemisia annua</i>	farnesyl diphosphate synthase. fps2.
AAB39276.1	L39789	<i>Zea mays</i>	farnesyl pyrophosphate synthetase. fps. putative.
AAD27558.1	AF111710	<i>Oryza sativa</i> subsp. <i>indica</i>	putative farnesyl pyrophosphate synthase. similar to <i>Oryza sativa</i> EST clones E10230_1A, C52647_1A, 232.
BAA36347.1	AB021979	<i>Oryza sativa</i>	farnesyl diphosphate synthase. FPPS2.
AAD37789.1	AF149257	<i>Artemisia annua</i>	farnesyl diphosphate synthase. FPP synthase.
BAB20822.1	AB045713	<i>Taraxacum japonicum</i>	putative FPP synthase. TJFPPS.
BAB16688.1	AB041627	<i>Eucommia ulmoides</i>	FPP synthase 2. EUFPPS2. putative.
BAB21061.1	AB046212	<i>Sonchus oleraceus</i>	putative FPP synthase. SoFPPS.
AAD45122.1	AF164026	<i>Xanthoceras sorbifolium</i>	synthesis of farnesyl pyrophosphate. farnesyl pyrophosphate synthase. FPS. prenyl transferase; farnesyl diphosphate synthetase.
AAB93951.1	U97330	<i>Nicotiana tabacum</i>	farnesylpyrophosphate synthase. FPPS.
BAB16687.1	AB041626	<i>Eucommia ulmoides</i>	FPP synthase 1. EUFPPS1. putative.
BAB39479.1	AB049086	<i>Youngia japonica</i>	putative FPP synthase 1. YjFPPS1.
AAB93984.1	AF005201	<i>Parthenium argentatum</i>	farnesyl pyrophosphate synthase. FPS3.

SEQ ID NO: 160

BAB03615.1	AP002522	<i>Oryza sativa</i>	putative gamma-glutamyltransferase. P0009G03.15. contains ESTs AU056150(S20332), AU056151(S20332).
BAB03616.1	AP002522	<i>Oryza sativa</i>	putative gamma-glutamyltransferase. P0009G03.16. contains EST AU056150(S20332).

SEQ ID NO: 162

- CAB96145.1 AJ250951 *Mesembryanthemum crystallinum*
phospholipid hydroperoxide glutathione peroxidase-like protein. gpxmc1.
- CAA42780.1 X60219 *Nicotiana sylvestris*
homologous to animal glutathione peroxidases.
- BAB16430.1 AB041518 *Nicotiana tabacum*
glutathione peroxidase Nt-SubC08. Nt-SubC08.
- CAA75054.1 Y14762 *Lycopersicon esculentum*
glutathione peroxidase. GPXle-1.
- AAB94892.1 AF037051 *Gossypium hirsutum*
glutathione peroxidase.
- CAB59893.1 AJ238697 *Hordeum vulgare*
GPX12Hv, glutathione peroxidase-like protein.
- BAA22194.1 D63425 *Spinacia oleracea*
phospholipid hydroperoxide glutathione peroxidase-like protein. similar to mammalian
phospholipid hydroperoxide glutathione peroxidases.
- CAB59895.1 AJ238745 *Hordeum vulgare*
glutathione peroxidase-like protein GPX54Hv.
- AAC78466.1 AF053311 *Zantedeschia aethiopica*
glutathione peroxidase. gpx.
- CAA04142.1 AJ000508 *Pisum sativum*
phospholipid glutathione peroxidase. plastid-localised.
- CAA75009.1 Y14707 *Helianthus annuus*
glutathione peroxidase. GPxha-2.
- CAB59894.1 AJ238744 *Hordeum vulgare*
glutathione peroxidase-like protein GPX15Hv.
- CAA74775.1 Y14429 *Helianthus annuus*
glutathione peroxidase. GPxha-1.
- CAC17628.1 AJ270955 *Oryza sativa*
putative role in antioxidative systems. putative phospholipid hydroperoxide glutathione
peroxidase. riPHGPX.
- BAA83594.1 AB009083 *Chlamydomonas* sp. W80
glutathione peroxidase.
- AAB66330.1 AF014927 *Chlamydomonas reinhardtii*
glutathione peroxidase homolog. gpsh.
- CAA75055.1 Y14763 *Lycopersicon esculentum*
glutathione peroxidase. GPXle-2.
- CAA09194.1 AJ010455 *Triticum aestivum*
glutathione peroxidase. PHGPX6.
- CAB66331.1 AJ279689 *Betula pendula*
glutathione peroxidase. gpx.

SEQ ID NO: 163

AAF67753.1	AF255651	Brassica rapa subsp. pekinensis	conversion of oxidized glutathione to reduced glutathione. cytosolic glutathione reductase. GR1.
AAC49980.2	AF008441	Brassica rapa	glutathione reductase. BcGR1. cytosolic.
BAA11214.1	D78136	Oryza sativa	Glutathione Reductase. putative.
CAA66924.1	X98274	Pisum sativum	glutathione reductase. cytosolic.
BAA36283.1	D85751	Oryza sativa	glutathione reductase.
BAA37092.1	AB009592	Oryza sativa	conversion of oxidized glutathione to reduced glutathione. cytosolic glutathione reductase. RGRC2. Amino Acids 1-496.
BAA07108.1	D37870	Spinacia oleracea	Glutathione Reductase precursor. Chloroplastic glutathione reductase.
CAC13956.1	AJ400816	Mesembryanthemum crystallinum	reduction of glutathione. glutathione reductase. gr1.
CAB66332.1	AJ279690	Betula pendula	glutathione reductase. gr.
CAA53925.1	X76293	Nicotiana tabacum	glutathione reductase (NADPH). gor.
CAA42921.1	X60373	Pisum sativum	glutathione reductase (NADPH). Protein sequence is in conflict with the conceptual translation.
AAK27157.1	AF349449	Brassica juncea	glutathione reductase. GR2.
AAD28177.1	AF109694	Brassica juncea	glutathione reductase. GR1.
CAA62482.1	X90996	Pisum sativum	glutathione reductase (NADPH). gr. alpha II subunit.
AAF26175.1	AF105199	Glycine max	glutathione reductase. GR-5.
AAB70837.1	AF019907	Vitis vinifera	glutathione reductase (NADPH). GOR. VvGR1.
AAA33962.1	L11632	Glycine max	glutathione reductase. GR.
CAA54043.1	X76533	Nicotiana tabacum	glutathione reductase (NADPH). gor.
CAA06835.1	AJ006055	Zea mays	NADPH-dependent reduction of glutathione disulphide. glutathione reductase. gor1.
CAA53993.1	X76455	Nicotiana tabacum	glutathione reductase. gor.

AAB30526.1	S70187	Glycine max	ferric leghemoglobin reductase. ferric leghemoglobin reductase, FLbR. Method: conceptual translation with partial peptide sequencing; This sequence comes from Fig. 3; FLbR.
AAC26053.1	AF074940	Glycine max	ferric leghemoglobin reductase-2 precursor. FLbR homolog;FLbR-2.
AAD53185.1	AF181096	Vigna unguiculata	ferric leghemoglobin reductase. flbr.
AAA60979.1	U06461	Pisum sativum	catalyzes the conversion of monodehydroascorbate to ascorbate, oxidizing NADH in the process, binds to flavin as a single subunit. monodehydroascorbate reductase.
BAA05408.1	D26392	Cucumis sativus	monodehydroascorbate reductase.
AAC41654.1	L41345	Lycopersicon esculentum	ascorbate free radical reductase. AFRR.
AAD53522.1	AF158602	Zantedeschia aethiopica	monodehydroascorbate reductase. MDAR. putative.
AAD28178.1	AF109695	Brassica juncea	monodehydroascorbate reductase. MDAR1.
BAA77214.1	D85764	Oryza sativa	cytosolic monodehydroascorbate reductase.
SEQ ID NO: 164			
CAA04391.1	AJ000923	Carica papaya	glutathione transferase. PGST1.
AAC18566.1	AF048978	Glycine max	2,4-D inducible glutathione S-transferase. GSTa.
AAG34800.1	AF243365	Glycine max	glutathione S-transferase GST 10.
AAF22647.1	AF193439	Lycopersicon esculentum	glutathione S-transferase/oxidase. BI-GST/GPX.
CAA71784.1	Y10820	Glycine max	glutathione transferase.
AAG34799.1	AF243364	Glycine max	glutathione S-transferase GST 9.
AAG16760.1	AY007562	Lycopersicon esculentum	putative glutathione S-transferase T5.
CAA48717.1	X68819	Glycine max	lactoylglutathione lyase. glyoxalase I.
CAC24549.1	AJ296343	Cichorium intybus x Cichorium endivia	glutathione S-transferase. chi-GST1. auxin-induced GST.
AAC28101.1	AF079511	Mesembryanthemum crystallinum	glutathione S-transferase.
AAG34806.1	AF243371	Glycine max	glutathione S-transferase GST 16.

AAF23357.1	AF109194	Hordeum vulgare glutathione-S-transferase.
CAA73369.1	Y12862	Zea mays glutathione transferase. GST5.
AAG32470.1	AF309377	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU5.
CAA74197.1	Y13898	Brassica juncea glutathione-S-transferase. gst.
AAG34827.1	AF244684	Zea mays glutathione S-transferase GST 19.
AAC05216.1	AF050102	Oryza sativa glutathione s-transferase. GST1.
AAC32118.1	AF051214	Picea mariana probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAG16758.1	AY007560	Lycopersicon esculentum putative glutathione S-transferase T3.
AAG34798.1	AF243363	Glycine max glutathione S-transferase GST 8.
AAG34842.1	AF244699	Zea mays glutathione S-transferase GST 34.
AAG34807.1	AF243372	Glycine max glutathione S-transferase GST 17.
AAG34809.1	AF243374	Glycine max glutathione S-transferase GST 19.
AAG34839.1	AF244696	Zea mays glutathione S-transferase GST 31.
AAG34804.1	AF243369	Glycine max glutathione S-transferase GST 14.
AAG34844.1	AF244701	Zea mays glutathione S-transferase GST 36.
AAG34831.1	AF244688	Zea mays glutathione S-transferase GST 23.
AAG34797.1	AF243362	Glycine max glutathione S-transferase GST 7.
AAG34832.1	AF244689	Zea mays glutathione S-transferase GST 24.
AAG32471.1	AF309378	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU4.
AAG34796.1	AF243361	Glycine max glutathione S-transferase GST 6.
AAG34810.1	AF243375	Glycine max glutathione S-transferase GST 20.

AAG34835.1 AF244692 *Zea mays*
glutathione S-transferase GST 27.

AAC32139.1 AF051238 *Picea mariana*
probable glutathione S-transferase. Sb52. similar to *Nicotiana tabacum* probable glutathione S-transferase encoded by GenBank Accession Number X56266.

SEQ ID NO: 165

CAA71878.1 Y10984 *Brassica juncea*
ATP-dependent addition of glycine to gamma-glutamylcysteine. glutathione synthetase. gshII.

AAB71231.1 AF017984 *Lycopersicon esculentum*
glutathione synthetase. GSH2.

AAF98157.1 AF258320 *Phaseolus vulgaris*
homoglutathione synthetase. hgshs.

AAF98156.1 AF258319 *Pisum sativum*
putative homoglutathione synthetase. hgshs.

CAB91078.1 AJ272035 *Glycine max*
homoglutathione synthetase. hGS. putatively predicted to be targetted to the chloroplast.

AAF98121.1 AF231137 *Pisum sativum*
glutathione synthetase precursor: gshs. putative mitochondrial protein.

AAD29848.1 AF075699 *Medicago truncatula*
putative glutathione synthetase. GSHS1.

AAD29849.1 AF075700 *Medicago truncatula*
putative glutathione synthetase. GSHS2.

SEQ ID NO: 166

BAA83711.1 AB014484 *Nicotiana tabacum*
heat shock factor. NtHSF2.

AAF37579.1 AF235958 *Medicago sativa*
heat shock transcription factor. HSFA4-6. MsHSFA4-6.

CAA58117.1 X82943 *Zea mays*
heat shock factor. hsfb.

CAA47868.1 X67599 *Lycopersicon esculentum*
heat stress transcription factor 8. hsf8.

CAA47869.1 X67600 *Lycopersicon peruvianum*
heat shock transcription factor 8. hsf8.

CAA47870.1 X67601 *Lycopersicon peruvianum*
heat stress transcription factor HSF30. hsf30.

AAF74563.1 AF208544 *Lycopersicon peruvianum*
heat stress transcription factor A3. HSFA3.

CAA87080.1 Z46956 *Glycine max*
heat shock transcription factor 5. HSF.

CAA87076.1 Z46952 *Glycine max*
heat shock transcription factor 21. HSF.

CAA39034.1 X55347 *Lycopersicon peruvianum*
heat stress transcription factor. Lp-HSF24.

BAA83710.1	AB014483	Nicotiana tabacum	heat shock factor. NtHSF1.
CAA87077.1	Z46953	Glycine max	heat shock transcription factor 34. HSF. corresponds to longest open reading frame; preceeded by four short open reading frames in the 5' leader sequence.
BAB19067.1	AP002744	Oryza sativa	putative heat shock factor protein 1 (HSF 1). P0006C01.9.
CAA09301.1	AJ010644	Pisum sativum	heat shock transcription factor (HSFA). hsfA.
CAA87079.1	Z46955	Glycine max	heat shock transcription factor 31. HSF.
CAA87075.1	Z46951	Glycine max	heat shock transcription factor 29. HSF.
CAA09300.1	AJ010643	Pisum sativum	heat shock transcription factor (HSFA). hsfA.
SEQ ID NO: 168			
BAA83710.1	AB014483	Nicotiana tabacum	heat shock factor. NtHSF1.
CAA39034.1	X55347	Lycopersicon peruvianum	heat stress transcription factor. Lp-HSF24.
CAA87077.1	Z46953	Glycine max	heat shock transcription factor 34. HSF. corresponds to longest open reading frame; preceeded by four short open reading frames in the 5' leader sequence.
CAA87080.1	Z46956	Glycine max	heat shock transcription factor 5. HSF.
CAA47869.1	X67600	Lycopersicon peruvianum	heat shock transcription factor 8. hsf8.
CAA47868.1	X67599	Lycopersicon esculentum	heat stress transcription factor 8. hsf8.
BAA83711.1	AB014484	Nicotiana tabacum	heat shock factor. NtHSF2.
CAA58117.1	X82943	Zea mays	heat shock factor. hsfB.
CAA87075.1	Z46951	Glycine max	heat shock transcription factor 29. HSF.
CAA87076.1	Z46952	Glycine max	heat shock transcription factor 21. HSF.
CAA47870.1	X67601	Lycopersicon peruvianum	heat stress transcription factor HSF30. hsf30.
AAF74563.1	AF208544	Lycopersicon peruvianum	heat stress transcription factor A3. HSFA3.
AAF37579.1	AF235958	Medicago sativa	heat shock transcription factor. HSFA4-6. MsHSFA4-6.

CAA87079.1	Z46955	Glycine max	heat shock transcription factor 31. HSF.
BAB19067.1	AP002744	Oryza sativa	putative heat shock factor protein 1 (HSF 1). P0006C01.9.
CAA09301.1	AJ010644	Pisum sativum	heat shock transcription factor (HSFA). hsfA.
CAA09300.1	AJ010643	Pisum sativum	heat shock transcription factor (HSFA). hsfA.
SEQ ID NO: 169			
AAB72109.1	AF022217	Brassica rapa	low molecular weight heat-shock protein. BcHSP17.6. 17.6 kDa; cytosolic class I.
CAB93512.1	AJ243565	Brassica oleracea	putative class I small heat shock protein. HSP17.7-a protein. hsp17.7-a.
CAA37847.1	X53851	Daucus carota	heat shock protein.
AAD49336.1	AF166277	Nicotiana tabacum	low molecular weight heat-shock protein. LHS-1. TLHS-1.
BAA33062.1	AB017273	Cuscuta japonica	low-molecular-weight heat shock protein. CJHSP17.
CAB36910.1	AJ000691	Quercus suber	stress protein chaperone. heat shock protein 17.4. hsp17.
CAA08908.1	AJ009880	Castanea sativa	molecular chaperone. cytosolic class I small heat-shock protein HSP17.5. hsp17.5.
AAA33975.1	M11395	Glycine max	small heat shock protein.
CAA25578.1	X01104	Glycine max	heat shock protein 6871 (aa 1-153).
AAB03893.1	M11318	Glycine max	17.5 kd heat shock protein Gmhsp17.6L.
CAA41547.1	X58711	Medicago sativa	heat shock protein.
AAB63310.1	U46544	Helianthus annuus	18.6 kDa heat-shock protein. Class I low-molecular-weight heat-shock protein.
CAB08441.1	Z95153	Helianthus annuus	17.6 kD class I small heat-shock protein HSP17.6. Ha hsp17.6.
CAA42222.1	X59701	Helianthus annuus	17.6 kDa heat shock protein.
CAA37848.1	X53852	Daucus carota	heat shock protein.
AAC39360.1	U63631	Fragaria x ananassa	LMW heat shock protein.

AAA33672.1	M33899	Pisum sativum	18.1 kDa heat shock protein (hsp18.1).
AAB63311.1	U46545	Helianthus annuus	17.7 kDa heat shock protein. Class I low-molecular-weight heat-shock protein.
AAA33974.1	M11317	Glycine max	17.6 kd heat shock protein Gmhsp17.6L.
CAA63903.1	X94193	Pennisetum glaucum	heat shock protein 17.9. hsp17.9.
AAA61632.1	U08601	Papaver somniferum	low molecular weight heat-shock protein.
CAB55634.2	AJ237596	Helianthus annuus	17.9 kDa heat-shock protein. hsp17.9.
AAC78392.1	U83669	Oryza sativa	low molecular mass heat shock protein Oshsp17.3. OSHSP17.3. class I LMMHSP.
AAA33910.1	M80939	Oryza sativa	16.9 kDa heat shock protein.
BAA02160.1	D12635	Oryza sativa	'low molecular weight heat shock protein'.
CAA43210.1	X60820	Oryza sativa	16.9 KD low molecular weight heat shock protein.
CAA37864.1	X53870	Chenopodium rubrum	heat-shock protein.
AAA33909.1	M80938	Oryza sativa	16.9 kDa heat shock protein.
AAC78393.1	U83670	Oryza sativa	low molecular mass heat shock protein Oshsp18.0. OSHSP18.0. class I LMMHSP.
AAB39856.1	U81385	Oryza sativa	heat shock protein. Oshsp16.9C. class I, low molecular mass.
AAD30454.1	AF123257	Lycopersicon esculentum	17.6 kD class I small heat shock protein. HSP17.6.
AAA33671.1	M33900	Pisum sativum	17.9 kDa heat shock protein (hsp17.9).
AAC78394.1	U83671	Oryza sativa	low molecular mass heat shock protein Oshsp17.7. OSHSP17.7. class I LMMHSP.
CAB93514.1	AJ243567	Brassica oleracea	Putative class I small heat shock protein. HSP17.x protein. hsp17.x.
CAA63901.1	X94191	Pennisetum glaucum	heat shock protein 17.0. hsp17.0.
CAA63902.1	X94192	Pennisetum glaucum	heat shock protein 16.9. hsp16.9.
AAD30452.1	AF123255	Lycopersicon esculentum	17.7 kD class I small heat shock protein. HSP17.7.

CAA46641.1	X65725	Zea mays	heat shock protein 17.2. Zmhsp 17.2. Class I low molecular weight heat shock protein.
CAA39603.1	X56138	Lycopersicon esculentum	small heat shock protein (class I).
CAA63570.1	X92983	Pseudotsuga menziesii	low molecular weight heat-shock protein.
AAD30453.1	AF123256	Lycopersicon esculentum	17.8 kD class I small heat shock protein. HSP17.8.
CAA63571.1	X92984	Pseudotsuga menziesii	low molecular weight heat-shock protein.
CAA31785.1	X13431	Triticum aestivum	put. heat shock protein (AA 1 -151).
CAA53286.1	X75616	Oryza sativa	heat shock protein 17.8.
SEQ ID NO: 170			
AAC14577.1	U72396	Lycopersicon esculentum	class II small heat shock protein Le-HSP17.6. heat treatment/chilling tolerance related protein from tomato fruit.
AAA33670.1	M33901	Pisum sativum	17.7 kDa heat shock protein (hsp17.7).
CAA82653.1	Z29554	Helianthus annuus	17.9 kDa heat-shock protein.
AAD41409.1	AF159562	Prunus dulcis	cytosolic class II low molecular weight heat shock protein. hsp17.5.
CAA65020.1	X95716	Petroselinum crispum	small heat shock protein. cytoplasmic class II HSP.
AAC36312.1	AF090115	Lycopersicon esculentum	cytosolic class II small heat shock protein HCT2. HSP17.4.
AAB01561.1	L47717	Picea glauca	heat shock protein 17.0. EMB27.
AAB39336.1	M99430	Ipomoea nil	small heat shock protein.
AAB01562.1	L47740	Picea glauca	class II cytoplasmic small molecular weight heat shock protein 17.1. EMB29, SMW HSP17.1.
CAA67206.1	X98617	Medicago sativa	17kD heat shock protein.
BAA99529.1	AP002484	Oryza sativa	putative heat shock protein, 18K - maize. P0489A01.20. contains ESTs C99035(E4351),AU093460(E3974).
CAA41218.1	X58279	Triticum aestivum	heat shock protein 17.3. Tahsp17.3.
CAA67726.1	X99346	Picea abies	small heat shock protein.

CAA38012.1	X54075	Zea mays	18kDa heat shock protein.
CAA38013.1	X54076	Zea mays	18kDa heat shock protein.
AAB26481.1	S59777	Zea mays	HSP18. HSP18. 18 kda heat shock protein; This sequence comes from Fig. 2B.
AAB39335.1	M99429	Ipomoea nil	small heat shock protein.
AAD09184.1	AF089845	Funaria hygrometrica	cytosolic II small heat shock protein HSP16.4II. HSP16.4II.
BAA04841.1	D21817	Lilium longiflorum	small heat shock protein. LIM11.
AAD09185.1	AF089846	Funaria hygrometrica	cytosolic II small heat shock protein HSP18.3II. HSP18.3II.
BAA04842.1	D21818	Lilium longiflorum	small heat shock protein. LIM12.
CAA63570.1	X92983	Pseudotsuga menziesii	low molecular weight heat-shock protein.
CAA63571.1	X92984	Pseudotsuga menziesii	low molecular weight heat-shock protein.
AAC39360.1	U63631	Fragaria x ananassa	LMW heat shock protein.
AAD09178.1	AF087640	Funaria hygrometrica	cytosolic I small heat shock protein HSP17.2IA. HSP17.2IA.
AAD09182.1	AF089843	Funaria hygrometrica	cytosolic I small heat shock protein HSP17.2IC. HSP17.2IC.
BAA04840.1	D21816	Lilium longiflorum	small heat shock protein. LIM10.
CAB93514.1	AJ243567	Brassica oleracea	Putative class I small heat shock protein. HSP17.x protein. hsp17.x.
AAD30452.1	AF123255	Lycopersicon esculentum	17.7 kD class I small heat shock protein. HSP17.7.
AAB63311.1	U46545	Helianthus annuus	17.7 kDa heat shock protein: Class I low-molecular-weight heat-shock protein.
CAA31785.1	X13431	Triticum aestivum	put. heat shock protein (AA 1 -151).
CAA63901.1	X94191	Pennisetum glaucum	heat shock protein 17.0. hsp17.0.
AAA33672.1	M33899	Pisum sativum	18.1 kDa heat shock protein (hsp18.1).
CAA41547.1	X58711	Medicago sativa	heat shock protein.

CAA46641.1	X65725	Zea mays	heat shock protein 17.2. Zmhspl 17.2. Class I low molecular weight heat shock protein.
AAB39856.1	U81385	Oryza sativa	heat shock protein. Oshspl6.9C. class I, low molecular mass.
AAC78394.1	U83671	Oryza sativa	low molecular mass heat shock protein Oshspl17.7. OSHSP17.7. class I LMMHSP.
AAC78392.1	U83669	Oryza sativa	low molecular mass heat shock protein Oshspl17.3. OSHSP17.3. class I LMMHSP.
CAA39603.1	X56138	Lycopersicon esculentum	small heat shock protein (class I).
AAA33910.1	M80939	Oryza sativa	16.9 kDa heat shock protein.
AAA33909.1	M80938	Oryza sativa	16.9 kDa heat shock protein.
CAA43210.1	X60820	Oryza sativa	16.9 KD low molecular weight heat shock protein.
AAD30453.1	AF123256	Lycopersicon esculentum	17.8 kD class I small heat shock protein. HSP17.8.
AAA34294.1	L14444	Triticum aestivum	heat shock protein 16.9C. hsp16.9C.
CAA69172.1	Y07844	Hordeum vulgare	17 kDa class I small heat shock protein. hsp17. putative.
AAD30454.1	AF123257	Lycopersicon esculentum	17.6 kD class I small heat shock protein. HSP17.6.
SEQ ID NO: 171			
CAA82653.1	Z29554	Helianthus annuus	17.9 kDa heat-shock protein.
AAC14577.1	U72396	Lycopersicon esculentum	class II small heat shock protein Le-HSP17.6. heat treatment/chilling tolerance related protein from tomato fruit.
CAA65020.1	X95716	Petroselinum crispum	small heat shock protein. cytoplasmic class II HSP.
AAB39336.1	M99430	Ipomoea nil	small heat shock protein.
AAA33670.1	M33901	Pisum sativum	17.7 kDa heat shock protein (hsp17.7).
AAD41409.1	AF159562	Prunus dulcis	cytosolic class II low molecular weight heat shock protein. hsp17.5.
CAA67206.1	X98617	Medicago sativa	17kD heat shock protein.
BAA99529.1	AP002484	Oryza sativa	putative heat shock protein, 18K - maize. P0489A01.20. contains ESTs C99035(E4351),AU093460(E3974).

AAC36312.1	AF090115	<i>Lycopersicon esculentum</i>	cytosolic class II small heat shock protein HCT2. HSP17.4.
CAA38012.1	X54075	<i>Zea mays</i>	18kDa heat shock protein.
CAA38013.1	X54076	<i>Zea mays</i>	18kDa heat shock protein.
CAA41218.1	X58279	<i>Triticum aestivum</i>	heat shock protein 17.3. Tahsp17.3.
AAB26481.1	S59777	<i>Zea mays</i>	HSP18. HSP18. 18 kda heat shock protein; This sequence comes from Fig. 2B.
AAB01561.1	L47717	<i>Picea glauca</i>	heat shock protein 17.0. EMB27.
AAB39335.1	M99429	<i>Ipomoea nil</i>	small heat shock protein.
AAB01562.1	L47740	<i>Picea glauca</i>	class II cytoplasmic small molecular weight heat shock protein 17.1. EMB29, SMW HSP17.1.
CAA67726.1	X99346	<i>Picea abies</i>	small heat shock protein.
AAD09184.1	AF089845	<i>Funaria hygrometrica</i>	cytosolic II small heat shock protein HSP16.4II. HSP16.4II.
BAA04841.1	D21817	<i>Lilium longiflorum</i>	small heat shock protein. LIM11.
BAA04842.1	D21818	<i>Lilium longiflorum</i>	small heat shock protein. LIM12.
AAD09185.1	AF089846	<i>Funaria hygrometrica</i>	cytosolic II small heat shock protein HSP18.3II. HSP18.3II.
BAA04840.1	D21816	<i>Lilium longiflorum</i>	small heat shock protein. LIM10.
CAA63570.1	X92983	<i>Pseudotsuga menziesii</i>	low molecular weight heat-shock protein.
CAA63571.1	X92984	<i>Pseudotsuga menziesii</i>	low molecular weight heat-shock protein.
AAD30452.1	AF123255	<i>Lycopersicon esculentum</i>	17.7 kD class I small heat shock protein. HSP17.7.
AAD09178.1	AF087640	<i>Funaria hygrometrica</i>	cytosolic I small heat shock protein HSP17.2IA. HSP17.2IA.
AAB63311.1	U46545	<i>Helianthus annuus</i>	17.7 kDa heat shock protein. Class I low-molecular-weight heat-shock protein.
CAA39603.1	X56138	<i>Lycopersicon esculentum</i>	small heat shock protein (class I).
AAC39360.1	U63631	<i>Fragaria x ananassa</i>	LMW heat shock protein.

AAA33672.1	M33899	Pisum sativum	18.1 kDa heat shock protein (hsp18.1).
AAD30453.1	AF123256	Lycopersicon esculentum	17.8 kD class I small heat shock protein. HSP17.8.
AAD30454.1	AF123257	Lycopersicon esculentum	17.6 kD class I small heat shock protein. HSP17.6.
CAA41547.1	X58711	Medicago sativa	heat shock protein.
CAA31785.1	X13431	Triticum aestivum	put. heat shock protein (AA 1 -151).
AAB39856.1	U81385	Oryza sativa	heat shock protein. Oshsp16.9C. class I, low molecular mass.
CAA41546.1	X58710	Medicago sativa	heat shock protein.
CAB93514.1	AJ243567	Brassica oleracea	Putative class I small heat shock protein. HSP17.x protein. hsp17.x.
CAA63901.1	X94191	Pennisetum glaucum	heat shock protein 17.0. hsp17.0.
AAA33910.1	M80939	Oryza sativa	16.9 kDa heat shock protein.
AAA33909.1	M80938	Oryza sativa	16.9 kDa heat shock protein.
CAA43210.1	X60820	Oryza sativa	16.9 KD low molecular weight heat shock protein.
AAB03097.1	U21723	Glycine max	Hsp22.3. Gmhsp22.3. low molecular weight heat shock protein.
AAC78394.1	U83671	Oryza sativa	low molecular mass heat shock protein Oshsp17.7. OSHSP17.7. class I LMMHSP.
AAC78392.1	U83669	Oryza sativa	low molecular mass heat shock protein Oshsp17.3. OSHSP17.3. class I LMMHSP.
AAD09182.1	AF089843	Funaria hygrometrica	cytosolic I small heat shock protein HSP17.2IC. HSP17.2IC.

SEQ ID NO: 173

AAD30456.1	AF123259	Lycopersicon esculentum	heat shock protein 90. HSP90.
AAF31705.1	AF221856	Euphorbia esula	heat-shock protein 80.
AAC32131.1	AF051230	Picea mariana	heat shock protein. Sb40. similar to Oryza sativa heat shock protein 82 encoded by GenBank Accession Number Z11920.
AAF64453.1	AF239931	Euphorbia esula	putative heat-shock protein 90. GRP94; similar to endoplasmic reticulum homolog precursor; contains the endoplasmic reticulum targeting sequence KDEL at the 3'-tail.

CAA78738.1	Z15018	Oryza sativa	heat shock protein. heat shock protein hsp82. hsp82.
SEQ ID NO: 174			
AAG43546.1	AF211528	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 4. ACRE4. similar to Nicotiana glutinosa Ntr truncated N resistance protein encoded by GenBank Accession Number U15605.
AAA50763.1	U15605	Nicotiana glutinosa	virus resistance. N.
CAA08797.1	AJ009719	Solanum tuberosum	disease resistance. NL25. nl25.
CAA08798.1	AJ009720	Solanum tuberosum	disease resistance. NL27. nl27.
AAG09951.1	AF175388	Glycine max	resistance protein LM6.
AAG09954.1	AF175399	Glycine max	resistance protein MG13.
AAD25974.1	AF093647	Linum usitatissimum	flax rust resistance protein. L.
AAD25966.1	AF093639	Linum usitatissimum	flax rust resistance protein. L.
AAD25969.1	AF093642	Linum usitatissimum	flax rust resistance protein. L.
AAD25965.1	AF093638	Linum usitatissimum	flax rust resistance protein. L.
AAD25968.1	AF093641	Linum usitatissimum	flax rust resistance protein. L.
AAA91021.1	U27081	Linum usitatissimum	rust resistance. L6tr. L6: The shorter of two alternate protein products of The L6 gene that results from retention of intron 3 in the mRNA; truncated L6 gene product.
AAA91022.1	U27081	Linum usitatissimum	rust resistance. L6. L6. The longer of two alternate proteins encoded by the L6 gene.
AAD25967.1	AF093640	Linum usitatissimum	flax rust resistance protein. L.
AAK28803.1	AF310958	Linum usitatissimum	resistance-like protein P1-A. p1-A.
AAK28808.1	AF310961	Linum usitatissimum	resistance-like protein P3-A. p3-A.
AAK28805.1	AF310960	Linum usitatissimum	resistance-like protein P2-A. p2-A.
AAD25976.1	AF093649	Linum usitatissimum	flax rust resistance protein. L.
AAD25973.1	AF093646	Linum usitatissimum	flax rust resistance protein. L.

AAD25972.1	AF093645	Linum usitatissimum flax rust resistance protein. L.
AAD25971.1	AF093644	Linum usitatissimum flax rust resistance protein. L.
AAD25970.1	AF093643	Linum usitatissimum flax rust resistance protein. L.
AAD25975.1	AF093648	Linum usitatissimum flax rust resistance protein. L.
AAG48132.1	AF322632	Glycine max putative resistance protein. L20a.
AAG01052.1	AF175395	Glycine max resistance protein MG23.
CAC35330.1	AJ310155	Linum usitatissimum N1-D protein. N1-D. N locus resistance gene homolog: TIR-NBS-LRR protein.
CAC35333.1	AJ310158	Linum usitatissimum N2-C protein. N2-C. N locus rust resistance gene homolog: TIR-NBS-LRR protein.
AAG48133.1	AF322633	Glycine max putative resistance protein. L33.
AAF61452.1	AF139523	Tagetes erecta disease-resistance protein NRSA1.
CAC35334.1	AJ310159	Linum usitatissimum N2-D protein. N2-D. N locus rust resistance gene homolog: TIR-NBS-LRR protein.
CAC35337.1	AJ310162	Linum usitatissimum Nbi-C protein. Nbi-C. N locus rust resistance gene homolog: TIR-NBS-LRR protein.
CAC35339.1	AJ310164	Linum usitatissimum Nho-C protein. Nho-C. N locus rust resistance gene homolog: TIR-NBS-LRR protein.
CAC35326.1	AJ310151	Linum usitatissimum Ngc-C protein. Ngc-C. N rust resistance gene homolog: TIR-NBS-LRR protein.
AAG01051.1	AF175394	Glycine max resistance protein LM12.
CAC35338.1	AJ310163	Linum usitatissimum Nbi-D protein. Nbi-D. N locus rust resistance gene homolog: TIR-NBS-LRR protein.
CAC35329.1	AJ310154	Linum usitatissimum N1-C protein. N1-C. N locus resistance gene homolog: TIR-NBS-LRR protein.
AAK28804.1	AF310959	Linum usitatissimum resistance-like protein P1-B. p1-B.
AAK28809.1	AF310962	Linum usitatissimum resistance-like protein P3-B. p3-B.
CAC35332.1	AJ310157	Linum usitatissimum N2-B protein. N2-B. N locus rust resistance gene homolog: TIR-NBS-LRR protein.
CAC35328.1	AJ310153	Linum usitatissimum N1-B protein. N1-B. N locus resistance gene homolog: TIR-NBS-LRR protein.

CAC35325.1	AJ310150	Linum usitatissimum	Ngc-B protein. Ngc-B. N rust resistance gene homolog: TIR-NBS-LRR protein.
CAC35336.1	AJ310161	Linum usitatissimum	Nbi-B protein. Nbi-B. N locus rust resistance gene homolog: TIR-NBS-LRR protein.
CAC35321.1	AJ310150	Linum usitatissimum	Ngc-D protein. Ngc-D. N rust resistance gene: TIR-NBS-LRR protein.
CAC35331.1	AJ310156	Linum usitatissimum	N2-A protein. N2-A. N locus rust resistance gene homolog: TIR-NBS-LRR protein.
CAC35323.1	AJ310150	Linum usitatissimum	Ngc-A protein. Ngc-A. N rust resistance gene homolog: TIR-NBS-LRR protein.
AAB47618.1	U73916	Linum usitatissimum	rust resistance protein M. nucleotide-binding site, leucine-rich repeat class of plant disease resistance protein.
AAG01053.1	AF175396	Glycine max	resistance protein MG55.
CAC35327.1	AJ310152	Linum usitatissimum	N1-A protein. N1-A. N locus resistance gene homolog: TIR-NBS-LRR protein.
AAK28811.1	AF310966	Linum usitatissimum	resistance-like protein P-B. p-B.
SEQ ID NO: 175			
CAB52796.1	AJ245861	Solanum tuberosum	respiratory chain. putative internal rotenone-insensitive NADH dehydrogenase. nda1.
CAB52797.1	AJ245862	Solanum tuberosum	respiratory chain. putative external rotenone-insensitive NADH dehydrogenase. ndb1.
SEQ ID NO: 176			
BAA05648.1	D26601	Nicotiana tabacum	protein kinase.
CAA08997.1	AJ010093	Brassica napus	MAP3K beta 1 protein kinase. MAP3K beta 1.
CAA08995.1	AJ010091	Brassica napus	MAP3K alpha 1 protein kinase. MAP3K alpha 1.
AAF34436.1	AF172282	Oryza sativa	similar to mitogen-activated protein kinases, DUPR11.32.
CAB54520.1	AJ238845	Brassica napus	putative role in cell cycle control. MAP3K epsilon 1 protein kinase. MAP3Ke1.
CAA08758.1	AJ009609	Brassica napus	BnMAP4K alpha2.
CAA08757.1	AJ009608	Brassica napus	BnMAP4K alpha1.
AAC83393.1	U83625	Zea mays	protein kinase ZmMEK1. mitogen-activated; ERK-activating protein kinase (MEK) homolog.

AAG53979.1	AF325168	Nicotiana tabacum	mitogen-activated protein kinase 2. MEK2. upstream kinase for SIPK and WIPK, two tobacco MAP kinases.
AAG40578.1	AF216314	Oryza sativa	MAP kinase kinase 1. protein kinase; MEK1.
CAA04261.2	AJ000728	Lycopersicon esculentum	MAP kinase kinase. mek1.
AAF67262.1	AF165186	Nicotiana tabacum	MAP kinase kinase.
AAG45491.1	AY013245	Oryza sativa	36I5.3. putative serine/threonine kinase.
BAB32405.1	AB055514	Nicotiana tabacum	NQK1 MAPKK. nqk1.
AAG49001.1	AY013246	Hordeum vulgare	putative serine/threonine kinase. 635P2.3.
AAF19403.1	AF203481	Lycopersicon esculentum	phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca ²⁺ /CaM kinase family; lacks the autoinhibitory region and EF hands.
AAF19402.1	AF203480	Lycopersicon esculentum	phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca ²⁺ /CaM kinase family; lacks the autoinhibitory region and EF hands.
CAC24705.1	AJ302651	Nicotiana tabacum	protein kinase. MAP kinase. mek1.
BAA06731.1	D31964	Nicotiana tabacum	NPK2. protein kinase.
AAG31141.1	AF305911	Oryza sativa	EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAF19401.1	AF203479	Glycine max	phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca ²⁺ /CaM kinase family; lacks the autoinhibitory region and EF hands.
AAD46406.1	AF096250	Lycopersicon esculentum	ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.
CAA73722.1	Y13273	Lycopersicon esculentum	putative protein kinase.
BAA05649.1	D26602	Nicotiana tabacum	protein kinase.
AAD23582.1	AF128443	Glycine max	probably involved in plant stress responses possibly regulates gene expression. SNF-1-like serine/threonine protein kinase. expressed in nodules, roots and leaves.
CAA06334.1	AJ005077	Lycopersicon esculentum	protein kinase. TCTR2 protein. TCTR2.

AAD10057.1	AF110519	<i>Lycopersicon esculentum</i> ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.
CAB89082.1	AJ277534	<i>Asparagus officinalis</i> S6 ribosomal protein kinase. pk1. putative.
AAC78558.1	AF030879	<i>Solanum tuberosum</i> protein kinase CPK1.
AAD10056.1	AF110518	<i>Lycopersicon esculentum</i> ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.
AAK18832.1	AC082645	<i>Oryza sativa</i> putative protein kinase. OSJNBb0033N16.9.
AAG31142.1	AF305912	<i>Hordeum vulgare</i> EDR1. EDR1. MAP kinase kinase kinase; similar to <i>Arabidopsis thaliana</i> EDR1.
AAC24961.1	AF009337	<i>Tradescantia virginiana</i> CDPK-related protein kinase. CRK1.
BAB21278.1	AP002844	<i>Oryza sativa</i> putative MAP kinase. P0410E03.9.
AAA61682.1	L27484	<i>Zea mays</i> calcium-dependent protein kinase. CDPK.
CAA56313.1	X79992	<i>Avena sativa</i> putative pp70 ribosomal protein S6 kinase. Aspk11.
AAD31900.1	AF145482	<i>Mesembryanthemum crystallinum</i> putative serine/threonine protein kinase.
AAC25423.1	AF072908	<i>Nicotiana tabacum</i> calcium-dependent protein kinase. CDPK1.
CAA71142.1	Y10036	<i>Cucumis sativus</i> SNF1-related protein kinase.
BAA83689.1	AB011968	<i>Oryza sativa</i> OsPK7. OsPK7. protein kinase.
CAA46554.1	X65604	<i>Hordeum vulgare</i> protein kinase. BKIN12.
CAA46556.1	X65606	<i>Hordeum vulgare</i> protein kinase. BKIN12.
CAA65500.1	X96723	<i>Medicago sativa</i> protein kinase. CDPK.
AAF05112.1	AF158091	<i>Mesembryanthemum crystallinum</i> day/night regulation of carbon fixation by crassulacean acid metabolism pathway. phosphoenolpyruvate carboxylase-kinase. SNIK. protein kinase; salt/night induced kinase; phosphorylase; member of Ca ²⁺ /Cam protein kinase family; lacks both CAM domain and autoinhibitory domain; Ser/Thr kinase.
AAD17800.1	AF090835	<i>Mesembryanthemum crystallinum</i> Ca ²⁺ -dependent protein kinase. CPK1. serine/threonine protein kinase.

CAA07813.1 AJ007990 *Hordeum vulgare*
SnRK1-type protein kinase. kin12a.

SEQ ID NO: 177

BAB16335.1 AP002818 *Oryza sativa*
putative NAM protein. P0436E04.18. contains ESTs E10793(C19698),E10793(C99379).

BAA84803.1 AP000559 *Oryza sativa*
Similar to NAM like protein (AC005310).

BAB19365.1 AP002542 *Oryza sativa*
putative NAM (no apical meristem) protein. P0679C08.4.

BAB16328.1 AP002818 *Oryza sativa*
putative NAM protein. P0436E04.11. contains ESTs R4069(AU032425),R4069(AU082730).

CAA63102.2 X92205 *Petunia x hybrida*
apical meristem formation. NAM.

CAA63101.1 X92204 *Petunia x hybrida*
apical meristem formation. NAM.

AAK13151.1 AC078829 *Oryza sativa*
putative NAM (no apical meristem) protein. OSJNBa0026O12.6.

BAB03447.1 AP002817 *Oryza sativa*
ESTs C96615(C10106),C26336(C12127),D21959(C10106) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21; NAM (no apical meristem) - like protein (AL021889).

BAA92400.1 AP001366 *Oryza sativa*
ESTs C96615(C10106),C26336(C12127),D21959(C10106) correspond to a region of the predicted gene. Similar to NAM (AL021889).

SEQ ID NO: 178

BAA25434.1 AB000708 *Raphanus sativus*
SAUR.

AAG14454.1 AF283706 *Tulipa gesneriana*
auxin-induced protein TGSAUR12. SAUR12. small auxin upregulated RNA.

AAG14455.1 AF283707 *Tulipa gesneriana*
auxin-induced protein TGSAUR21. SAUR21. small auxin upregulated RNA.

AAG14456.1 AF283708 *Tulipa gesneriana*
auxin-induced protein TGSAUR22. SAUR22. small auxin upregulated RNA.

SEQ ID NO: 179

BAA78738.1 AB023482 *Oryza sativa*
EST AU055776(S20048) corresponds to a region of the predicted gene.; Similar to Arabidopsis thaliana AP2 domain containing protein RAP2.10 mRNA, partial cds.(AF003103).

CAB96899.1 AJ251249 *Catharanthus roseus*
transcription factor. AP2-domain DNA-binding protein. orca3.

CAB96900.1 AJ251250 *Catharanthus roseus*
transcription factor. AP2-domain DNA-binding protein. orca3.

AAF76898.1	AF274033	Atriplex hortensis	apetala2 domain-containing protein.
CAC12822.1	AJ299252	Nicotiana tabacum	AP2 domain-containing transcription factor. ap2.
AAC14323.1	AF058827	Nicotiana tabacum	TSI1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pti6.
BAA97123.1	AB016265	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
CAB93940.1	AJ238740	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca2.
AAC24587.1	AF071893	Prunus armeniaca	AP2 domain containing protein. AP2DCP.
BAB03248.1	AB037183	Oryza sativa	ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
BAB16083.1	AB036883	Oryza sativa	transcriptional repressor. osERF3. osERF3. ERF protein family ERF3 associated repression domain.
BAA76734.1	AB024575	Nicotiana tabacum	ethylene responsive element binding factor.
CAB93939.1	AJ238739	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca1.
AAG43545.1	AF211527	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.
AAG43548.1	AF211530	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
AAG43549.1	AF211531	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
AAF23899.1	AF193803	Oryza sativa	transcription factor EREBP1. EREBP/AP2-like transcription factor.
AAK31271.1	AC079890	Oryza sativa	putative transcriptional factor. OSJNBb0089A17.22.
AAF63205.1	AF245119	Mesembryanthemum crystallinum	AP2-related transcription factor. CDBP. stress induced transcription factor.
BAA07321.1	D38123	Nicotiana tabacum	ERF1. ethylene-responsive transcription factor.
BAA97122.1	AB016264	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.
BAA97124.1	AB016266	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.

BAA94514.2 AP001800 *Oryza sativa*

Similar to *Arabidopsis thaliana* chromosome 4, BAC clone F9D16; putative Ap2 domain protein (AL035394).

AAC62619.1 AF057373 *Nicotiana tabacum*

transcription factor. ethylene response element binding protein 1. EREBP1.

AAK01088.1 AF298230 *Hordeum vulgare*

CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.

BAA99376.1 AP002526 *Oryza sativa*

ESTs AU093391(E60370), AU091593(C60458), AU093392(E60370) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* BAC F21J9; AP2 domain protein. (AC000103).

AAK01089.1 AF298231 *Hordeum vulgare*

CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.

AAG59618.1 AF239616 *Hordeum vulgare*

CRT/DRE-binding factor. CBF.

SEQ ID NO: 181

CAB71134.1 AJ271667 *Cicer arietinum*

putative proteasome regulatory subunit.

SEQ ID NO: 185

BAA85440.1 AP000616 *Oryza sativa*

ESTs AU055729(S20023), AU055730(S20023) correspond to a region of the predicted gene.; similar to *Medicago nodulin* N21-like protein (AC004218).

CAB53493.1 AJ245900 *Oryza sativa*

CAA303720.1 protein. q3037.20. Similar to *Medicago nodulin* N21 (MtN21).

BAB17350.1 AP002747 *Oryza sativa*

putative nodulin. P0698G03.34. contains ESTs D39891(S1543), D41717(S4395), AU033037(S1543).

SEQ ID NO: 186

BAA02724.1 D13506 *Glycine max*
early nodulin.

BAA33816.1 AB018378 *Glycine max*
early nodulin. GmENOD93.

BAA83560.1 AP000399 *Oryza sativa*

EST AU077941(C12908) corresponds to a region of the predicted gene. Similar to OsENOD93a gene for early nodulin (AB018375).

BAA33815.1 AB018377 *Oryza sativa*
early nodulin. OsENOD93b.

BAA83566.1 AP000399 *Oryza sativa*

ESTs C98280(C1391), D15843(C1391) correspond to a region of the predicted gene. Similar to OsENOD93a gene for early nodulin (AB018375).

BAA83568.1 AP000399 *Oryza sativa*

EST AU077972(C53511) corresponds to a region of the predicted gene. Similar to OsENOD93a gene for early nodulin (AB018375).

BAA83565.1	AP000399	Oryza sativa	ESTs C98096(C0688),C98097(C0688) correspond to a region of the predicted gene. Similar to OsENOD93a gene for early nodulin (AB018375).
AAD30134.1	AF140229	Oryza sativa	early nodulin.
BAA33814.1	AB018376	Oryza sativa	early nodulin. OsENOD93a.
BAA33813.1	AB018375	Oryza sativa	early nodulin. OsENOD93a.
BAA83567.1	AP000399	Oryza sativa	EST C97982(C0324) corresponds to a region of the predicted gene. Similar to OsENOD93a gene for early nodulin (AB018375).
BAA83559.1	AP000399	Oryza sativa	EST C97982(C0324) corresponds to a region of the predicted gene. Similar to OsENOD93a gene for early nodulin (AB018375).
BAA83557.1	AP000399	Oryza sativa	Similar to OsENOD93a gene for early nodulin (AB018375).
SEQ ID NO: 188			
AAA33811.1	L02830	Solanum tuberosum	calcium-binding protein.
AAG43547.1	AF211529	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 31. ACRE31. similar to Solanum tuberosum CAST calcium binding protein encoded by GenBank Accession Number L02830.
CAB63264.1	AJ251808	Lotus japonicus	calcium-binding protein. cbp1.
AAA34015.1	L01433	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-4. putative.
AAA92677.1	U13736	Pisum sativum	binds calcium. calmodulin-like protein.
AAF31152.1	AF078680	Olea europaea	calcium-binding protein. PCA23. Pca23.
AAA33948.1	L19359	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-5. putative.
AAD10245.1	AF030033	Phaseolus vulgaris	calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
AAF31151.1	AF078679	Olea europaea	calcium-binding protein. PCA18. Pca18.
AAA19571.1	U10150	Brassica napus	calcium binding. calmodulin. bcml.
AAC49587.1	U49105	Triticum aestivum	calmodulin TaCaM4-1. calcium-binding protein.

AAC49586.1	U49104	Triticum aestivum calmodulin TaCaM3-3. calcium-binding protein.
AAC49585.1	U49103	Triticum aestivum calmodulin TaCaM3-2. calcium-binding protein.
AAC49584.1	U48693	Triticum aestivum calmodulin TaCaM3-1. calcium-binding protein.
AAC49580.1	U48689	Triticum aestivum calmodulin TaCaM1-3. calcium-binding protein.
AAC49579.1	U48688	Triticum aestivum calmodulin TaCaM1-2. calcium binding protein.
AAC49578.1	U48242	Triticum aestivum calmodulin TaCaM1-1. calcium-binding.
AAA85157.1	U20297	Solanum tuberosum calcium-binding protein. calmodulin.
AAA85156.1	U20296	Solanum tuberosum calcium-binding protein. calmodulin.
AAA62351.1	U20295	Solanum tuberosum calcium-binding protein. calmodulin.
AAA85155.1	U20294	Solanum tuberosum calcium-binding protein. calmodulin.
AAA34014.1	L01432	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-3. putative.
AAA03580.1	L01431	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-2. putative.
AAA34013.1	L01430	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-1. putative.
AAA33901.1	L18913	Oryza sativa calcium binding protein, signal transduction. calmodulin. putative.
AAA33900.1	L18914	Oryza sativa calcium binding protein, signal transduction. calmodulin.
AAA92681.1	U13882	Pisum sativum calcium-binding protein. calmodulin.
CAA78288.1	Z12828	Oryza sativa calcium binding protein, signal transduction. calmodulin.
SEQ ID NO: 190		
AAF72197.1	AF263737	Euphorbia esula glutathione S-transferase. theta class GST.
AAG34815.1	AF243380	Glycine max glutathione S-transferase GST 25.
AAG34825.1	AF244682	Zea mays glutathione S-transferase GST 17.

AAG32474.1	AF309381	Oryza sativa subsp. japonica	putative glutathione S-transferase OsGSTZ1.
AAG34826.1	AF244683	Zea mays	glutathione S-transferase GST 18.
AAA33277.1	M64268	Dianthus caryophyllus	glutathione transferase. CARSR8.
CAA41279.1	X58390	Dianthus caryophyllus	glutathione s-transferase. CARSR8.
AAD09190.1	AF109714	Triticum aestivum	glutathione S-transferase. GST.
AAB60886.1	AF002211	Triticum aestivum	glutathione-S-transferase.
AAA51450.1	L05916	Dianthus caryophyllus	glutathione s-transferase. GST2.
AAC50036.1	U42463	Coccomyxa sp. PA	glutathione S-transferase. GST.
AAG34801.1	AF243366	Glycine max	glutathione S-transferase GST 11.
AAG32469.1	AF309376	Oryza sativa subsp. japonica	putative glutathione S-transferase OsGSTU6.
AAG34850.1	AF244707	Zea mays	glutathione S-transferase GST 42.
AAG34807.1	AF243372	Glycine max	glutathione S-transferase GST 17.
CAB38119.1	AJ010296	Zea mays	Glutathione transferase III(b). gst3b.
AAF23357.1	AF109194	Hordeum vulgare	glutathione-S-transferase.
AAG34849.1	AF244706	Zea mays	glutathione S-transferase GST 41.
CAB38118.1	AJ010295	Zea mays	Glutathione transferase III(a). gst3a.
AAG32475.1	AF309382	Oryza sativa subsp. japonica	putative glutathione S-transferase OsGSTF5.
AAB65163.1	AF002692	Solanum commersonii	glutathione S-transferase, class-phi. GST1. low temperature induced.
AAF29773.1	AF159229	Gossypium hirsutum	glutathione S-transferase. GST.
BAB39927.1	AP002914	Oryza sativa	putative glutathione S-transferase. P0493G01.1. contains ESTs
AU031696(R0596),C97559(C60386),C28218(C60386), D28287(R0596).			
AAG32473.1	AF309380	Oryza sativa subsp. japonica	putative glutathione S-transferase OsGSTU2.

CAA09188.1	AJ010449	<i>Alopecurus myosuroides</i> glutathione transferase. GST1b.
AAG34846.1	AF244703	<i>Zea mays</i> glutathione S-transferase GST 38.
AAG34812.1	AF243377	<i>Glycine max</i> glutathione S-transferase GST 22.
CAA55039.1	X78203	<i>Hyoscyamus muticus</i> glutathione transferase.
AAG34803.1	AF243368	<i>Glycine max</i> glutathione S-transferase GST 13.
CAA09189.1	AJ010450	<i>Alopecurus myosuroides</i> glutathione transferase. GST1c.
AAG34808.1	AF243373	<i>Glycine max</i> glutathione S-transferase GST 18.
AAG34813.1	AF243378	<i>Glycine max</i> glutathione S-transferase GST 23.
AAD10129.1	AF004358	<i>Aegilops tauschii</i> chloroacetamide herbicide metabolism. glutathione S-transferase TSI-1. GST isozyme.
AAG41204.1	AF321437	<i>Suaeda maritima</i> glutathione transferase.
AAG34810.1	AF243375	<i>Glycine max</i> glutathione S-transferase GST 20.
AAG34804.1	AF243369	<i>Glycine max</i> glutathione S-transferase GST 14.
AAG34814.1	AF243379	<i>Glycine max</i> glutathione S-transferase GST 24.
AAG32472.1	AF309379	<i>Oryza sativa</i> subsp. <i>japonica</i> putative glutathione S-transferase OsGSTU3.
AAG32471.1	AF309378	<i>Oryza sativa</i> subsp. <i>japonica</i> putative glutathione S-transferase OsGSTU4.
CAA09187.1	AJ010448	<i>Alopecurus myosuroides</i> glutathione transferase. GST1a.
AAG34835.1	AF244692	<i>Zea mays</i> glutathione S-transferase GST 27.
AAF64449.1	AF239927	<i>Euphorbia esula</i> glutathione S-transferase. theta class GST.
AAG16758.1	AY007560	<i>Lycopersicon esculentum</i> putative glutathione S-transferase T3.
AAG34848.1	AF244705	<i>Zea mays</i> glutathione S-transferase GST 40.

SEQ ID NO: 191

AAD32141.1 AF123503 *Nicotiana tabacum*
Nt-gh3 deduced protein.

CAA42636.1 X60033 *Glycine max*
auxin-responsive GH3 product. GH3.

BAA96221.1 AP002094 *Oryza sativa*
ESTs C19814(E10971), AU090481(E10971) correspond to a region of the predicted gene.
Similar to *Arabidopsis thaliana* chromosome 2, sequence from clones T3F17, F11C10,
F13A10; auxin-responsive GH3-like protein (AC006526).

SEQ ID NO: 192

AAG13589.1 AC051633 *Oryza sativa*
putative ubiquitin protein. OSJNBb0015I11.23.

SEQ ID NO: 193

CAC09348.1 AL442007 *Oryza sativa*
putative phosphoglycerate dehydrogenase. H0212B02.4.

CAA79702.2 Z21493 *Solanum tuberosum*
mitochondrial formate dehydrogenase precursor.

BAA77337.1 AB019533 *Oryza sativa*
Nad-dependent formate dehydrogenase.

BAA36181.1 D88272 *Hordeum vulgare*
formate dehydrogenase.

SEQ ID NO: 194

AAD46412.1 AF096262 *Lycopersicon esculentum*
ER6 protein. ethylene-inducible; similar to sequence F21M12 from *Arabidopsis thaliana*
encoded by GenBank Accession Number AC000132.

SEQ ID NO: 195

AAK13154.1 AC078829 *Oryza sativa*
putative casein kinase. OSJNBa0026O12.5.

BAA92986.1 AP001550 *Oryza sativa*
ESTs D41826(S4655), C22685(S4655) correspond to a region of the predicted gene.; Similar
to *Arabidopsis thaliana* chromosome 4, BAC clone F16A16; protein kinase-like protein
(AL035353).

AAF19807.1 AF180356 *Brassica oleracea*
casein kinase I-like protein. CK1b. strong similarity to *Arabidopsis thaliana* casein kinase 1.

AAD20819.1 AF107592 *Dendrobium grex Madame Thong-In*
putative casein kinase I. otg16.

AAF19403.1 AF203481 *Lycopersicon esculentum*
phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca²⁺/CaM kinase
family; lacks the autoinhibitory region and EF hands.

AAF19402.1 AF203480 *Lycopersicon esculentum*
phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca²⁺/CaM kinase
family; lacks the autoinhibitory region and EF hands.

BAA05648.1 D26601 *Nicotiana tabacum*
protein kinase.

AAF23901.2	AF194414	Oryza sativa	calcium-dependent protein kinase. CDPK5. OsCDPK5.
AAC04324.1	U73937	Nicotiana tabacum	ethylene signal transduction. PK12 protein kinase. PK12. component of the LAMMER family of protein kinases; dual-specificity protein kinase.
AAF23900.1	AF194413	Oryza sativa	calcium-dependent protein kinase. CDPK1. OsCDPK1.
BAA34675.1	AB011670	Triticum aestivum	wpk4 protein kinase. wpk4.
BAA13440.1	D87707	Ipomoea batatas	calcium dependent protein kinase. CDPK.
AAD17800.1	AF090835	Mesembryanthemum crystallinum	Ca ²⁺ -dependent protein kinase. CPK1. serine/threonine protein kinase.
CAA57157.1	X81394	Oryza sativa	calcium-dependent protein kinase. OSCP2.
AAD23582.1	AF128443	Glycine max	probably involved in plant stress responses possibly regulates gene expression. SNF-1-like serine/threonine protein kinase. expressed in nodules, roots and leaves.
CAA39936.1	X56599	Daucus carota	calcium- dependent protein kinase. DcPK431.
BAA12715.1	D85039	Zea mays	calcium-dependent protein kinase.
CAA58750.1	X83869	Daucus carota	CDPK-related protein kinase. CRK (or PK421).
AAB80693.1	U69174	Glycine max	calmodulin-like domain protein kinase isoenzyme gamma. CDPK gamma.
AAF21062.1	AF216527	Dunaliella tertiolecta	calcium-dependent protein kinase. CPK1; CDPK.
CAA74646.1	Y14274	Sorghum bicolor	putative serine/threonine protein kinase. SNFL3.
AAD28192.2	AF115406	Solanum tuberosum	calcium-dependent protein kinase. CDPK; catalytic domain.
BAA05649.1	D26602	Nicotiana tabacum	protein kinase.
AAA69507.1	U28376	Zea mays	calcium-dependent protein kinase. MZECDPK2.
AAB05457.1	U55768	Oryza sativa	SNF1-related protein kinase. RSk1. Ser/Thr protein kinase homolog.
AAG36872.1	AF239819	Zea mays	protein kinase CK2 catalytic subunit CK2 alpha-3.
CAA89202.1	Z49233	Chlamydomonas eugametos	calcium-stimulated protein kinase.

CAA72362.1	Y11649	Zea mays	protein kinase CK2, alpha subunit.
CAA72290.1	Y11526	Zea mays	casein kinase II alpha subunit. CK2.
CAA43659.1	X61387	Zea mays	casein kinase II alpha subunit. ZMACK2.
CAA65244.1	X95997	Solanum tuberosum	SNF1-related protein kinase. PKIN1.
AAF76187.1	AF271237	Zea mays	casein kinase II alpha subunit.
BAB21591.1	AB036788	Oryza sativa	casein kinase II alpha subunit. OSCKA2.
BAB21589.1	AB036786	Oryza sativa	casein kinase II alpha subunit. OSCKA2.
CAB89082.1	AJ277534	Asparagus officinalis	S6 ribosomal protein kinase. pk1. putative.
AAF06970.1	AF162662	Kalanchoe fedtschenkoi	phosphoenolpyruvate carboxylase kinase. calcium-independent protein kinase.
AAF06969.1	AF162661	Kalanchoe fedtschenkoi	phosphoenolpyruvate carboxylase kinase. calcium-independent protein kinase.
CAA41172.1	X58194	Oryza sativa	cdc2+/CDC28-related protein kinase.
CAA65500.1	X96723	Medicago sativa	protein kinase. CDPK.
BAA12691.1	D84507	Zea mays	CDPK-related protein kinase. Does not require calcium for its activity (by similarity).
AAB47181.1	S82324	Zea mays	/gene="calcium/calmodulin-dependent protein kinase. This sequence comes from Fig. 1.
CAA07481.1	AJ007366	Zea mays	calcium-dependent protein kinase.
BAA99439.1	AP002743	Oryza sativa	putative protein kinase. P0710E05.26. contains ESTs C22394(C30013),C22393(C30013).
BAB12687.1	AP002746	Oryza sativa	putative protein kinase. P0671B11.2. contains ESTs C22394(C30013),C22393(C30013).
AAF40430.1	AF234652	Mesembryanthemum crystallinum	protein kinase MK5.
BAB21081.1	AP002819	Oryza sativa	putative calcium-dependent protein kinase. P0501G01.10.
SEQ ID NO: 196			
AAF37267.1	AF220406	Vitis riparia	26S proteasome regulatory ATPase subunit S10b. Rev136-3.
SEQ ID NO: 197			

BAA08104.1	D45074	<i>Panicum miliaceum</i> 2-oxoglutarate/malate translocator. mitochondrial 2-oxoglutarate/malate translocator.
BAA08103.1	D45073	<i>Panicum miliaceum</i> 2-oxoglutarate/malate translocator. mitochondrial 2-oxoglutarate/malate translocator.
BAA08105.1	D45075	<i>Panicum miliaceum</i> 2-oxoglutarate/malate translocator. mitochondrial 2-oxoglutarate/malate translocator.
CAA72107.1	Y11220	<i>Solanum tuberosum</i> mitochondrial uncoupling protein.
CAC12820.1	AJ299250	<i>Nicotiana tabacum</i> mitochondrial 2-oxoglutarate/malate carrier protein. momc1.
AAB71744.1	U75346	<i>Chlamydomonas reinhardtii</i> envelope protein. LIP-36G2. low CO2 inducible carrier protein LIP-36 with a molecular weight of 36 kDa.
AAB71743.1	U75345	<i>Chlamydomonas reinhardtii</i> envelope protein. LIP-36G1. low CO2 inducible carrier protein LIP-36 with a molecular weight of 36 kDa.
CAA07568.1	AJ007580	<i>Ribes nigrum</i> Mitochondrial carrier protein. prib7.
BAB40117.1	AP003311	<i>Oryza sativa</i> putative peroxisomal Ca-dependent solute carrier protein. P0024G09.9.
BAB16462.1	AP002483	<i>Oryza sativa</i> putative peroxisomal Ca-dependent solute carrier protein. P0019D06.21.
CAA56325.1	X80023	<i>Triticum turgidum</i> ATP/ADP carrier protein.
CAA46311.1	X65194	<i>Chlamydomonas reinhardtii</i> mitochondrial ADP/ATP translocator protein. CRANT.
CAA67107.1	X98474	<i>Solanum tuberosum</i> mitochondrial energy transfer protein. brittle1.
CAC27140.1	AJ132535	<i>Picea abies</i> ADP, ATP carrier protein precursor.
CAA69726.1	Y08499	<i>Betula pendula</i> mitochondrial phosphate translocator.
BAA31583.1	AB016064	<i>Zea mays</i> mitochondrial phosphate transporter.
CAB61741.1	AJ275306	<i>Cicer arietinum</i> mitochondrial phosphate transporter.
AAG45489.1	AY013245	<i>Oryza sativa</i> 36I5.1. putative mitochondrial carrier protein.
BAA31584.1	AB016065	<i>Oryza sativa</i> mitochondrial phosphate transporter.
BAA92520.1	AP001383	<i>Oryza sativa</i> ESTs AU068633(C30614),AU068634(C30614) correspond to a region of the predicted gene. Similar to <i>Bos taurus</i> mitochondrial solute carrier protein. (AF049236).

SEQ ID NO: 199

BAA03455.1 D14605 Daucus carota
AX110P. AX110.

SEQ ID NO: 204

AAD21872.1 AF078082 Phaseolus vulgaris
receptor-like protein kinase homolog RK20-1.

AAC23542.1 U20948 Ipomoea trifida
receptor protein kinase. IRK1.

CAA73133.1 Y12530 Brassica oleracea
serine /threonine kinase. ARLK.

CAA67145.1 X98520 Brassica oleracea
receptor-like kinase. SFR2.

CAB41879.1 Y18260 Brassica oleracea
SRK15 protein. SRK15. receptor-like kinase.

BAA92836.1 AB032473 Brassica oleracea
S18 S-locus receptor kinase. SRK18.

CAA74662.1 Y14286 Brassica oleracea
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular
kinase domain: from 1413.

AAB93834.1 U82481 Zea mays
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein
kinase.

CAB41878.1 Y18259 Brassica oleracea
SRK5 protein. SRK5. receptor-like kinase.

CAA73134.1 Y12531 Brassica oleracea
serine/threonine kinase. BRLK.

CAA74661.1 Y14285 Brassica oleracea
SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular
kinase domain: 1412-2554.

BAA23676.1 AB000970 Brassica rapa
receptor kinase 1. BcRK1.

AAA33000.1 M76647 Brassica oleracea
receptor protein kinase. SKR6.

AAA62232.1 U00443 Brassica napus
S-receptor kinase. protein contains an immunoglobulin-like domain.

CAB89179.1 AJ245479 Brassica napus subsp. napus
ser /thr kinase. S-locus receptor kinase. srk.

AAA33008.1 M97667 Brassica napus
serine/threonine kinase receptor.

BAA21132.1 D88193 Brassica rapa
S-receptor kinase. SRK9 (B.c).

BAA06285.1 D30049 Brassica rapa
S-receptor kinase SRK9.

AAK02023.1	AC074283	Oryza sativa	Putative protein kinase-like. OSJNBa0087H07.5.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrk1.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
CAB51836.1	AJ243961	Oryza sativa	Putative Ser/Thr protein kinase. I1332.7.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
BAA94529.2	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).

BAA94509.1 AB041503 Populus nigra
protein kinase 1. PnPK1.

SEQ ID NO: 211

AAG13478.1 AC026758 Oryza sativa
putative trehalose-6-phosphate phosphatase. OSJNBa0015J15.3.

SEQ ID NO: 212

AAC27894.1 AF023164 Zea mays
leucine-rich repeat transmembrane protein kinase 1. Itk1.

AAC27895.1 AF023165 Zea mays
leucine-rich repeat transmembrane protein kinase 2. Itk2.

AAK21965.1 AY028699 Brassica napus
receptor protein kinase PERK1.

AAC61805.1 U28007 Lycopersicon esculentum
serine/threonine protein kinase. Pto kinase interactor 1. Pti1. Pti1 kinase.

BAB21241.1 AP002953 Oryza sativa
Putative Pto kinase interactor 1. P0426D06.21. contains ESTs
AU108280(E0721),D48017(S13927).

AAF91336.1 AF249317 Glycine max
Pti1 kinase-like protein. Pti1a. protein kinase.

AAF91337.1 AF249318 Glycine max
Pti1 kinase-like protein. Pti1b. protein kinase.

BAA82394.1 AP000367 Oryza sativa
ESTs D23521(C2939),C22481(C2939) correspond to a region of the predicted gene.; Similar
to serine/threonine protein kinase like protein. (AL022140).

BAA87853.1 AP000816 Oryza sativa
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative
NAK-like Ser/Thr protein kinase. (AF001308).

AAG16628.1 AY007545 Brassica napus
protein serine/threonine kinase BNK1.

BAB07999.1 AP002525 Oryza sativa
putative protein kinase. P0462H08.22. contains EST C22619(S11214).

BAB03429.1 AP002817 Oryza sativa
EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis
thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).

BAB16871.1 AP002537 Oryza sativa
putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs
C22608(R3192),D25110(R3192).

BAA94510.1 AB041504 Populus nigra
protein kinase 2. PnPK2.

BAB39409.1 AP002901 Oryza sativa
putative protein kinase. P0456F08.9. contains EST C23560(R0290).

BAA94509.1 AB041503 Populus nigra
protein kinase 1. PnPK1.

BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAA78764.1	AB023482	Oryza sativa	ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
AAB09771.1	U67422	Zea mays	CRINKLY4 precursor. cr4. receptor kinase homolog.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
AAG25966.1	AF302082	Nicotiana tabacum	cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).
BAB40081.1	AP003074	Oryza sativa	putative receptor protein kinase. OSJNBa0004G10.30.
BAB18321.1	AP002865	Oryza sativa	putative receptor protein kinase. P0034C11.11.
AAD38286.1	AC007789	Oryza sativa	putative protein kinase. OSJNBa0049B20.13.
CAB51480.1	Y14600	Sorghum bicolor	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

BAB19337.1 AP003044 *Oryza sativa*
putative protein kinase. P0038C05.10. contains ESTs
AU056335(S20481),AU056336(S20481).

AAF91324.1 AF244890 *Glycine max*
receptor-like protein kinase 3. RLK3. GmRLK3.

AAF91323.1 AF244889 *Glycine max*
receptor-like protein kinase 2. RLK2. GmRLK2.

BAB16326.1 AP002818 *Oryza sativa*
putative receptor ser/thr protein kinase. P0436E04.9. contains ESTs
S10111(AU070304),S10111(AU083519).

BAA82556.1 AB030083 *Populus nigra*
lectin-like protein kinase. PnLPK.

BAA94516.1 AP001800 *Oryza sativa*
Similar to *Zea mays* S-domain receptor-like protein kinase (AJ010166).

BAB07906.1 AP002835 *Oryza sativa*
putative S-receptor kinase. P0417G05.14.

AAF59906.1 AF197947 *Glycine max*
receptor protein kinase-like protein. CLV1B.

AAF59905.1 AF197946 *Glycine max*
receptor protein kinase-like protein. CLV1A.

BAB07904.1 AP002835 *Oryza sativa*
putative S-receptor kinase. P0417G05.12.

SEQ ID NO: 214

AAB51442.1 U63012 *Sophora japonica*
lectin precursor.

CAA93829.1 Z69999 *Phaseolus lunatus*
lectin 3.

BAA36415.1 AB012634 *Robinia pseudoacacia*
lectin.

CAA93828.1 Z69998 *Phaseolus lunatus*
lectin 2.

AAC49137.1 U21959 *Cladrastis kentukea*
lectin precursor.

AAC49150.1 U21940 *Cladrastis kentukea*
storage protein precursor. lectin.

CAB96391.1 AJ271873 *Phaseolus lunatus*
carbohydrate-binding. lectin. lbl5.

CAB96392.1 AJ271874 *Phaseolus lunatus*
carbohydrate-binding. lectin. lbl6.

CAA76366.1 Y16754 *Medicago sativa*
lectin. lec2.

BAA82556.1 AB030083 *Populus nigra*
lectin-like protein kinase. PnLPK.

CAA93830.1	Z70000	Phaseolus lunatus lectin 4.
AAG16779.1	AF190633	Ulex europaeus lectin II.
AAC49136.1	U21958	Cladrastis kentukea lectin precursor.
AAB39933.1	U65009	Maackia amurensis lectin precursor.
AAB39934.1	U65010	Maackia amurensis lectin precursor.
AAA33766.1	L26237	Phaseolus lunatus lectin II.
AAA33143.1	M34270	Dolichos biflorus seed lectin.
CAA57697.1	X82216	Medicago truncatula lectin. lec3.
BAA36413.1	AB012632	Robinia pseudoacacia lectin.
AAA80182.1	U12783	Robinia pseudoacacia lectin.
BAA04604.1	D17757	Robinia pseudoacacia lectin precursor.
CAA68497.1	Y00440	Pisum sativum lectin-precursor (AA -30 to 245).
AAC49271.1	U24249	Robinia pseudoacacia lectin precursor.
AAA80181.1	U12782	Robinia pseudoacacia lectin.
BAA36416.1	AB012635	Robinia pseudoacacia lectin-related polypeptide.
AAA33676.1	M18160	Pisum sativum lectin.
CAA47011.1	X66368	Pisum sativum Psl lectin. psl.
AAA33141.1	J02721	Dolichos biflorus lectin subunit I precursor.
BAA36414.1	AB012633	Robinia pseudoacacia lectin.
BAA02049.1	D12481	Bauhinia purpurea lectin.
AAA80183.1	U12784	Robinia pseudoacacia lectin.

AAC49272.1	U24250	Robinia pseudoacacia	lectin precursor.
AAA82737.1	U18296	Medicago sativa	lectin. Mslec1.
AAA74571.1	U22468	Arachis hypogaea	agglutinin. galactose-binding lectin precursor. lec. lectin.
AAB51441.1	U63011	Sophora japonica	lectin precursor.
AAA74574.1	U22471	Arachis hypogaea	agglutinin. galactose-binding lectin precursor. lec. lectin.
AAG00508.1	AF285121	Sophora flavescens	lectin.
AAB39932.1	U65008	Maackia amurensis	lectin precursor.
SEQ ID NO: 215			
CAA64327.1	X94624	Brassica napus	acyl-CoA synthetase.
CAA96523.1	Z72153	Brassica napus	acyl CoA synthetase.
CAC19877.1	AJ401089	Brassica napus	activation of free fatty acids. long chain acyl-CoA synthetase. acs6. activity confirmed by expression in E. coli.
CAA06820.1	AJ006025	Cicer arietinum	acyl-coA synthetase.
AAC39365.1	AF008183	Populus x generosa	4-coumarate:CoA ligase 2. 4CL2.
CAA31697.1	X13325	Petroselinum crispum	4-coumarate:CoA ligase Pc4Cl-2 (AA 1-544).
CAA31696.1	X13324	Petroselinum crispum	4-coumarate:CoA ligase Pc4Cl-1 (AA 1-544).
AAC39366.1	AF008184	Populus x generosa	4-coumarate:CoA ligase 1. 4CL1.
AAF37734.1	AF052223	Lolium perenne	4-coumarate--CoA ligase 4CL3.
AAF91309.1	AF239686	Rubus idaeus	4-coumarate:coA ligase 2. adenylate-forming enzyme; 4CL2.
AAF37733.1	AF052222	Lolium perenne	4-coumarate--CoA ligase 4CL2.
CAA36850.1	X52623	Oryza sativa	4-coumarate-CoA ligase.
BAA07828.1	D43773	Nicotiana tabacum	4-coumarate:coenzyme A ligase.

BAA08365.1	D49366	Lithospermum erythrorhizon
4-coumarate:CoA ligase.		
AAB18637.1	U50845	Nicotiana tabacum
4-coumarate:coenzyme A ligase. 4CL1. Nt4CL-1.		
AAD40664.1	AF150686	Solanum tuberosum
4-coumarate:coenzyme A ligase. 4CL-2a.		
AAA33842.1	M62755	Solanum tuberosum
4-coumarate--CoA ligase. St4CL-1.		
AAB18638.1	U50846	Nicotiana tabacum
4-coumarate:coenzyme A ligase. 4CL2. Nt4CL-19.		
AAF91310.1	AF239687	Rubus idaeus
4-coumarate:coA ligase 1. adenylate-forming enzyme; 4CL1.		
AAC24503.1	AF041049	Populus tremuloides
4-coumarate:CoA ligase.		
AAF37732.1	AF052221	Lolium perenne
4-coumarate--CoA ligase 4CL1.		
AAA92669.1	U12013	Pinus taeda
4-coumarate-CoA ligase enzyme.		
AAB42382.1	U39404	Pinus taeda
4-coumarate:CoA ligase. lp4CL-2.		
AAB42383.1	U39405	Pinus taeda
4-coumarate:CoA ligase. lp4CL-1.		
AAF91308.1	AF239685	Rubus idaeus
4-coumarate:coA ligase 3. adenylate-forming enzyme; 4CL3.		
AAC24504.1	AF041050	Populus tremuloides
4-coumarate:CoA ligase.		
AAA92668.1	U12012	Pinus taeda
4-coumarate-CoA ligase enzyme.		
CAC36095.1	X69955	Glycine max
4-coumarate:Coenzyme A ligase isoenzyme 4. 4CL4.		
AAG43823.1	AF212317	Capsicum annuum
4-coumarate:coenzyme A ligase. 4CL.		
AAA69580.1	L43362	Oryza sativa
4-coumarate:CoA ligase isoform 2. 4cl.2. putative.		
BAA08366.2	D49367	Lithospermum erythrorhizon
4-coumarate:CoA ligase.		
CAA49575.1	X69954	Glycine max
4-coumarate--CoA ligase.		
CAB97359.1	AJ278455	Juglans nigra
4-coumarate-CoA ligase. 4CL.		
AAF73995.2	AF144502	Pinus armandii
4-coumarate:CoA ligase. 4CL.		

AAAF73994.2 AF144501 *Pinus armandii*
4-coumarate:CoA ligase. 4CL.

AAAF74018.2 AF144525 *Tsuga canadensis*
4-coumarate:CoA ligase. 4CL.

AAAF74010.2 AF144517 *Abies holophylla*
4-coumarate:CoA ligase. 4CL.

AAAF74020.2 AF144527 *Pseudolarix amabilis*
4-coumarate:CoA ligase. 4CL.

AAAF74016.2 AF144523 *Nothotsuga longibracteata*
4-coumarate:CoA ligase. 4CL.

AAAF73997.2 AF144504 *Picea smithiana*
4-coumarate:CoA ligase. 4CL.

AAAF74013.2 AF144520 *Abies beshanzuensis*
4-coumarate:CoA ligase. 4CL.

AAAF74008.2 AF144515 *Abies firma*
4-coumarate:CoA ligase. 4CL.

AAAF74022.2 AF144529 *Cedrus atlantica*
4-coumarate:CoA ligase. 4CL.

AAAF74005.2 AF144512 *Larix gmellini*
4-coumarate:CoA ligase. 4CL.

AAAF74021.2 AF144528 *Pseudolarix amabilis*
4-coumarate:CoA ligase. 4CL.

AAAF74003.2 AF144510 *Pseudotsuga sinensis*
4-coumarate:CoA ligase. 4CL.

AAAF74019.2 AF144526 *Tsuga canadensis*
4-coumarate:CoA ligase. 4CL.

SEQ ID NO: 221

AAB37246.1 U58971 *Nicotiana tabacum*
calmodulin-binding protein. TCB60.

SEQ ID NO: 224

BAB19413.1 AP002870 *Oryza sativa*
putative acetone-cyanohydrin lyase. P0458A05.22.

AAC49184.1 U40402 *Hevea brasiliensis*
hydroxynitrile lyase. hnl.

CAA11219.1 AJ223281 *Manihot esculenta*
alpha-hydroxynitrile lyase. HNL4.

CAA82334.1 Z29091 *Manihot esculenta*
alpha-hydroxynitrile lyase.

SEQ ID NO: 225

BAB16335.1 AP002818 *Oryza sativa*
putative NAM protein. P0436E04.18. contains ESTs E10793(C19698),E10793(C99379).

AAK13151.1	AC078829	Oryza sativa	putative NAM (no apical meristem) protein. OSJNBa0026O12.6.
CAA63102.2	X92205	Petunia x hybrida	apical meristem formation. NAM.
CAA63101.1	X92204	Petunia x hybrida	apical meristem formation. NAM.
BAB16328.1	AP002818	Oryza sativa	putative NAM protein. P0436E04.11. contains ESTs R4069(AU032425),R4069(AU082730).
BAB19365.1	AP002542	Oryza sativa	putative NAM (no apical meristem) protein. P0679C08.4.
BAA84803.1	AP000559	Oryza sativa	Similar to NAM like protein (AC005310).
BAB03447.1	AP002817	Oryza sativa	ESTs C96615(C10106),C26336(C12127),D21959(C10106) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21; NAM (no apical meristem) - like protein (AL021889).
BAA92400.1	AP001366	Oryza sativa	ESTs C96615(C10106),C26336(C12127),D21959(C10106) correspond to a region of the predicted gene. Similar to NAM (AL021889).
SEQ ID NO: 226			
BAA96221.1	AP002094	Oryza sativa	ESTs C19814(E10971),AU090481(E10971) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, sequence from clones T3F17, F11C10, F13A10; auxin-responsive GH3-like protein (AC006526).
AAD32141.1	AF123503	Nicotiana tabacum	Nt-gh3 deduced protein.
CAA42636.1	X60033	Glycine max	auxin-responsive GH3 product. GH3.
SEQ ID NO: 227			
CAA70403.1	Y09204	Nicotiana tabacum	histidinol-phosphate aminotransferase. hpa.
CAC20728.1	AJ278767	Nicotiana plumbaginifolia	essential for histidine biosynthesis. histidinol phosphate aminotransferase. hpa.
SEQ ID NO: 229			
AAF33670.1	AF079872	Nicotiana tabacum	cyclic nucleotide-gated calmodulin-binding ion channel. CBP4.
AAF33669.1	AF079871	Nicotiana tabacum	cyclic nucleotide-gated calmodulin-binding ion channel. CBP7.
AAK16188.1	AC079887	Oryza sativa	putative cyclic nucleotide and calmodulin-regulated ion channel protein. OSJNBa0040E01.13.
AAB53255.1	U65390	Nicotiana tabacum	cyclic nucleotide gated channel protein. CaMB-channel protein. channel protein homolog.

CAB54856.1	AJ132686	Zea mays	potassium channel protein ZMK2. ZMK2.
AAD16278.1	AF099095	Samanea saman	pulvinus inward-rectifying channel for potassium SPICK1. similar to Arabidopsis potassium channel AKT3.
CAA71598.1	Y10579	Vicia faba	potassium channel.
CAA56175.1	X79779	Solanum tuberosum	K+ channel inward rectifying. KST1.
CAC05489.1	AJ271447	Populus tremula x Populus tremuloides	potassium channel. potassium channel 2. ptk2.
AAD39492.1	AF145272	Samanea saman	pulvinus inward-rectifying channel SPICK2. potassium channel; similar to AKT2/3.
CAA70870.1	Y09699	Solanum tuberosum	putative inward rectifying potassium channel. SKT2.
CAB62555.1	AJ249962	Daucus carota	potassium channel. kdc1.
BAA96192.1	AP002093	Oryza sativa	Similar to Arabidopsis thaliana potassium channel protein (M86990).
BAA96150.1	AP002092	Oryza sativa	Similar to Arabidopsis thaliana potassium channel protein (M86990).
BAA84085.1	AB032074	Nicotiana paniculata	potassium channel. NpKT1.
AAF81251.1	AF267755	Mesembryanthemum crystallinum	potassium channel protein Mkt2p.
CAA68912.1	Y07632	Zea mays	potassium channel. ZMK1.
CAA60016.1	X86021	Solanum tuberosum	potassium channel. SKT1 gene. putative start codon.
CAA65254.1	X96390	Lycopersicon esculentum	potassium channel. LKT1.
CAA12645.1	AJ225805	Egeria densa	inward potassium channel alpha subunit. homologous to the sequences of the family of inwardly rectifying potassium channels in plants which is structurally related to the shaker family of outwardly rectifying channels in Drosophila.
AAF36832.1	AF207745	Triticum aestivum	AKT1-like potassium channel. TaAKT1.
CAC10514.1	AJ299019	Samanea saman	potassium release. outwardly rectifying potassium channel. spork1.
AAF81249.1	AF267753	Mesembryanthemum crystallinum	putative potassium channel protein Mkt1p.
CAC05488.1	AJ271446	Populus tremula x Populus tremuloides	potassium channel. outward rectifying potassium channel. ptork.

SEQ ID NO: 232

AAA80575.1 U13148 *Pennisetum ciliare*
possible apospory-associated protein.

AAF34174.1 AF195243 *Chlamydomonas reinhardtii*
apospory-associated protein C. APOC.

SEQ ID NO: 233

AAB97366.1 AF039531 *Oryza sativa*
lysophospholipase homolog. LPL1.

SEQ ID NO: 235

AAC61839.1 AF025430 *Papaver somniferum*
berberine bridge enzyme. bbe1. (S)-reticuline:oxygen oxidoreductase (methylene bridge forming).

AAC39358.1 AF005655 *Eschscholzia californica*
oxidizes the N-methyl group of (S)-reticuline to the berberine bridge carbon C-8 of (S)-scoulerine in berberine and benzophenanthridine alkaloid biosynthesis. berberine bridge enzyme. bbe1. covalently-bound FAD-dependent oxidase; elicitor-inducible.

AAB20352.1 S65550 *Eschscholzia californica*
(S)-reticuline:oxygen oxidoreductase (methylene-bridge-forming). /gene="(S)-reticuline:oxygen oxidoreductase. This sequence comes from Fig 2; berberine bridge enzyme.

AAD17487.1 AF049347 *Berberis stolonifera*
Catalyzes the oxidative cyclization of the N-methyl group of (S)-reticuline into the berberine bridge carbon (C-8) of (S)-scoulerine. berberine bridge enzyme. bbe1. Covalently flavinylated oxidase of isoquinoline alkaloid biosynthesis in plants.

SEQ ID NO: 244

AAD17487.1 AF049347 *Berberis stolonifera*
Catalyzes the oxidative cyclization of the N-methyl group of (S)-reticuline into the berberine bridge carbon (C-8) of (S)-scoulerine. berberine bridge enzyme. bbe1. Covalently flavinylated oxidase of isoquinoline alkaloid biosynthesis in plants.

AAB20352.1 S65550 *Eschscholzia californica*
(S)-reticuline:oxygen oxidoreductase (methylene-bridge-forming). /gene="(S)-reticuline:oxygen oxidoreductase. This sequence comes from Fig 2; berberine bridge enzyme.

AAC39358.1 AF005655 *Eschscholzia californica*
oxidizes the N-methyl group of (S)-reticuline to the berberine bridge carbon C-8 of (S)-scoulerine in berberine and benzophenanthridine alkaloid biosynthesis. berberine bridge enzyme. bbe1. covalently-bound FAD-dependent oxidase; elicitor-inducible.

AAC61839.1 AF025430 *Papaver somniferum*
berberine bridge enzyme. bbe1. (S)-reticuline:oxygen oxidoreductase (methylene bridge forming).

SEQ ID NO: 247

AAF37267.1 AF220406 *Vitis riparia*
26S proteasome regulatory ATPase subunit S10b. Rev136-3.

SEQ ID NO: 248

-
- BAA78764.1 AB023482 *Oryza sativa*
ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to *Arabidopsis thaliana* APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
-
- BAA94509.1 AB041503 *Populus nigra*
protein kinase 1. PnPK1.
-
- AAG16628.1 AY007545 *Brassica napus*
protein serine/threonine kinase BNK1.
-
- BAB03429.1 AP002817 *Oryza sativa*
EST C22619(S11214) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
-
- BAB07999.1 AP002525 *Oryza sativa*
putative protein kinase. P0462H08.22. contains EST C22619(S11214).
-
- BAA94510.1 AB041504 *Populus nigra*
protein kinase 2. PnPK2.
-
- AAK11674.1 AF339747 *Lophopyrum elongatum*
protein kinase. ESI47.
-
- AAF43496.1 AF131222 *Lophopyrum elongatum*
protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
-
- BAB16871.1 AP002537 *Oryza sativa*
putative protein kinase APK1A*Arabidopsis thaliana*. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
-
- BAA87853.1 AP000816 *Oryza sativa*
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
-
- BAB39409.1 AP002901 *Oryza sativa*
putative protein kinase. P0456F08.9. contains EST C23560(R0290).
-
- BAB39873.1 AP002882 *Oryza sativa*
putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
-
- BAB21240.1 AP002953 *Oryza sativa*
Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
-
- AAK21965.1 AY028699 *Brassica napus*
receptor protein kinase PERK1.
-
- AAK00425.1 AC069324 *Oryza sativa*
Putative protein kinase. OSJNBa0071K19.11.
-
- AAG03090.1 AC073405 *Oryza sativa*
Similar to an *Arabidopsis* somatic embryogenesis receptor-like kinase (AC007504).
-
- AAG59657.1 AC084319 *Oryza sativa*
putative protein kinase. OSJNBa0004B24.20.
-
- AAF91336.1 AF249317 *Glycine max*
Ptil kinase-like protein. Ptila. protein kinase.
-

AAF91337.1	AF249318	Glycine max	Ptil kinase-like protein. Ptilb. protein kinase.
BAB21241.1	AP002953	Oryza sativa	Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721),D48017(S13927).
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
AAC61805.1	U28007	Lycopersicon esculentum	serine/threonine protein kinase. Pto kinase interactor 1. Ptil. Ptil kinase.
AAG33377.1	AF290411	Oryza meyeriana	serine/threonine protein kinase. R1.
AAC27894.1	AF023164	Zea mays	leucine-rich repeat transmembrane protein kinase 1. ltk1.
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).
AAC27895.1	AF023165	Zea mays	leucine-rich repeat transmembrane protein kinase 2. ltk2.
AAB61708.1	U93048	Daucus carota	somatic embryogenesis receptor-like kinase. SERK.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
AAK11566.1	AF318490	Lycopersicon hirsutum	Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
CAB51480.1	Y14600	Sorghum bicolor	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
AAG25966.1	AF302082	Nicotiana tabacum	cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
AAG00510.1	AF285172	Phaseolus vulgaris	leaf senescence-associated receptor-like protein kinase. SARK.
AAC48932.1	U13923	Lycopersicon pimpinellifolium	Fen. putative serine/threonine protein kinase; similar to product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.
AAB47424.1	U59317	Lycopersicon pimpinellifolium	serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.
AAF76307.1	AF220602	Lycopersicon pimpinellifolium	Fen kinase.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.

BAA92221.1 AP001278 *Oryza sativa*
Similar to *Arabidopsis thaliana* chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).

BAA87852.1 AP000816 *Oryza sativa*
Similar to putative Ser/Thr protein kinase. (AC004218).

AAK11567.1 AF318491 *Lycopersicon hirsutum*
Pto-like protein kinase F. LhirPtoF.

CAA73134.1 Y12531 *Brassica oleracea*
serine/threonine kinase. BRLK.

BAB19337.1 AP003044 *Oryza sativa*
putative protein kinase. P0038C05.10. contains ESTs
AU056335(S20481), AU056336(S20481).

SEQ ID NO: 249

BAA22422.1 AB001379 *Glycyrrhiza echinata*
cytochrome P450. CYP81E1.

BAA74465.1 AB022732 *Glycyrrhiza echinata*
cytochrome P450. CYP Ge-31.

BAA93634.1 AB025016 *Lotus japonicus*
cytochrome P450.

CAB43505.1 AJ239051 *Cicer arietinum*
cytochrome P450. cyp81E2.

CAB41490.1 AJ238439 *Cicer arietinum*
cytochrome P450 monooxygenase. cyp81E3v2.

CAA10067.1 AJ012581 *Cicer arietinum*
cytochrome P450. cyp81E3.

CAA04117.1 AJ000478 *Helianthus tuberosus*
fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l. chimeric sequence (from 5'-
race).

CAA04116.1 AJ000477 *Helianthus tuberosus*
fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

AAK38079.1 AF321855 *Lolium rigidum*
putative cytochrome P450.

AAK38080.1 AF321856 *Lolium rigidum*
putative cytochrome P450.

AAK38081.1 AF321857 *Lolium rigidum*
putative cytochrome P450.

AAC34853.1 AF082028 *Hemerocallis* hybrid cultivar
putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3.
mRNA accumulates in senescing petals.

AAB94590.1 AF022461 *Glycine max*
CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.

CAB56742.1 AJ249800 *Cicer arietinum*
cytochrome P450 monooxygenase. cyp81E5.

AAD56282.1	AF155332	Petunia x hybrida flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
AAG09208.1	AF175278	Pisum sativum wound-inducible P450 hydroxylase. CYP82A1.
CAA71515.1	Y10491	Glycine max putative cytochrome P450.
CAA71516.1	Y10492	Glycine max putative cytochrome P450.
AAC49188.2	U29333	Pisum sativum cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
CAA71876.1	Y10982	Glycine max putative cytochrome P450.
BAA12159.1	D83968	Glycine max Cytochrome P-450 (CYP93A1).
AAC39454.1	AF014802	Eschscholzia californica (S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome P-450-dependent, homologous to wound-inducible CYP82A1 of Pisum sativum GenBank Accession Number U29333.
CAA65580.1	X96784	Nicotiana tabacum cytochrome P450. hsr515.
BAA13076.1	D86351	Glycine max cytochrome P-450 (CYP93A2).
AAA32913.1	M32885	Persea americana cytochrome P-450LXXIA1 (cyp71A1).
CAA71877.1	Y10983	Glycine max putative cytochrome P450.
AAG44132.1	AF218296	Pisum sativum cytochrome P450. P450 isolog.
CAA64635.1	X95342	Nicotiana tabacum cytochrome P450. hsr515. hypersensitivity-related gene.
AAB94587.1	AF022458	Glycine max CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
AAD38930.1	AF135485	Glycine max cytochrome P450 monooxygenase CYP93D1. CYP93E1.
BAA84072.1	AB028152	Torenia hybrida flavone synthase II. cytochrome P450. TFNS5.
BAA74466.1	AB022733	Glycyrrhiza echinata cytochrome P450. CYP Ge-51.
BAA22423.1	AB001380	Glycyrrhiza echinata cytochrome P450. CYP93B1.
BAA35080.1	AB015762	Nicotiana tabacum putative cytochrome P450. CYP82E1.

BAA92894.1	AB006790	Petunia x hybrida cytochrome P450. IMT-2.
AAC32274.1	AF081575	Petunia x hybrida flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.
CAB56743.1	AJ249801	Cicer arietinum cytochrome P450 monooxygenase. cyp81E4.
BAA84071.1	AB028151	Antirrhinum majus flavone synthase II. cytochrome P450. AFNS2.
SEQ ID NO: 250		
AAD55566.1	AF110784	Volvox carteri f. nagariensis protein disulfide isomerase precursor. pdi.
AAD02069.1	AF036939	Chlamydomonas reinhardtii redox-regulator of 5'UTR psbA mRNA binding complex and translation. protein disulfide isomerase. localized to ER and chloroplast.
AAC49896.1	AF027727	Chlamydomonas reinhardtii involved in the redox-regulated binding of chloroplast poly(A)-binding protein to the 5'-UTR of psbA mRNA; regulates chloroplast translational activation. protein disulfide isomerase RB60. PDI.
AAD28260.1	AF131223	Datisca glomerata protein disulfide isomerase homolog. PDI.
AAB08519.1	L39014	Zea mays protein disulfide isomerase. pdi. putative.
AAA19660.1	U11496	Triticum aestivum protein disulfide isomerase. PDI.
CAC21230.1	AJ277379	Triticum turgidum subsp. durum catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.
CAC21228.1	AJ277377	Triticum turgidum subsp. durum catalyzes the formation of disulfide bonds. protein disulfide isomerase. Pdi.
AAA70345.1	L33251	Hordeum vulgare catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.
AAA70344.1	L33250	Hordeum vulgare catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.
AAB05641.1	U41385	Ricinus communis protein disulphide isomerase PDI. molecular chaperone.
CAA77575.1	Z11499	Medicago sativa protein disulfide isomerase.
CAC21231.1	AJ277380	Triticum turgidum subsp. durum catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.
CAC21229.1	AJ277378	Triticum turgidum subsp. durum catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.
BAB18780.1	AB047268	Cucumis sativus disulfide isomerase.

BAA92322.1	AB039278	Oryza sativa	protein disulfide isomerase. Pdi.
AAA70346.1	L33252	Hordeum vulgare	catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.
CAA72092.1	Y11209	Nicotiana tabacum	protein disulfide-isomerase precursor. PDI.
AAG13988.1	AF298829	Prunus avium	putative protein disulfide-isomerase. PDI.
SEQ ID NO: 251			
CAA61275.1	X88797	Eucalyptus gunnii	cinnamyl alcohol dehydrogenase. CAD1.
AAC06319.1	AF053084	Malus x domestica	putative cinnamyl alcohol dehydrogenase. CAD.
SEQ ID NO: 253			
CAB61745.1	AJ275311	Cicer arietinum	farnesylated protein.
AAD09515.1	U64917	Glycine max	putative metal-binding protein. GMFP7. farnesylated protein.
SEQ ID NO: 254			
BAB19757.1	AB052785	Glycine max	nitrate transporter NRT1-2. NRT1-2.
BAB19756.1	AB052784	Glycine max	nitrate transporter NRT1-1. NRT1-1.
BAB19760.1	AB052788	Glycine max	nitrate transporter NRT1-5. NRT1-5.
AAC32034.1	AF023472	Hordeum vulgare	peptide transporter. ptr1. PTR1; integral membrane protein.
AAD01600.1	AF016713	Lycopersicon esculentum	LeOPT1. LeOPT1. oligopeptide transporter.
BAB40113.1	AP003311	Oryza sativa	putative peptide transport protein. P0024G09.4. contains ESTs D40448(S2437),C71800(E0368),AU102190(E2393), AU055921(S20154),AU102191(E2393),AU055922(S20154), C98524(E0368),AU097146(S2437).
BAB16458.1	AP002483	Oryza sativa	putative peptide transport protein. P0019D06.16. contains ESTs D40448(S2437),C71800(E0368),AU102190(E2393), AU055921(S20154),AU102191(E2393),AU055922(S20154), C98524(E0368),AU097146(S2437).
CAA93316.1	Z69370	Cucumis sativus	nitrite transporter. NiTR1.
AAK15441.1	AC037426	Oryza sativa	putative nitrate transporter. OSJNBb0014I11.9.

AAG21898.1 AC026815 *Oryza sativa*
putative peptide transport protein. OSJNBa0079L16.13.

CAC00544.1 AJ277084 *Nicotiana plumbaginifolia*
ion transport. putative low-affinity nitrate transporter. nrt1.1.

AAG46153.1 AC018727 *Oryza sativa*
putative peptide transporter. OSJNBa0056G17.8.

CAC00545.1 AJ277085 *Nicotiana plumbaginifolia*
ion transport. putative low-affinity nitrate transporter. nrt1.2.

AAG21906.1 AC026815 *Oryza sativa*
putative peptide transport protein. OSJNBa0079L16.9.

AAF20002.1 AF213936 *Prunus dulcis*
amino acid/peptide transporter. PTR2. similar to transporters of nitrogenous compounds.

AAF07875.1 AF140606 *Oryza sativa*
nitrate transporter. NRT1.

BAB16322.1 AP002818 *Oryza sativa*
putative peptide transporter-like protein. P0436E04.4.

BAB19758.1 AB052786 *Glycine max*
putative nitrate transporter NRT1-3. NRT1-3.

AAA80582.1 U17987 *Brassica napus*
putative nitrate transporter. RCH2 protein.

CAC07206.1 AJ278966 *Brassica napus*
Low-affinity nitrate transporter. nitrate transporter. nrt1.

AAG46154.1 AC018727 *Oryza sativa*
putative peptide transporter. OSJNBa0056G17.27.

AAB69642.1 AF000392 *Lotus japonicus*
peptide transporter. LjNOD65.

BAB19759.1 AB052787 *Glycine max*
putative nitrate transporter NRT1-4. NRT1-4.

AAD16016.1 AF080545 *Nepenthes alata*
peptide transporter. PTR1.

AAD42860.1 AF154930 *Prunus dulcis*
transporter-like protein. TLP1.

AAG13513.1 AC068924 *Oryza sativa*
putative peptide transporter. OSJNBa0026L12.7.

SEQ ID NO: 255

AAB01567.1 L47672 *Picea glauca*
EMB34. embryo-abundant protein.

SEQ ID NO: 257

AAB71743.1 U75345 *Chlamydomonas reinhardtii*
envelope protein. LIP-36G1. low CO₂ inducible carrier protein LIP-36 with a molecular weight of 36 kDa.

AAB71744.1	U75346	<i>Chlamydomonas reinhardtii</i>	envelope protein. LIP-36G2. low CO ₂ inducible carrier protein LIP-36 with a molecular weight of 36 kDa.
BAA92520.1	AP001383	<i>Oryza sativa</i>	ESTs AU068633(C30614),AU068634(C30614) correspond to a region of the predicted gene. Similar to <i>Bos taurus</i> mitochondrial solute carrier protein. (AF049236).
BAB16462.1	AP002483	<i>Oryza sativa</i>	putative peroxisomal Ca-dependent solute carrier protein. P0019D06.21.
BAB40117.1	AP003311	<i>Oryza sativa</i>	putative peroxisomal Ca-dependent solute carrier protein. P0024G09.9.
CAA07568.1	AJ007580	<i>Ribes nigrum</i>	Mitochondrial carrier protein. prib7.
CAC27140.1	AJ132535	<i>Picea abies</i>	ADP, ATP carrier protein precursor.
CAA56325.1	X80023	<i>Triticum turgidum</i>	ATP/ADP carrier protein.
CAC12820.1	AJ299250	<i>Nicotiana tabacum</i>	mitochondrial 2-oxoglutarate/malate carrier protein. momc1.
AAG48999.1	AY013246	<i>Hordeum vulgare</i>	putative mitochondrial carrier protein. 635P2.1.
SEQ ID NO: 258			
CAA05276.1	AJ002236	<i>Lycopersicon pimpinellifolium</i>	resistance gene. Hcr9-9E. Hcr9-9E.
AAC78591.1	AF053993	<i>Lycopersicon esculentum</i>	disease resistance protein. Cf-5.
AAC78596.1	AF053998	<i>Lycopersicon esculentum</i>	Hcr2-5D. Hcr2-5D. similar to <i>Lycopersicon pimpinellifolium</i> disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.
CAA05279.1	AJ002237	<i>Lycopersicon esculentum</i>	Hcr9-0. Hcr9-0. homologue of <i>Cladosporium fulvum</i> disease resistance gene Cf-9.
AAC78593.1	AF053995	<i>Lycopersicon esculentum</i>	Hcr2-0B. Hcr2-0B. similar to <i>Lycopersicon pimpinellifolium</i> disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.
AAA65235.1	U15936	<i>Lycopersicon pimpinellifolium</i>	Cf-9 precursor. Cf-9. this is the ninth resistance gene to disease caused by <i>Cladosporium fulvum</i> to be isolated.
CAA05274.1	AJ002236	<i>Lycopersicon pimpinellifolium</i>	resistance gene. Cf-9. Cf-9.
AAC78592.1	AF053994	<i>Lycopersicon esculentum</i>	Hcr2-0A. Hcr2-0A. similar to <i>Lycopersicon pimpinellifolium</i> disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.

AAC78595.1	AF053997	Lycopersicon esculentum	Hcr2-5B. Hcr2-5B. similar to Lycopersicon pimpinellifolium disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.
AAC78594.1	AF053996	Lycopersicon pimpinellifolium	Hcr2-2A. Hcr2-2A. similar to Lycopersicon pimpinellifolium disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.
BAA96776.1	AP002521	Oryza sativa	Similar to Lycopersicon esculentum disease resistance protein (AF053993).
BAB08215.1	AP002539	Oryza sativa	Similar to Lycopersicon esculentum disease resistance protein (AF053993).
CAA05268.1	AJ002235	Lycopersicon hirsutum	Resistance gene. Cf-4. Cf-4.
AAG21897.1	AC026815	Oryza sativa	putative disease resistance protein (3' partial). OSJNBa0079L16.21.
AAD50430.1	AF166121	Hordeum vulgare	Cf2/Cf5 disease resistance protein homolog. Big1. leucine rich repeat protein.
AAG21917.1	AC026815	Oryza sativa	putative disease resistance protein. OSJNBa0079L16.5.
AAG21909.1	AC026815	Oryza sativa	putative disease resistance protein. OSJNBa0079L16.3.
CAB55409.1	AL117265	Oryza sativa	zhb0001.1. Incomplete at 5'end, Similar to disease resistance protein; Method: conceptual translation with partial peptide sequencing.
AAC49123.1	U37133	Oryza sativa	receptor kinase-like protein. Xa21. Xa21 disease resistance gene.
AAC80225.1	U72723	Oryza longistaminata	receptor kinase-like protein. Xa21. disease resistance gene.
SEQ ID NO: 259			
CAB52689.1	AJ132224	Lycopersicon esculentum	hexose transporter. ht2.
CAA09419.1	AJ010942	Lycopersicon esculentum	hexose transporter protein.
BAB19864.1	AB052885	Oryza sativa	monosaccharide transporter 3. OsMST3.
AAA18534.1	L21753	Saccharum hybrid cultivar H65-7052	glucose transporter. putative.
CAA47324.1	X66856	Nicotiana tabacum	monosaccharid transporter. MST1.
AAB06594.1	U38651	Medicago truncatula	sugar transporter.
AAA79761.1	L08196	Ricinus communis	hexose transport. sugar carrier protein. RCSTC.

CAA04511.1	AJ001061	Vitis vinifera	hexose uptake. hexose transporter.
CAA70777.1	Y09590	Vitis vinifera	hexose transporter.
AAC61852.1	AF061106	Petunia x hybrida	putative monosaccharide transporter 1. pmt1. similar to hexose transporter protein; PMT1.
AAA79857.1	L08188	Ricinus communis	hexose transport. hexose carrier protein. HEX6.
CAB06079.1	Z83829	Picea abies	monosaccharide transporter. PaMst-1. PaMst-1.
BAB19863.1	AB052884	Oryza sativa	monosaccharide transporter 2. OsMST2.
BAA83554.1	AP000399	Oryza sativa	Similar to hexose carrier protein HEX6 & RCCHCP_1 (Q07423).
AAK31286.1	AC079890	Oryza sativa	putative hexose carrier protein. OSJNBb0089A17.11.
CAA53192.1	X75440	Chlorella kessleri	hexose transporter like protein. HUP3.
CAA68813.1	Y07520	Chlorella kessleri	H(+)/hexose cotransporter (AA 1-533).
CAA39036.1	X55349	Chlorella kessleri	H(+)/hexose-cotransporter. HUP1.
BAB19862.1	AB052883	Oryza sativa	monosaccharide transporter 1. OsMST1.
AAA18533.1	L21752	Saccharum hybrid cultivar H65-7052	glucose transporter. putative.
CAB52688.1	AJ132223	Lycopersicon esculentum	hexose transporter. ht1.
AAD55054.1	AF173655	Beta vulgaris	glucose transporter. Gt.
CAB52690.1	AJ132225	Lycopersicon esculentum	hexose transporter. ht3.
AAA33875.1	L31352	Ricinus communis	hexose transport. hexose carrier. Hex9. putative.
AAK13147.1	AC083945	Oryza sativa	Putative sugar transporter. OSJNBa0058E19.22.
AAB68029.1	U64903	Beta vulgaris	BvcDNA-397. putative sugar transporter; member of major facilitative superfamily; integral membrane protein.
AAB68028.1	U64902	Beta vulgaris	BvcDNA-205. putative sugar transporter; member of major facilitative superfamily; integral membrane protein.

AAG43998.1	AF215837	<i>Apium graveolens</i> var. dulce	mannitol transporter. Mat1.
AAF74568.1	AF215854	<i>Zea mays</i>	transport of hexoses across the plastid inner envelope membrane. hexose transporter. pGlcT.
AAF74567.1	AF215853	<i>Solanum tuberosum</i>	transport of hexoses across the plastid inner envelope membrane. hexose transporter. pGlcT.
AAF74566.1	AF215852	<i>Nicotiana tabacum</i>	transport of hexoses across the plastid inner envelope membrane. hexose transporter. pGlcT.
AAF74565.1	AF215851	<i>Spinacia oleracea</i>	transport of hexoses across the plastid inner envelope membrane. hexose transporter. pGlcT.
AAG46179.1	AC018727	<i>Oryza sativa</i>	putative sugar transporter protein. OSJNBa0056G17.3.
AAG00995.1	AF286906	<i>Mesembryanthemum crystallinum</i>	putative glucose translocator. metabolite transporter; targeted to plastid inner envelope membrane.
AAB53155.1	U43629	<i>Beta vulgaris</i>	putative sugar transporter. integral membrane protein. member of major facilitator superfamily.
AAB88879.1	AF000952	<i>Prunus armeniaca</i>	putative sugar transporter.
AAA33874.1	L31353	<i>Ricinus communis</i>	hexose transport. hexose carrier. Hex10. putative.
AAD37424.1	AF149282	<i>Phaseolus vulgaris</i>	hexose carrier protein 1. HCP1.
AAD45934.1	AF168773	<i>Betula pendula</i>	hexose transport protein. HEX2.
SEQ ID NO: 260			
AAA33915.1	L27821	<i>Oryza sativa</i>	receptor type serine/threonine kinase. protein kinase.
AAF34428.1	AF172282	<i>Oryza sativa</i>	receptor-like protein kinase. DUPR11.18.
BAA92954.1	AP001551	<i>Oryza sativa</i>	Similar to <i>Oryza sativa</i> protein kinase (OSPK10) mRNA. (L27821).
BAB07906.1	AP002835	<i>Oryza sativa</i>	putative S-receptor kinase. P0417G05.14.
BAA94516.1	AP001800	<i>Oryza sativa</i>	Similar to <i>Zea mays</i> S-domain receptor-like protein kinase (AJ010166).
BAA94528.1	AP001800	<i>Oryza sativa</i>	Similar to <i>Arabidopsis thaliana</i> chromosome 2 BAC T20K24; putative receptor-like protein kinase (AC002392).
BAA94517.1	AP001800	<i>Oryza sativa</i>	Similar to <i>Zea mays</i> S-domain receptor-like protein kinase (AJ010166).

BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.
BAA94529.2	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07904.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.12.
BAA94518.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
CAA47962.1	X67733	Zea mays	receptor-like protein kinase. PK1.
BAA83573.1	AP000399	Oryza sativa	Similar to serine/threonine-specific protein kinase PK10 precursor (AL021811).
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAB17345.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.29.
BAB17348.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.32.
BAB17342.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.26.
BAB39451.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.24.
BAB17126.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.16.
BAB19337.1	AP003044	Oryza sativa	putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
CAB51480.1	Y14600	Sorghum bicolor	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
BAB17339.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.23.
AAB61708.1	U93048	Daucus carota	somatic embryogenesis receptor-like kinase. SERK.
AAF78016.1	AF238472	Oryza sativa	receptor-like kinase. RLG15. protein kinase.
AAD46420.1	AF100771	Hordeum vulgare	receptor-like kinase. Hv3ARK. similar to wheat ARK1AS.
AAC49629.1	U51330	Triticum aestivum	rust resistance kinase Lr10. LRK10.

BAB17139.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.31.
BAB17331.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.12.
AAC01746.1	AF044489	Oryza sativa	receptor-like protein kinase. drpk1.
AAC27489.1	AF077130	Oryza sativa	receptor-like protein kinase.
AAC02535.1	AF044260	Oryza sativa	receptor serine/threonine kinase. protein kinase.
BAB39434.1	AP003338	Oryza sativa	receptor-like kinase. OJ1212_B09.1.
AAF78020.1	AF238476	Oryza sativa	receptor-like kinase. RLG11. protein kinase.
BAA92953.1	AP001551	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).
AAF78018.1	AF238474	Oryza sativa	receptor-like kinase. RLG16. protein kinase.
AAD46917.1	AF164021	Oryza sativa	receptor kinase.
BAB39438.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.7.
BAB39435.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.2.
BAB17129.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.20.
BAB17321.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.1.
AAF68398.1	AF237568	Oryza sativa	receptor-like protein kinase. RLG2.
BAB39437.1	AP003338	Oryza sativa	receptor-like kinase. OJ1212_B09.6.
AAF78019.1	AF238475	Oryza sativa	receptor-like kinase. RLG17. protein kinase.
SEQ ID NO: 261			
AAD09343.1	AF026538	Hordeum vulgare	ABA-responsive protein.
SEQ ID NO: 263			
BAA22813.1	D26015	Nicotiana tabacum	aspartic protease activity. CND41, chloroplast nucleoid DNA binding protein. cnd41.

BAB21205.1	AP002913	Oryza sativa	nucleoid DNA-binding protein cnd41-like protein. P0480E02.11. contains ESTs AU166073(E31027),AU029516(E31027).
SEQ ID NO: 270			
BAB12719.1	AP002746	Oryza sativa	putative regulatory protein NPR1. P0671B11.35.
BAB16860.1	AP002537	Oryza sativa	Arabidopsis thaliana regulatory protein NPR1 like protein. P0001B06.13.
SEQ ID NO: 271			
AAG35658.1	AF204925	Petroselinum crispum	transcription factor WRKY4. WRKY4. binds to W box (TTGACC) elements.
BAA87058.1	AB028022	Nicotiana tabacum	WIZZ. wizz. wound-induced transcription factor.
BAA86031.1	AB026890	Nicotiana tabacum	transcription factor NtWRKY4.
AAD16139.1	AF096299	Nicotiana tabacum	DNA-binding protein 2. WRKY2. transcription factor.
BAA77383.1	AB020590	Nicotiana tabacum	transcription factor NtWRKY2.
AAF23898.1	AF193802	Oryza sativa	zinc finger transcription factor WRKY1.
AAD55974.1	AF121353	Petroselinum crispum	zinc-finger type transcription factor WRKY1. WRKY1.
CAB97004.1	AJ278507	Solanum tuberosum	putative transcription factor. WRKY DNA binding protein. WRKY1.
BAA82107.1	AB022693	Nicotiana tabacum	transcription factor. NtWRKY1.
AAD32677.1	AF140554	Avena sativa	DNA-binding protein WRKY1. wrky1. putative transcription factor.
BAB16432.1	AB041520	Nicotiana tabacum	WRKY transcription factor Nt-SubD48. Nt-SubD48.
AAD16138.1	AF096298	Nicotiana tabacum	DNA-binding protein 1. WRKY1. transcription factor.
AAD32676.1	AF140553	Avena sativa	DNA-binding protein WRKY3. wrky3. putative transcription factor.
AAD27591.1	AF121354	Petroselinum crispum	binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.
AAF61864.1	AF193771	Nicotiana tabacum	DNA-binding protein 4. WRKY4. transcription factor.
AAG35659.1	AF204926	Petroselinum crispum	transcription factor WRKY5. WRKY5. binds to W box (TTGACC) elements.

AAF61863.1	AF193770	Nicotiana tabacum
DNA-binding protein 3. WRKY3. transcription factor.		
SEQ ID NO: 272		
BAA07395.1	D38220	Brassica napus
nitrate reductase.		
BAA07394.1	D38219	Brassica napus
nitrate reductase.		
AAG30576.1	AF314093	Ricinus communis
nitrate reductase. NIA.		
CAA32217.1	X14059	Nicotiana tabacum
nitrate reductase.		
AAA33713.1	L13691	Petunia x hybrida
nitrate reductase. putative.		
CAA32218.1	X14060	Lycopersicon esculentum
nitrate reductase.		
AAA33712.1	L11563	Petunia x hybrida
nitrate reductase apoenzyme. nia.		
CAA32216.1	X14058	Nicotiana tabacum
nitrate reductase.		
CAA56696.1	X80670	Lotus japonicus
nitrate reductase (NADH). NIA.		
AAB52786.1	U95317	Solanum tuberosum
NADH nitrate reductase. StNR3.		
AAB18985.1	U76701	Solanum tuberosum
NADH nitrate reductase. StNR2.		
AAA95940.1	U01029	Phaseolus vulgaris
nitrate reductase. PVNR2.		
AAA34033.1	M32600	Spinacia oleracea
NADH nitrate reductase.		
CAA38031.1	X54097	Betula pendula
nitrate reductase (NADH). nial.		
BAA13047.1	D86226	Spinacia oleracea
nitrate reductase.		
AAA33114.1	M33154	Cucurbita maxima
nitrate reductase.		
AAD19790.1	AF055369	Glycine max
nitrate reductase. nr2.		
CAA58909.1	X84103	Cichorium intybus
nitrate reductase (NADH). nia.		
AAA96813.1	U13987	Glycine max
inducible nitrate reductase 2. INR2.		

CAA37672.1	X53603	Phaseolus vulgaris nitrate reductase.
AAA96727.1	L23854	Glycine max nitrate reductase. INR1.
AAA62316.1	U20450	Zea mays nitrate reductase.
AAD38068.1	AF153448	Zea mays nitrate reductase. NR1.
CAA40975.1	X57844	Hordeum vulgare nitrate reductase. cDNA is 9bp short of atg.
CAA40976.1	X57845	Hordeum vulgare nitrate reductase.
CAA42739.1	X60173	Hordeum vulgare nitrate reductase (NAD(P)H). nar7.
AAB93560.1	AF022780	Glycine max nitrate reductase. BCNR-A.
AAF17595.1	AF203033	Chlamydomonas reinhardtii nitrate reductase. NIT1.
CAA45497.1	X64136	Volvox carteri nitrate reductase (NADH). nitA.
AAC49460.1	U39931	Chlorella vulgaris nitrate reductase.
AAC49459.1	U39930	Chlorella vulgaris nitrate reductase.
CAA29497.1	X06134	Nicotiana tabacum nitrate reductase.
AAA18377.1	U08029	Spinacia oleracea reduces nitrate to nitrite with NADH. NADH:nitrate reductase.
AAB39553.1	U64308	Agrostemma githago nitrate reductase. agnr1. NADH; similar to agnr2 product encoded by GenBank Accession Number U64309 and to agnr3 product encoded by GenBank Accession Number U64310.
AAA03202.1	M27821	Zea mays NADH:nitrate reductase; (EC 1.6.6.1).
AAA33483.1	M77792	Zea mays enzyme. nitrate reductase. NAR1S.
AAB39555.1	U64310	Agrostemma githago nitrate reductase. agnr3. NADH; similar to agnr1 product encoded by GenBank Accession Number U64308 and agnr2 product encoded by GenBank Accession Number U64309.
AAB39554.1	U64309	Agrostemma githago nitrate reductase. agnr2. NADH; similar to agnr1 product encoded by GenBank Accession Number U64308 and agnr3 product encoded by GenBank Accession Number U64310.

CAA33819.1	X15820	Oryza sativa	nitrate reductase apoenzyme (AA 472-916); Protein sequence is in conflict with the conceptual translation.
CAA33817.1	X15819	Oryza sativa	nitrate reductase apoenzyme.
AAA33998.1	L23853	Glycine max	nitrate reductase. mutant.
CAA58908.1	X84102	Cichorium intybus	nitrate reductase (NADH). nia.
CAA40090.1	X56771	Chlorella vulgaris	nitrate reductase (NADH).
CAA45776.1	X64446	Zea mays	nitrate reductase (NAD(P)H). nar.
AAD17694.1	AF077372	Zea mays	possible reduction of Fe ³⁺ -chelates. cytochrome b5 reductase. NFR.
AAA96242.1	L40147	Avena strigosa	nitrate reductase.
AAB20155.1	S61885	Nicotiana plumbaginifolia	nitrate reductase heme domain. nitrate reductase heme domain, NR. This sequence comes from fig3; NR.
AAA96245.1	L40151	Hordeum pusillum	nitrate reductase.
AAA96247.1	L40153	Hordeum stenostachys	nitrate reductase.
SEQ ID NO: 273			
BAA07395.1	D38220	Brassica napus	nitrate reductase.
BAA07394.1	D38219	Brassica napus	nitrate reductase.
AAA33713.1	L13691	Petunia x hybrida	nitrate reductase. putative.
CAA32218.1	X14060	Lycopersicon esculentum	nitrate reductase.
AAA33712.1	L11563	Petunia x hybrida	nitrate reductase apoenzyme. nia.
AAG30576.1	AF314093	Ricinus communis	nitrate reductase. NIA.
CAA32217.1	X14059	Nicotiana tabacum	nitrate reductase.
CAA32216.1	X14058	Nicotiana tabacum	nitrate reductase.
AAA33114.1	M33154	Cucurbita maxima	nitrate reductase.

AAB52786.1	U95317	Solanum tuberosum	NADH nitrate reductase. StNR3.
AAB18985.1	U76701	Solanum tuberosum	NADH nitrate reductase. StNR2.
AAA34033.1	M32600	Spinacia oleracea	NADH nitrate reductase.
BAA13047.1	D86226	Spinacia oleracea	nitrate reductase.
CAA38031.1	X54097	Betula pendula	nitrate reductase (NADH). nia1.
CAA56696.1	X80670	Lotus japonicus	nitrate reductase (NADH). NIA.
AAA95940.1	U01029	Phaseolus vulgaris	nitrate reductase. PVNR2.
CAA58909.1	X84103	Cichorium intybus	nitrate reductase (NADH). nia.
AAD19790.1	AF055369	Glycine max	nitrate reductase. nr2.
AAA96813.1	U13987	Glycine max	inducible nitrate reductase 2. INR2.
CAA40976.1	X57845	Hordeum vulgare	nitrate reductase.
AAA96727.1	L23854	Glycine max	nitrate reductase. INR1.
CAA37672.1	X53603	Phaseolus vulgaris	nitrate reductase.
CAA33819.1	X15820	Oryza sativa	nitrate reductase apoenzyme (AA 472-916); Protein sequence is in conflict with the conceptual translation.
AAD38068.1	AF153448	Zea mays	nitrate reductase. NR1.
CAA40975.1	X57844	Hordeum vulgare	nitrate reductase. cDNA is 9bp short of atg.
AAB93560.1	AF022780	Glycine max	nitrate reductase. BCNR-A.
AAA62316.1	U20450	Zea mays	nitrate reductase.
CAA42739.1	X60173	Hordeum vulgare	nitrate reductase (NAD(P)H). nar7.
AAF17595.1	AF203033	Chlamydomonas reinhardtii	nitrate reductase. NIT1.
CAA45497.1	X64136	Volvox carteri	nitrate reductase (NADH). nitA.

AAC49460.1	U39931	Chlorella vulgaris	nitrate reductase.
AAC49459.1	U39930	Chlorella vulgaris	nitrate reductase.
CAA29497.1	X06134	Nicotiana tabacum	nitrate reductase.
AAA18377.1	U08029	Spinacia oleracea	reduces nitrate to nitrite with NADH. NADH:nitrate reductase.
AAB39553.1	U64308	Agrostemma githago	nitrate reductase. agnr1. NADH; similar to agnr2 product encoded by GenBank Accession Number U64309 and to agnr3 product encoded by GenBank Accession Number U64310.
AAA03202.1	M27821	Zea mays	NADH:nitrate reductase; (EC 1.6.6.1).
AAA33483.1	M77792	Zea mays	enzyme. nitrate reductase. NAR1S.
AAB39555.1	U64310	Agrostemma githago	nitrate reductase. agnr3. NADH; similar to agnr1 product encoded by GenBank Accession Number U64308 and agnr2 product encoded by GenBank Accession Number U64309.
AAB39554.1	U64309	Agrostemma githago	nitrate reductase. agnr2. NADH; similar to agnr1 product encoded by GenBank Accession Number U64308 and agnr3 product encoded by GenBank Accession Number U64310.
CAA33817.1	X15819	Oryza sativa	nitrate reductase apoenzyme.
CAA58908.1	X84102	Cichorium intybus	nitrate reductase (NADH). nia.
AAA33998.1	L23853	Glycine max	nitrate reductase. mutant.
CAA40090.1	X56771	Chlorella vulgaris	nitrate reductase (NADH).
CAA45776.1	X64446	Zea mays	nitrate reductase (NAD(P)H). nar.
AAD17694.1	AF077372	Zea mays	possible reduction of Fe ³⁺ -chelates. cytochrome b5 reductase. NFR.
AAA96242.1	L40147	Avena strigosa	nitrate reductase.
AAA96250.1	L40149	Hordeum chilense	nitrate reductase.
AAA96245.1	L40151	Hordeum pusillum	nitrate reductase.
AAA96247.1	L40153	Hordeum stenostachys	nitrate reductase.
SEQ ID NO: 274			

AAC39318.1	AF029858	<i>Sorghum bicolor</i> second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p-hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.
BAB40323.1	AB037244	<i>Asparagus officinalis</i> cytochrome P450. ASPI-1.
AAA32913.1	M32885	<i>Persea americana</i> cytochrome P-450LXXIA1 (cyp71A1).
BAB40324.1	AB037245	<i>Asparagus officinalis</i> cytochrome P450. ASPI-2.
AAA19701.1	L24438	<i>Thlaspi arvense</i> cytochrome P450.
CAA71513.1	Y10489	<i>Glycine max</i> putative cytochrome P450.
AAB94589.1	AF022460	<i>Glycine max</i> CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.
AAB94588.1	AF022459	<i>Glycine max</i> CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
AAB61965.1	U48435	<i>Solanum chacoense</i> putative cytochrome P450.
CAA70575.1	Y09423	<i>Nepeta racemosa</i> cytochrome P450. CYP71A5.
CAA71517.1	Y10493	<i>Glycine max</i> putative cytochrome P450.
AAD47832.1	AF166332	<i>Nicotiana tabacum</i> cytochrome P450.
AAK38084.1	AF321860	<i>Lolium rigidum</i> putative cytochrome P450.
AAB94584.1	AF022157	<i>Glycine max</i> capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
AAF27282.1	AF122821	<i>Capsicum annuum</i> cytochrome P450. PepCYP.
AAK38083.1	AF321859	<i>Lolium rigidum</i> putative cytochrome P450.
CAA50312.1	X70981	<i>Solanum melongena</i> P450 hydroxylase. CYPEG2.
CAB56503.1	AJ238612	<i>Catharanthus roseus</i> cytochrome P450.
AAB61964.1	U48434	<i>Solanum chacoense</i> putative cytochrome P450.
AAK38087.1	AF321863	<i>Lolium rigidum</i> putative cytochrome P450.

CAA71514.1	Y10490	Glycine max putative cytochrome P450.
CAA50645.1	X71654	Solanum melongena P450 hydroxylase.
BAA03635.1	D14990	Solanum melongena Cytochrome P-450EG4.
AAD44151.1	AF124816	Mentha x piperita cytochrome p450 isoform PM17.
AAD44152.1	AF124817	Mentha x piperita cytochrome p450 isoform PM2.
CAA83941.1	Z33875	Mentha x piperita cytochrome P-450 oxidase.
AAD44150.1	AF124815	Mentha spicata cytochrome p450.
AAB69644.1	AF000403	Lotus japonicus putative cytochrome P450. LjNP450.
BAB40322.1	AB036772	Triticum aestivum cytochrome P450. N-1.
CAC27827.1	AJ295719	Catharanthus roseus geraniol hydroxylase. cytochrome P450. cyp71.
AAG44132.1	AF218296	Pisum sativum cytochrome P450. P450 isolog.
AAD56282.1	AF155332	Petunia x hybrida flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
AAG14963.1	AF214009	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H3.
AAD37433.1	AF150881	Lycopersicon esculentum x Lycopersicon peruvianum catalyzes the hydroxylation of ferulic acid to 5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome P450-dependent monooxygenase; F5H; FAH1.
BAB39252.1	AP002968	Oryza sativa putative cytochrome P450. P0416G11.1.
AAK38088.1	AF321864	Lolium rigidum putative cytochrome P450.
CAA65580.1	X96784	Nicotiana tabacum cytochrome P450. hsr515.
AAG14961.1	AF214007	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H1.
AAG14962.1	AF214008	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H2.
AAB17562.1	U72654	Eustoma grandiflorum flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
SEQ ID NO: 279		

AAA34122.1	M84466	Nicotiana tabacum	phenylalanine ammonia lyase. tpal.
BAA22948.1	AB008200	Nicotiana tabacum	phenylalanine ammonia-lyase. palB.
AAA34176.1	M90692	Lycopersicon esculentum	phenylalanine ammonia-lyase. PAL5.
AAF40224.1	AF237955	Rubus idaeus	phenylalanine ammonia-lyase 2. PAL2. PAL; phenylpropanoid; multigene; flavonoid.
CAA37129.1	X52953	Glycine max	phenylalanine ammonia-lyase. PAL1.
CAA68036.1	X99705	Triticum aestivum	phenylalanine ammonia-lyase. PAL.
AAA33389.1	M29232	Ipomoea batatas	phenylalanine ammonia-lyase.
AAA34179.2	M83314	Lycopersicon esculentum	deamination of phenylalanine to coumarate. phenylalanine ammonia lyase. pal.
BAA21643.1	D30656	Populus kitakamiensis	phenylalanine ammonia-lyase.
AAB67733.1	U43338	Citrus limon	phenylalanine ammonia-lyase. pal6.
BAA95629.1	AB042520	Catharanthus roseus	phenylalanine ammonia lyase.
BAA05643.1	D26596	Camellia sinensis	phenylalanine ammonia-lyase.
CAA73065.1	Y12461	Helianthus annuus	phenylalanine ammonia lyase. PAL.
BAA24929.1	D83076	Lithospermum erythrorhizon	phenylalanine ammonia-lyase.
BAA24928.1	D83075	Lithospermum erythrorhizon	phenylalanine ammonia-lyase.
BAA00885.1	D10001	Pisum sativum	phenylalanine ammonia-lyase.
AAA84889.1	U39792	Pinus taeda	phenylalanine ammonia-lyase. lpPAL.
CAA61198.1	X87946	Oryza sativa	phenylalanine ammonia-lyase. ZB8.
CAA41169.1	X58180	Medicago sativa	phenylalanine ammonia-lyase. PAL.
BAA00887.1	D10003	Pisum sativum	phenylalanine ammonia-lyase. PAL2.
BAA00886.1	D10002	Pisum sativum	phenylalanine ammonia-lyase. PAL1.

AAA17993.1	M91192	Trifolium subterraneum	phenylalanine ammonia-lyase. PAL1.
AAA33805.1	L11747	Populus x generosa	phenylalanine ammonia lyase. PAL.
AAC78457.1	AF036948	Prunus avium	phenylalanine ammonia-lyase. PAL1.
BAA23367.1	D85850	Daucus carota	phenylalanine ammonia-lyase. gDcPAL1.
CAB42793.1	AJ238753	Citrus clementina x Citrus reticulata	phenylalanine-ammonia lyase. pal1.
AAA99500.1	L36822	Stylosanthes humilis	phenylalanine ammonia lyase. PAL17.1.
CAA55075.1	X78269	Nicotiana tabacum	phenylalanine ammonia-lyase.
BAA22963.1	D17467	Nicotiana tabacum	phenylalanine ammonia-lyase. TOBPAL1.
BAA22947.1	AB008199	Nicotiana tabacum	phenylalanine ammonia-lyase. palA.
CAA57057.1	X81159	Petroselinum crispum	phenylalanine ammonia-lyase 3. PAL3. tetramere subunit.
AAG49585.1	AF325496	Ipomoea nil	phenylalanine ammonia-lyase.
CAA57056.1	X81158	Petroselinum crispum	phenylalanine ammonia-lyase 2. PAL2. deaminase subunit.
CAB42794.1	AJ238754	Citrus clementina x Citrus reticulata	phenylalanine-ammonia lyase. pal2.
CAA05251.1	AJ002221	Digitalis lanata	phenylalanine ammonia lyase.
BAA07860.1	D43802	Populus kitakamiensis	phenylalanine ammonia-lyase.
CAB60719.1	AJ250836	Cicer arietinum	phenylpropanoid pathway. phenylalanine ammonia-lyase. pal.
CAA68256.1	X99997	Bromheadia finlaysoniana	phenylalanine ammonia-lyase. pal.
AAK15640.1	AF326116	Agastache rugosa	phenylalanine ammonia-lyase. PAL.
CAA34226.1	X16099	Oryza sativa subsp. japonica	phenylalanine ammonia-lyase.
AAF40223.1	AF237954	Rubus idaeus	phenylalanine ammonia-lyase 1. PAL1. PAL; phenylpropanoid; multigene; flavonoid.
BAA11459.1	D78640	Ipomoea batatas	Phenylalanine Ammonia-Lyase.

BAA06337.1 D30657 *Populus kitakamiensis*
phenylalanine ammonia-lyase.

AAD45384.1 AF165998 *Vigna unguiculata*
phenylalanine ammonia-lyase.

CAA53733.1 X76130 *Cucumis melo*
phenylalanine ammonia-lyase. pal.

AAA51873.1 U16130 *Persea americana*
phenylalanine ammonia lyase. PAL.

BAB19128.1 AB041361 *Dianthus caryophyllus*
phenylalanine ammonia-lyase. Dcpall.

CAA34715.1 X16772 *Petroselinum crispum*
phenylalanine ammonia-lyase (AA 137 - 716) (1 is 3rd base in codon).

BAA07861.1 D43803 *Populus kitakamiensis*
phenylalanine ammonia-lyase.

SEQ ID NO: 280

AAG43550.1 AF211532 *Nicotiana tabacum*
Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.

AAK00436.1 AC060755 *Oryza sativa*
putative zinc finger protein. OSJNBa0003O19.23.

BAA78746.1 AB023482 *Oryza sativa*
Similar to Arabidopsis thaliana RING-H2 finger protein RHX1a mRNA, partial cds.(AF079184).

CAA74911.1 Y14573 *Hordeum vulgare*
ring finger protein. putative.

AAG46117.1 AC073166 *Oryza sativa*
putative ring finger protein. OSJNBb0064P21.7.

BAA96875.1 AB045121 *Oryza sativa*
RING finger 1. RRF1.

BAA90357.1 AP001080 *Oryza sativa*
EST AU070319(S10788) corresponds to a region of the predicted gene. Similar to RING-H2 finger protein RHA2b (AC006200).

BAA90806.1 AP001168 *Oryza sativa*
ESTs C26000(C11448),AU082130(C11448) correspond to a region of the predicted gene.; Similar to mRNA for zinc-finger protein (Z36749).

SEQ ID NO: 286

AAG14454.1 AF283706 *Tulipa gesneriana*
auxin-induced protein TGSAUR12. SAUR12. small auxin upregulated RNA.

AAG14456.1 AF283708 *Tulipa gesneriana*
auxin-induced protein TGSAUR22. SAUR22. small auxin upregulated RNA.

AAG14455.1 AF283707 *Tulipa gesneriana*
auxin-induced protein TGSAUR21. SAUR21. small auxin upregulated RNA.

AAC08401.1 AF053564 *Mesembryanthemum crystallinum*
auxin-induced protein. similar to auxin-induced proteins from soybean.

SEQ ID NO: 290

AAB65498.1 U73856 *Chlamydomonas reinhardtii*
carbonic anhydrase, alpha type. CAH3.

AAC49983.1 U40871 *Chlamydomonas reinhardtii*
intracellular carbonic anhydrase, alpha type. CAH3.

AAF04292.2 AF190735 *Dunaliella salina*
carbonic anhydrase. CA.

AAC49378.1 U53811 *Dunaliella salina*
carbonic anhydrase. dca.

AAF22644.1 AF183939 *Dunaliella salina*
duplicated carbonic anhydrase. DCA1. DCA; carbonic anhydrase gene family member; salt-inducible; intra-duplicated.

AAD51633.1 AF170173 *Acetabularia acetabulum*
putative carbonic anhydrase 2. CA2. AaCA2.

AAD51634.1 AF170174 *Acetabularia acetabulum*
putative carbonic anhydrase 1. CA1. AaCA1.

AAD51635.1 AF170175 *Acetabularia acetabulum*
putative carbonic anhydrase 1. CA1. AaCA1.

BAA14232.1 D90206 *Chlamydomonas reinhardtii*
carbonic anhydrase.

BAA28217.1 AB013804 *Chlorella sorokiniana*
soluble carbonic anhydrase precursor. CAH1.

SEQ ID NO: 301

AAG03089.2 AC073405 *Oryza sativa*
similar to an Arabidopsis putative P-type transporting ATPase (AC010926).

BAA89544.1 AP001072 *Oryza sativa*
Similar to chromaffin granule ATPase II homolog. (U75321).

BAA88191.1 AP000836 *Oryza sativa*
Similar to chromaffin granule ATPase II homolog (U75321).

BAA90510.2 AP001111 *Oryza sativa*
rice EST AU030811, similar to rice Ca²⁺-ATPase (U82966).

AAD11618.1 AF050496 *Lycopersicon esculentum*
Ca²⁺-ATPase. LCA1B; alternative transcript.

AAA34138.1 M96324 *Lycopersicon esculentum*
The calcium ATPase is a calcium ion pump. Ca²⁺-ATPase. LCA1.

AAD11617.1 AF050495 *Lycopersicon esculentum*
Ca²⁺-ATPase. LCA1A; alternative transcript.

AAF73985.1 AF096871 *Zea mays*
calcium pump. calcium ATPase. cap1.

AAD31896.1 AF145478 *Mesembryanthemum crystallinum*
calcium ATPase.

AAG28436.1 AF195029 *Glycine max*
plasma membrane Ca²⁺-ATPase. SCA2.

CAA63790.1	X93592	Dunaliella bioculata
P-type ATPase. cal. calcium pumping; CA1.		
AAG28435.1	AF195028	Glycine max
plasma membrane Ca ²⁺ -ATPase. SCA1.		
CAA68234.1	X99972	Brassica oleracea
calmodulin-stimulated calcium-ATPase.		
AAB58910.1	U82966	Oryza sativa
Ca ²⁺ -ATPase.		
CAB69824.1	AJ271439	Prunus persica
plasma membrane H ⁺ ATPase. PPA1.		
AAB60276.1	U09989	Zea mays
H(+)-transporting ATPase. Mha1.		
BAA01058.1	D10207	Oryza sativa
H-ATPase. OSA1.		
CAC29435.1	AJ310523	Vicia faba
P-type H ⁺ -ATPase. vha4. predominantly expressed in flowers.		
AAD20330.1	AF110268	Oryza sativa
plasma membrane proton-ATPase gene OSA3.		
AAA34098.1	M80490	Nicotiana plumbaginifolia
plasma membrane H ⁺ ATPase. pma3.		
AAB84203.1	AF029257	Kosteletzkya virginica
plasma membrane H ⁺ -ATPase.		
CAC28224.1	AJ286749	Sesbania rostrata
p-type H ⁺ -ATPase. ha5.		
AAD46188.1	AF156691	Nicotiana plumbaginifolia
plasma membrane proton ATPase. pma9.		
AAA34173.1	M60166	Lycopersicon esculentum
H ⁺ -ATPase. LHA1.		
AAA34094.1	M80489	Nicotiana plumbaginifolia
plasma membrane H ⁺ ATPase. pma1.		
AAA34052.1	M27888	Nicotiana plumbaginifolia
H ⁺ -translocating ATPase.		
CAC28221.1	AJ286746	Sesbania rostrata
p-type H ⁺ -ATPase. ha2.		
CAA54045.1	X76535	Solanum tuberosum
H(+)-transporting ATPase. PHA2.		
BAA06629.1	D31843	Oryza sativa
plasma membrane H ⁺ -ATPase. OSA2.		
CAA64406.1	X94936	Phaseolus vulgaris
H(+)-transporting ATPase. BHA-2.		
AAF98344.1	AF275745	Lycopersicon esculentum
plasma membrane H ⁺ -ATPase. LHA2. P-type ion pump.		

AAD55399.1 AF179442 *Lycopersicon esculentum*
plasma membrane H⁺-ATPase isoform LHA2. LHA2.

CAA54046.1 X76536 *Solanum tuberosum*
H(+)-transporting ATPase. PHA1.

SEQ ID NO: 302

CAA70575.1 Y09423 *Nepeta racemosa*
cytochrome P450. CYP71A5.

CAA70576.1 Y09424 *Nepeta racemosa*
cytochrome P450. CYP71A6.

CAA50312.1 X70981 *Solanum melongena*
P450 hydroxylase. CYPEG2.

AAA32913.1 M32885 *Persea americana*
cytochrome P-450LXXIA1 (cyp71A1).

BAA03635.1 D14990 *Solanum melongena*
Cytochrome P-450EG4.

CAA50645.1 X71654 *Solanum melongena*
P450 hydroxylase.

CAA83941.1 Z33875 *Mentha x piperita*
cytochrome P-450 oxidase.

CAA71513.1 Y10489 *Glycine max*
putative cytochrome P450.

AAB94584.1 AF022157 *Glycine max*
capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10.
cytochrome P450 monooxygenase.

AAB61965.1 U48435 *Solanum chacoense*
putative cytochrome P450.

AAB69644.1 AF000403 *Lotus japonicus*
putative cytochrome P450. LjNP450.

BAB40324.1 AB037245 *Asparagus officinalis*
cytochrome P450. ASPI-2.

AAD47832.1 AF166332 *Nicotiana tabacum*
cytochrome P450.

AAB61964.1 U48434 *Solanum chacoense*
putative cytochrome P450.

BAB40323.1 AB037244 *Asparagus officinalis*
cytochrome P450. ASPI-1.

CAA71514.1 Y10490 *Glycine max*
putative cytochrome P450.

AAB94588.1 AF022459 *Glycine max*
CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.

AAF27282.1 AF122821 *Capsicum annuum*
cytochrome P450. PepCYP.

CAA50313.1	X70982	Solanum melongena	P450 hydroxylase. CYPEG3.
AAA19701.1	L24438	Thlaspi arvense	cytochrome P450.
BAA12159.1	D83968	Glycine max	Cytochrome P-450 (CYP93A1).
AAK38082.1	AF321858	Lolium rigidum	putative cytochrome P450.
BAB40322.1	AB036772	Triticum aestivum	cytochrome P450. N-1.
CAA71516.1	Y10492	Glycine max	putative cytochrome P450.
CAA65580.1	X96784	Nicotiana tabacum	cytochrome P450. hsr515.
AAK38083.1	AF321859	Lolium rigidum	putative cytochrome P450.
AAK38084.1	AF321860	Lolium rigidum	putative cytochrome P450.
CAA71517.1	Y10493	Glycine max	putative cytochrome P450.
CAA72196.1	Y11368	Zea mays	cytochrome p450. cyp71c4.
CAA57425.1	X81831	Zea mays	cytochrome P450. CYP71C4. family CYP71, subfamily CYP71C.
AAC39318.1	AF029858	Sorghum bicolor	second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p-hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.
AAD56282.1	AF155332	Petunia x hybrida	flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
CAB56503.1	AJ238612	Catharanthus roseus	cytochrome P450.
AAK38087.1	AF321863	Lolium rigidum	putative cytochrome P450.
CAA57421.1	X81827	Zea mays	cytochrome P450. CYP71C1. family CYP71, subfamily CYP71C.
CAA57422.1	X81828	Zea mays	cytochrome P450. CYP71C1. family CYP71, subfamily CYP71C.
BAB39252.1	AP002968	Oryza sativa	putative cytochrome P450. P0416G11.1.
BAA13076.1	D86351	Glycine max	cytochrome P-450 (CYP93A2).

AAB94589.1 AF022460 Glycine max
CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.

AAD38930.1 AF135485 Glycine max
cytochrome P450 monooxygenase CYP93D1. CYP93E1.

CAA57423.1 X81829 Zea mays
cytochrome P450. CYP71C2. family CYP71, subfamily CYP71C.

CAA72208.1 Y11404 Zea mays
cytochrome p450. cyp71c2.

AAG44132.1 AF218296 Pisum sativum
cytochrome P450. P450 isolog.

AAK38088.1 AF321864 Lolium rigidum
putative cytochrome P450.

CAA64635.1 X95342 Nicotiana tabacum
cytochrome P450. hsr515. hypersensitivity-related gene.

SEQ ID NO: 303

AAC49826.1 U71604 Catharanthus roseus
involved in the second to last step in vindoline biosynthesis. desacetoxyvindoline 4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase.

AAB97311.1 AF008597 Catharanthus roseus
desacetoxyvindoline-4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase; involved in the second to last step in vindoline biosynthesis.

AAC49827.1 U71605 Catharanthus roseus
involved in the second to last step in vindoline biosynthesis. desacetoxyvindoline 4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase.

BAA95828.1 AP002069 Oryza sativa
ESTs D47168(S12332), D46350(S10967) correspond to a region of the predicted gene. Similar to Prunus armeniaca ethylene-forming-enzyme-like dioxygenase. (U97530).

BAA37127.1 AB012203 Lactuca sativa
2-oxoglutarate-dependent dioxygenase. gibberelin 20-oxidase. Ls20ox1.

CAA54557.1 X77368 Solanum melongena
dioxygenase. DIOX.

BAA81862.1 AB026295 Oryza sativa
Similar to leucoanthocyanidin dioxygenase. (AI440611).

SEQ ID NO: 304

AAF61647.1 AF190634 Nicotiana tabacum
UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

BAA89009.1 AB027455 Petunia x hybrida
anthocyanin 5-O-glucosyltransferase. PH1.

AAF17077.1 AF199453 Sorghum bicolor
UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.

AAF98390.1 AF287143 *Brassica napus*
catalyzes the transfer of glucose from UDP-glucose to sinapate and some other
hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate
glucosyltransferase. SGT1. SGT.

BAA36423.1 AB013598 *Verbena x hybrida*
UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

AAK16181.1 AC079887 *Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.16.

BAA36421.1 AB013596 *Perilla frutescens*
UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.

BAB07962.1 AP002524 *Oryza sativa*
putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs
AU067881(C10481),AU067882(C10481).

AAK16178.1 AC079887 *Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.5.

BAA93039.1 AB033758 *Citrus unshiu*
limonoid UDP-glucosyltransferase. LGTase.

AAK16172.1 AC079887 *Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.14.

BAA36422.1 AB013597 *Perilla frutescens*
UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.

BAB17182.1 AP002843 *Oryza sativa*
putative UTP-glucose glucosyltransferase. P0407B12.19.

BAA12737.1 D85186 *Gentiana triflora*
UDP-glucose:flavonoid-3-glucosyltransferase.

AAG25643.1 AF303396 *Phaseolus vulgaris*
UDP-glucosyltransferase HRA25. putative; defense associated.

AAB48444.1 U82367 *Solanum tuberosum*
UDP-glucose glucosyltransferase.

BAA19659.1 AB002818 *Perilla frutescens*
flavonoid 3-O-glucosyltransferase. UDP glucose.

CAA54612.1 X77462 *Manihot esculenta*
UTP-glucose glucosyltransferase. CGT5.

BAA89008.1 AB027454 *Petunia x hybrida*
anthocyanidin 3-O-glucosyltransferase. PGT8.

AAK16175.1 AC079887 *Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.15.

BAA83484.1 AB031274 *Scutellaria baicalensis*
UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

AAB36652.1 U32643 *Nicotiana tabacum*
immediate-early salicylate-induced glucosyltransferase. IS10a.

AAK28304.1 AF346432 *Nicotiana tabacum*
phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.

AAB36653.1	U32644	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS5a.
AAD04166.1	AF101972	Phaseolus lunatus	catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
AAD21086.1	AF127218	Forsythia x intermedia	adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
CAA54611.1	X77461	Manihot esculenta	UTP-glucose glucosyltransferase. CGT2.
AAK28303.1	AF346431	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
CAA54609.1	X77459	Manihot esculenta	UTP-glucose glucosyltransferase. CGT1.
CAA54613.1	X77463	Manihot esculenta	UTP-glucose glucosyltransferase. CGT6.
BAB41026.1	AB047099	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
BAB41024.1	AB047097	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.
BAB41022.1	AB047095	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAB41017.1	AB047090	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.
BAB41020.1	AB047093	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
CAA59450.1	X85138	Lycopersicon esculentum	twil. homologous to glucosyltransferases.
BAB41025.1	AB047098	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
BAB41023.1	AB047096	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
BAB41018.1	AB047091	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents V. vinifera cv. Centennial.
SEQ ID NO: 306			
AAB06458.1	U64806	Brassica napus	pathogenesis-related protein PR1. Ypr1.
AAB01666.1	U21849	Brassica napus	PR-1a. LSC94.

AAB09587.1	U70666	Brassica napus	pathogenesis-related protein PR1. Ypr1.
CAA47374.1	X66942	Nicotiana tabacum	prb-1b. PRB-1B.
AAK30143.1	AF348141	Capsicum annuum	pathogenesis-related protein PR-1 precursor.
CAA36790.1	X52555	Nicotiana tabacum	PR-1 protein (AA 1-184).
CAA35666.1	X17681	Nicotiana tabacum	pathogenesis-related protein 1b (AA 1-168).
CAA31010.1	X12487	Nicotiana tabacum	PR1c preprotein.
CAA29023.1	X05454	Nicotiana tabacum	PR-1c protein.
CAA32228.1	X14065	Nicotiana tabacum	PRP 1 precursor (AA -23 to 154).
BAA14220.1	D90196	Nicotiana tabacum	PR1a protein precursor.
CAA31233.1	X12737	Nicotiana tabacum	PR-1a protein (AA 1 - 168).
CAA29392.1	X05959	Nicotiana tabacum	PR-1a precursor (AA -30 to 138).
CAA29660.1	X06361	Nicotiana tabacum	PR1a precursor (AA -30 to -1).
CAA09671.1	AJ011520	Lycopersicon esculentum	pathogenesis-related protein PR1a (P4). pr1a (P4).
AAA03615.1	M69247	Lycopersicon esculentum	pathogenesis-related protein P4. P4.
CAA30017.1	X06930	Nicotiana tabacum	PR-1a protein (AA 1 - 168).
CAA31008.1	X12485	Nicotiana tabacum	PR1a preprotein.
CAA52893.1	X74939	Hordeum vulgare	PR-1a pathogenesis related protein (Hv-1a).
CAB58263.1	AJ250136	Solanum tuberosum	pathogenesis related protein PR-1. pr1-1.
AAB49685.1	U89895	Oryza sativa	pathogenesis-related protein class 1. PR-1. induced by pathogen attack in plants.
CAA27183.1	X03465	Nicotiana tabacum	PR-1b precursor; (aa -30-138).
CAA35665.1	X17680	Nicotiana tabacum	pathogenesis-related protein 1b (AA 1-168).

BAA14221.1	D90197	Nicotiana tabacum
PR1b protein precursor.		
CAA48672.1	X68738	Lycopersicon esculentum
P1(p14) protein. pTE28.1.		
CAA81229.1	Z26320	Hordeum vulgare
pathogenesis-related protein. pathogenesis-related protein.		
AAA03616.1	M69248	Lycopersicon esculentum
pathogenesis-related protein P6. P6.		
CAA70042.1	Y08804	Lycopersicon esculentum
PR protein. PR1b1.		
AAB05225.1	U49241	Nicotiana glutinosa
pathogenesis-related protein-1.		
CAA31009.1	X12486	Nicotiana tabacum
PR1b preprotein.		
AAC25629.1	U82200	Zea mays
pathogenesis related protein-1. PR-1.		
AAF78528.1	AF195237	Pyrus pyrifolia
pathogenesis-related protein. PR-1b.		
AAD33696.1	AF136636	Glycine max
PR1a precursor. PR1a.		
CAA79703.1	Z21494	Hordeum vulgare
Pathogenesis-related protein 1.		
CAA52894.1	X74940	Hordeum vulgare
PR-1b pathogenesis related protein (Hv-8).		
CAA81234.1	Z26333	Hordeum vulgare
pathogenesis-related protein. pathogenesis-related protein.		
CAA81230.1	Z26321	Hordeum vulgare
pathogenesis-related protein. pathogenesis-related protein.		
CAA04881.1	AJ001627	Lycopersicon esculentum
pathogenesis-related protein. PR1d.		
CAA07473.1	AJ007348	Triticum aestivum
pathogenesis-related protein 1.1. PR-1.1.		
CAA07474.1	AJ007349	Triticum aestivum
pathogenesis-related protein 1.2. PR-1.2.		
CAA50596.1	X71592	Lycopersicon esculentum
PR-1a1.		
CAA70070.1	Y08844	Lycopersicon esculentum
PR protein. PR1a2.		
CAA38223.1	X54325	Zea mays
pathogenesis-related protein. PRms.		
AAF78527.1	AF195236	Pyrus pyrifolia
pathogenesis-related proteins. PR-1a.		

CAC03571.1 AJ278436 *Oryza sativa*
defence response. PR1a protein. Pr1a.

AAG44566.1 AF251277 *Oryza sativa* subsp. *japonica*
acidic PR-1 type pathogenesis-related protein PR-1a. PR-1a. induced by pathogen attack.

AAC06244.1 AF053343 *Capsicum annuum*
PR-1 protein precursor. pathogen-induced PR1 protein.

CAA56174.1 X79778 *Medicago truncatula*
PR-1.

SEQ ID NO: 307

AAF06347.1 AF195654 *Vitis vinifera*
SCUTL2. thaumatin-like protein.

BAA28872.1 AB006009 *Pyrus pyrifolia*
thaumatin-like protein precursor. PsTL1.

AAB38064.1 U32440 *Prunus avium*
thaumatin-like protein precursor.

BAA95017.1 AB031870 *Cestrum elegans*
thaumatin-like protein. CETLP.

BAA74546.2 AB000834 *Nicotiana tabacum*
thaumatin-like protein SE39b.

AAC36740.1 AF090143 *Malus x domestica*
thaumatin-like protein precursor Mdtl1. MDTL1. pathogenesis-related.

CAC10270.1 AJ243427 *Malus x domestica*
thaumatin-like protein. tl. allergen, pathogenesis-related.

AAB95118.1 U71244 *Brassica rapa*
pathogenesis-related group 5 protein. BFTP. thaumatin-like protein; PR-5.

CAC09477.1 AL442113 *Oryza sativa*
thaumatin-like protein. H0806H05.10.

CAB62167.1 AJ242828 *Castanea sativa*
antifungal. thaumatin-like protein. tl1.

CAA06927.1 AJ006233 *Nicotiana tabacum*
putative thaumatin-like protein precursor.

AAF06346.1 AF195653 *Vitis vinifera*
SCUTL1. thaumatin-like protein.

AAB02259.1 U57787 *Avena sativa*
permatin precursor. thaumatin-like protein.

AAD55090.1 AF178653 *Vitis riparia*
thaumatin. osmotin; pathogenesis-related protein.

CAA10492.1 AJ131731 *Pseudotsuga menziesii*
Thaumatin-like protein. 5A1A.16.

CAA09228.1 AJ010501 *Cicer arietinum*
thaumatin-like protein PR-5b.

BAA95165.1 AB029918 *Nicotiana tabacum*
pistil transmitting tissue specific thaumatin (SE39b)-like protein. SE39b.

AAF82264.1 AF227324 *Vitis vinifera*
thaumatin-like protein.

CAB85636.1 AJ237998 *Vitis vinifera*
putative thaumatin-like protein. TL2.

AAB53368.1 U77657 *Oryza sativa*
pathogenesis-related thaumatin-like protein.

AAB61590.1 AF003007 *Vitis vinifera*
VVTL1. osmotin-like protein, PR-5 protein; thaumatin-like protein.

AAB53367.1 U77656 *Oryza sativa*
pathogenesis-related thaumatin-like protein.

CAB85637.1 AJ237999 *Vitis vinifera*
putative thaumatin-like protein. TL1. alternative name grip 51.

SEQ ID NO: 308

BAA14143.1 D90115 *Armoracia rusticana*
peroxidase isozyme.

BAA14144.1 D90116 *Armoracia rusticana*
peroxidase isozyme.

BAA11853.1 D83225 *Populus nigra*
peroxidase.

CAA66035.1 X97349 *Populus balsamifera* subsp. *trichocarpa*
signal for ER. peroxidase.

CAA66036.1 X97350 *Populus balsamifera* subsp. *trichocarpa*
signal for ER. peroxidase.

BAA11852.1 D83224 *Populus nigra*
peroxidase.

CAA66034.1 X97348 *Populus balsamifera* subsp. *trichocarpa*
signal for ER. peroxidase.

CAA66037.1 X97351 *Populus balsamifera* subsp. *trichocarpa*
signal for ER. peroxidase.

BAA07241.1 D38051 *Populus kitakamiensis*
peroxidase. prxA4a.

AAB47602.1 L07554 *Linum usitatissimum*
peroxidase. FLXPER1.

BAA06334.1 D30652 *Populus kitakamiensis*
peroxidase.

AAC98519.1 AF007211 *Glycine max*
peroxidase precursor. GMIPER1. pathogen-induced.

AAB97734.1 AF014502 *Glycine max*
seed coat peroxidase precursor. Ep. H2O2 oxidoreductase; class III plant peroxidase.

BAA06335.1	D30653	Populus kitakamiensis	peroxidase.
AAD37427.1	AF149277	Phaseolus vulgaris	peroxidase 1 precursor. FBP1. secretory peroxidase.
CAA62226.1	X90693	Medicago sativa	peroxidase1B. prx1B.
CAA62227.1	X90694	Medicago sativa	peroxidase1C. prx1C.
AAB41811.1	L36157	Medicago sativa	peroxidase. pxdC. amino acid feature: conserved domains, aa 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 .. 73.
CAA62225.1	X90692	Medicago sativa	peroxidase1A. prx1A.
AAB41810.1	L36156	Medicago sativa	peroxidase. pxdA. amino acid feature: conserved motifs, aa 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
AAD37430.1	AF149280	Phaseolus vulgaris	peroxidase 5 precursor. FBP5. secretory peroxidase.
CAB94692.1	AJ242742	Ipomoea batatas	Removal of H ₂ O ₂ , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
AAA34108.1	J02979	Nicotiana tabacum	lignin-forming peroxidase precursor (EC 1.11.1.7).
CAA40796.1	X57564	Armoracia rusticana	peroxidase. peroxidase precursor.
BAA01877.1	D11102	Populus kitakamiensis	peroxidase. prxA1.
BAA01992.1	D11396	Nicotiana tabacum	'peroxidase'.
CAB67121.1	Y19023	Lycopersicon esculentum	peroxidase. cevi-1.
CAA50597.1	X71593	Lycopersicon esculentum	peroxidase. CEVI-1.
AAD43561.1	AF155124	Gossypium hirsutum	bacterial-induced peroxidase precursor. Perx_Goshiko.
BAA92500.1	AP001383	Oryza sativa	ESTs D39300(R3292),AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).
AAF63027.1	AF244924	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
AAB02554.1	L37790	Stylosanthes humilis	cationic peroxidase.

AAB06183.1	M37636	Arachis hypogaea	cationic peroxidase. PNC1.
CAA59487.1	X85230	Triticum aestivum	peroxidase. pox4.
BAA94962.1	AB042103	Asparagus officinalis	peroxidase. AspPOX1.
AAF63026.1	AF244923	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx14 precursor. type III peroxidase.
CAB99487.1	AJ276227	Hordeum vulgare	defence against plant pathogens. peroxidase. prx8.
CAA71492.1	Y10466	Spinacia oleracea	peroxidase. prxr5.
CAB65334.1	AJ250121	Picea abies	peroxidase. SPI2 protein. spi2.
AAA33121.1	M32742	Cucumis sativus	peroxidase (CuPer2).
CAA39486.1	X56011	Triticum aestivum	peroxidase.
BAA92422.1	AP001366	Oryza sativa	ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to A.thaliana mRNA for peroxidase ATP18a. (X98804).
BAA92497.1	AP001383	Oryza sativa	ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to peroxidase ATP18a. (X98804).
CAA59485.1	X85228	Triticum aestivum	peroxidase. POX2.
CAA76680.1	Y17192	Cucurbita pepo	peroxidase. aprx. type III peroxidase.
SEQ ID NO: 309			
BAA85400.1	AP000615	Oryza sativa	similar to OsMlo-h1. (Z95353).
CAB06083.1	Z83834	Hordeum vulgare	Mlo. Mlo.
CAA74909.1	Y14573	Hordeum vulgare	Mlo protein. Mlo.
AAG46114.1	AC073166	Oryza sativa	putative Mlo (pathogen resistance) protein. OSJNBb0064P21.5.
CAA06487.1	AJ005341	Linum usitatissimum	MLO. homolog.
SEQ ID NO: 310			
AAC63113.1	AF000307	Brassica napus	steroid sulfotransferase 3. BnST3.

AAC63112.1 AF000306 *Brassica napus*
steroid sulfotransferase 2. BnST2.

AAC63111.1 AF000305 *Brassica napus*
steroid sulfotransferase 1. BnST1.

AAA61638.1 U10275 *Flaveria bidentis*
O-sulfation of position 3 of flavonols. flavonol 3-sulfotransferase.

AAA33342.2 M84135 *Flaveria chloraefolia*
flavonol 3-sulfotransferase.

AAA87399.1 U10277 *Flaveria bidentis*
transfers sulfate group into flavonol. sulfotransferase-like flavonol.

AAA33343.1 M84136 *Flaveria chloraefolia*
O-sulfation of position 4' of flavonol. flavonol 4'-sulfotransferase.

SEQ ID NO: 312

AAD22970.1 AF124148 *Glycine max*
trehalase 1 GMTRE1. expressed constitutively in many tissues of soybean at a low level;
similar to the *Arabidopsis thaliana* trehalase precursor encoded by GenBank Accession
Number AC002343.

AAG13442.1 AC051634 *Oryza sativa*
putative trehalase. OSJNBb0018B10.19.

CAB50901.1 AJ238651 *Medicago truncatula*
trehalase. TRE1 protein. tre1.

SEQ ID NO: 313

BAA19928.1 AB003491 *Oryza sativa*
tryptophan synthase B. trpB.

AAA33491.1 M76685 *Zea mays*
tryptophan synthase beta-subunit. TSB2.

AAB97526.1 AF042321 *Camptotheca acuminata*
tryptophan synthase beta. TSB.

AAB97087.1 AF042320 *Camptotheca acuminata*
tryptophan synthase beta subunit.

AAA33490.1 M76684 *Zea mays*
tryptophan synthase beta-subunit. TSB1.

AAC25986.1 AF047024 *Chlamydomonas reinhardtii*
tryptophan synthase beta. MAA7.

SEQ ID NO: 314

AAG42689.1 AF271384 *Zea mays*
putative tryptophan synthase alpha. TSAlike.

CAA54131.1 X76713 *Zea mays*
tryptophan synthase, alpha subunit. trpA.

AAG42688.1 AF271383 *Zea mays*
putative tryptophan synthase alpha. TSAlike.

SEQ ID NO: 315

AAB97526.1 AF042321 *Camptotheca acuminata*
tryptophan synthase beta. TSB.

AAB97087.1 AF042320 *Camptotheca acuminata*
tryptophan synthase beta subunit.

BAA19928.1 AB003491 *Oryza sativa*
tryptophan synthase B. trpB.

AAA33491.1 M76685 *Zea mays*
tryptophan synthase beta-subunit. TSB2.

AAA33490.1 M76684 *Zea mays*
tryptophan synthase beta-subunit. TSB1.

AAC25986.1 AF047024 *Chlamydomonas reinhardtii*
tryptophan synthase beta. MAA7.

SEQ ID NO: 316

AAA33967.1 M76981 *Glycine max*
vegetative storage protein. vspA.

BAA23563.1 D50094 *Phaseolus vulgaris*
pod storage protein.

BAA19152.1 AB000585 *Phaseolus vulgaris*
pod storage protein. PSP.

AAA34020.1 M20037 *Glycine max*
vegetative storage protein.

AAA34022.1 M76980 *Glycine max*
vegetative storage protein. vspB.

AAA34021.1 M20038 *Glycine max*
vegetative storage protein.

SEQ ID NO: 321

BAA87043.1 AB035183 *Ipomoea batatas*
N-hydroxycinnamoyl/benzoyltransferase. hcbt.

CAB06427.1 Z84383 *Dianthus caryophyllus*
phytoalexin biosynthesis. anthranilate N-hydroxycinnamoyl/benzoyltransferase.

CAB06429.1 Z84385 *Dianthus caryophyllus*
phytoalexin biosynthesis. anthranilate N-hydroxycinnamoyl/benzoyltransferase.

CAB06430.1 Z84386 *Dianthus caryophyllus*
phytoalexin biosynthesis. anthranilate N-hydroxycinnamoyl/benzoyltransferase.

CAB11466.1 Z98758 *Dianthus caryophyllus*
carnation phytoalexin biosynthesis. anthranilate N-hydroxycinnamoyl/benzoyltransferase.

CAB06538.1 Z84571 *Dianthus caryophyllus*
phytoalexin biosynthesis. anthranilate N-hydroxycinnamoyl/benzoyltransferase.

CAB06428.1 Z84384 *Dianthus caryophyllus*
phytoalexin biosynthesis. anthranilate N-hydroxycinnamoyl/benzoyltransferase.

SEQ ID NO: 323

BAB12694.1 AP002746 *Oryza sativa*
putative zinc finger transcription factor. P0671B11.10. contains ESTs
AU098331(E31537),C91783(E31537).

SEQ ID NO: 325

BAB03447.1 AP002817 *Oryza sativa*
ESTs C96615(C10106),C26336(C12127),D21959(C10106) correspond to a region of the
predicted gene. Similar to *Arabidopsis thaliana* DNA chromosome 4, BAC clone T6K21;
NAM (no apical meristem) - like protein (AL021889).

BAA92400.1 AP001366 *Oryza sativa*
ESTs C96615(C10106),C26336(C12127),D21959(C10106) correspond to a region of the
predicted gene. Similar to NAM (AL021889).

BAB16335.1 AP002818 *Oryza sativa*
putative NAM protein. P0436E04.18. contains ESTs E10793(C19698),E10793(C99379).

BAB16328.1 AP002818 *Oryza sativa*
putative NAM protein. P0436E04.11. contains ESTs R4069(AU032425),R4069(AU082730).

CAA63102.2 X92205 *Petunia x hybrida*
apical meristem formation. NAM.

CAA63101.1 X92204 *Petunia x hybrida*
apical meristem formation. NAM.

AAK13151.1 AC078829 *Oryza sativa*
putative NAM (no apical meristem) protein. OSJNBa0026O12.6.

BAB19365.1 AP002542 *Oryza sativa*
putative NAM (no apical meristem) protein. P0679C08.4.

BAA84803.1 AP000559 *Oryza sativa*
Similar to NAM like protein (AC005310).

SEQ ID NO: 326

CAB51836.1 AJ243961 *Oryza sativa*
Putative Ser/Thr protein kinase. I1332.7.

BAB18292.1 AP002860 *Oryza sativa*
putative receptor-like protein kinase. P0409B08.19.

BAB39873.1 AP002882 *Oryza sativa*
putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

BAB21240.1 AP002953 *Oryza sativa*
Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).

AAA33000.1 M76647 *Brassica oleracea*
receptor protein kinase. SKR6.

CAA74661.1 Y14285 *Brassica oleracea*
SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular
kinase domain: 1412-2554.

CAB89179.1 AJ245479 *Brassica napus* subsp. *napus*
ser /thr kinase. S-locus receptor kinase. srk.

AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
AAB61708.1	U93048	Daucus carota	somatic embryogenesis receptor-like kinase. SERK.
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
SEQ ID NO: 327			
AAC04717.1	AF034131	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-G. similar to MYB A encoded by GenBank Accession Number L04497.
BAA23340.1	D88620	Oryza sativa	transfactor. OSMYB4. Osmyb4.
AAK19611.1	AF336278	Gossypium hirsutum	BNLGH1233. bnlghi6233. similar to myb.
AAA33482.1	M37153	Zea mays	c1 locus myb homologue; putative.
AAK09326.1	AF320613	Zea mays	activates anthocyanin transcription. anthocyanin regulatory C1. c1. transcription factor.
AAK09327.1	AF320614	Zea mays	activates anthocyanin transcription. anthocyanin regulatory C1. c1. transcription factor.
AAA82943.1	U39448	Picea mariana	MYB-like transcriptional factor MBF1. putative DNA binding region highly similar to the maize C1.
AAK19618.1	AF336285	Gossypium hirsutum	GHMYB38. ghmyb38. similar to myb.
CAA64614.1	X95296	Lycopersicon esculentum	transcription factor. THM27. myb-related.
AAK19619.1	AF336286	Gossypium hirsutum	GHMYB9. ghmyb9. similar to myb.

AAC04720.1 AF034134 *Gossypium hirsutum*
putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-O.
similar to MYB A encoded by GenBank Accession Number L04497.

AAC04718.1 AF034132 *Gossypium hirsutum*
putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-J.
similar to MYB A encoded by GenBank Accession Number L04497.

SEQ ID NO: 329

CAB93939.1 AJ238739 *Catharanthus roseus*
putative transcription factor. AP2-domain DNA-binding protein. orca1.

AAF76898.1 AF274033 *Atriplex hortensis*
apetala2 domain-containing protein.

AAG43545.1 AF211527 *Nicotiana tabacum*
Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.

CAC12822.1 AJ299252 *Nicotiana tabacum*
AP2 domain-containing transcription factor. ap2.

BAA78738.1 AB023482 *Oryza sativa*
EST AU055776(S20048) corresponds to a region of the predicted gene.; Similar to
Arabidopsis thaliana AP2 domain containing protein RAP2.10 mRNA, partial
cds.(AF003103).

AAC14323.1 AF058827 *Nicotiana tabacum*
TSI1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pti6.

BAA97122.1 AB016264 *Nicotiana sylvestris*
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-
related) gene of higher plant. ethylene-responsive element binding factor. nserf2.

CAB93940.1 AJ238740 *Catharanthus roseus*
putative transcription factor. AP2-domain DNA-binding protein. orca2.

BAA76734.1 AB024575 *Nicotiana tabacum*
ethylene responsive element binding factor.

CAB96900.1 AJ251250 *Catharanthus roseus*
transcription factor. AP2-domain DNA-binding protein. orca3.

CAB96899.1 AJ251249 *Catharanthus roseus*
transcription factor. AP2-domain DNA-binding protein. orca3.

AAF63205.1 AF245119 *Mesembryanthemum crystallinum*
AP2-related transcription factor. CDBP. stress induced transcription factor.

AAC24587.1 AF071893 *Prunus armeniaca*
AP2 domain containing protein. AP2DCP.

BAA94514.2 AP001800 *Oryza sativa*
Similar to *Arabidopsis thaliana* chromosome 4, BAC clone F9D16; putative Ap2 domain
protein (AL035394).

BAA97124.1 AB016266 *Nicotiana sylvestris*
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-
related) gene of higher plant. ethylene-responsive element binding factor. nserf4.

BAA07321.1	D38123	Nicotiana tabacum	ERF1. ethylene-responsive transcription factor.
BAB16083.1	AB036883	Oryza sativa	transcriptional repressor. osERF3. osERF3. ERF protein family ERF3 associated repression domain.
BAB03248.1	AB037183	Oryza sativa	ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
BAA97123.1	AB016265	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
AAF23899.1	AF193803	Oryza sativa	transcription factor EREBP1. EREBP/AP2-like transcription factor.
AAK31271.1	AC079890	Oryza sativa	putative transcriptional factor. OSJNBb0089A17.22.
AAC62619.1	AF057373	Nicotiana tabacum	transcription factor. ethylene response element binding protein 1. EREBP1.
AAG43548.1	AF211530	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
BAA90812.1	AP001168	Oryza sativa	Similar to mRNA for DREB1A (AB007787).
AAG43549.1	AF211531	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
BAA99376.1	AP002526	Oryza sativa	ESTs AU093391(E60370), AU091593(C60458), AU093392(E60370) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana BAC F21J9; AP2 domain protein. (AC000103).
AAK01089.1	AF298231	Hordeum vulgare	CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.
AAG59618.1	AF239616	Hordeum vulgare	CRT/DRE-binding factor. CBF.
AAG59619.1	AF243384	Oryza sativa	CRT/DRE binding factor. CBF. DREB.
AAK01088.1	AF298230	Hordeum vulgare	CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
AAC49567.1	U41466	Zea mays	Glossy15. Glossy15. AP2 DNA-binding domain protein; similar to the Arabidopsis floral homeotic gene APETALA2; maize AP2-domain regulator of leaf epidermal traits; homeotic regulator of leaf epidermal cell identity; allele: W64A; putative transcription factor.
SEQ ID NO: 330			
AAC67571.1	AF060884	Brassica napus	desiccation protein. Cdes. induced by dehydration.

AAA61564.1	U08108	Glycine max	putative desiccation protectant protein, homolog of Lea14, GenBank Accession Number M88321.
AAA18543.1	M88322	Gossypium hirsutum	probable desiccation protectant. Group 4 late embryogenesis-abundant protein. Lea14-A. This CDS is colinear and 66% identical with that in cDNA clone pcC27-45 from <i>Cratogeomys</i> plantagineum desiccated leaves (Piatkowski et al., 1990, Plant Physiol. 94: 1682-1688).; putative.
AAA18542.1	M88321	Gossypium hirsutum	probable desiccation protectant. Group 4 late embryogenesis-abundant protein. Lea14-A. putative.
AAD25354.1	AF115314	Glycine max	possible desiccation protectant. seed maturation protein PM22. PM22. similar to desiccation protectant protein encoded by GenBank Accession Number U08108; late embryogenesis abundant protein; LEA protein.
AAF64451.1	AF239929	Euphorbia esula	late-embryogenesis abundant protein. similar to desiccation protectant protein and late-embryogenesis abundant protein LEA14.
AAB96796.1	U77719	Lycopersicon esculentum	ethylene-responsive late embryogenesis-like protein. ER5. LEA-like protein; drought-inducible; ABA-inducible; putative desiccation protectant protein; similar to cotton Lea14A product encoded by GenBank Accession Number M88321.
SEQ ID NO: 345			
AAF61647.1	AF190634	Nicotiana tabacum	UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
BAA36423.1	AB013598	Verbena x hybrida	UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
BAA89009.1	AB027455	Petunia x hybrida	anthocyanin 5-O-glucosyltransferase. PH1.
BAA36421.1	AB013596	Perilla frutescens	UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.
BAA93039.1	AB033758	Citrus unshiu	limonoid UDP-glucosyltransferase. LGTase.
BAA36422.1	AB013597	Perilla frutescens	UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.
AAF98390.1	AF287143	Brassica napus	catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
BAB07962.1	AP002524	Oryza sativa	putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).

AAAF17077.1	AF199453	<i>Sorghum bicolor</i>	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
AAK16172.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.14.
AAB36653.1	U32644	<i>Nicotiana tabacum</i>	immediate-early salicylate-induced glucosyltransferase. IS5a.
AAK28303.1	AF346431	<i>Nicotiana tabacum</i>	phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
BAA83484.1	AB031274	<i>Scutellaria baicalensis</i>	UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAK16181.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.16.
AAD21086.1	AF127218	<i>Forsythia x intermedia</i>	adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
AAB36652.1	U32643	<i>Nicotiana tabacum</i>	immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	<i>Nicotiana tabacum</i>	phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
CAA59450.1	X85138	<i>Lycopersicon esculentum</i>	twil. homologous to glucosyltransferases.
AAK16178.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.5.
AAK16175.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.15.
AAK16180.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.21.
CAB56231.1	Y18871	<i>Dorotheanthus bellidiformis</i>	betanidin-5-O-glucosyltransferase.
BAA12737.1	D85186	<i>Gentiana triflora</i>	UDP-glucose:flavonoid-3-glucosyltransferase.
AAG25643.1	AF303396	<i>Phaseolus vulgaris</i>	UDP-glucosyltransferase HRA25. putative; defense associated.
BAB41017.1	AB047090	<i>Vitis labrusca</i> x <i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents <i>V. labruscana</i> cv. Ishiharawase.
AAB81683.1	AF000372	<i>Vitis vinifera</i>	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41020.1	AB047093	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
BAB41022.1	AB047095	<i>Vitis vinifera</i>	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.

BAB41019.1	AB047092	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
AAB81682.1	AF000371	Vitis vinifera	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41025.1	AB047098	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
BAB41023.1	AB047096	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
BAB41021.1	AB047094	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
BAB41026.1	AB047099	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
BAB41024.1	AB047097	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.
BAB41018.1	AB047091	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents V. vinifera cv. Centennial.
BAB17182.1	AP002843	Oryza sativa	putative UTP-glucose glucosyltransferase. P0407B12.19.
BAA19659.1	AB002818	Perilla frutescens	flavonoid 3-O-glucosyltransferase. UDP glucose.
BAA89008.1	AB027454	Petunia x hybrida	anthocyanidin 3-O-glucosyltransferase. PGT8.
BAB17176.1	AP002843	Oryza sativa	putative UTP-glucose glucosyltransferase. P0407B12.13.
AAB86473.1	AF028237	Ipomoea purpurea	UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.
SEQ ID NO: 350			
CAA44216.1	X62343	Nicotiana tabacum	cinnamyl-alcohol dehydrogenase. CAD14.
BAA03099.1	D13991	Aralia cordata	cinnamyl alcohol dehydrogenase. cadacl.
CAA79622.1	Z19568	Populus deltoides	lignin biosynthesis. cinnamyl alcohol dehydrogenase.
CAC07423.1	AJ295837	Populus balsamifera subsp. trichocarpa	lignin monomer biosynthesis. cinnamyl alcohol dehydrogenase. cad.
AAF43140.1	AF217957	Populus tremuloides	cinnamyl alcohol dehydrogenase. CAD.
CAA44217.1	X62344	Nicotiana tabacum	cinnamyl-alcohol dehydrogenase. CAD19.
CAA79625.1	Z19573	Medicago sativa	lignin biosynthesis. cinnamyl alcohol dehydrogenase.

AAC35845.1	AF083332	Medicago sativa	cinnamyl-alcohol dehydrogenase. MsaCad2.
AAC07987.1	AF038561	Eucalyptus globulus	catalyses the reduction of cinnamaldehydes to the corresponding cinnamyl alcohols as the last step in the production of lignin monomers. cinnamyl alcohol dehydrogenase. CAD.
CAA46585.1	X65631	Eucalyptus gunnii	cinnamyl-alcohol dehydrogenase. cad.
AAG15553.1	AF294793	Eucalyptus saligna	cinnamyl alcohol dehydrogenase. cad. CAD.
CAA53211.1	X75480	Eucalyptus gunnii	cinnamyl-alcohol dehydrogenase. CAD.
AAB70908.1	AF010290	Lolium perenne	cinnamyl alcohol dehydrogenase. CAD.
CAA74070.1	Y13733	Zea mays	cinnamyl alcohol dehydrogenase. cad.
CAA06687.1	AJ005702	Zea mays	cinnamyl alcohol dehydrogenase. cad.
CAA13177.1	AJ231135	Saccharum officinarum	lignin biosynthesis. cinnamyl alcohol dehydrogenase. cad.
BAA19487.1	D86590	Zinnia elegans	cinnamyl alcohol dehydrogenase. ZCAD1.
CAA51226.1	X72675	Picea abies	cinnamyl-alcohol dehydrogenase.
CAA05097.1	AJ001926	Picea abies	cinnamyl alcohol dehydrogenase. cad8.
CAA05096.1	AJ001925	Picea abies	cinnamyl alcohol dehydrogenase. cad7.
CAA05095.1	AJ001924	Picea abies	cinnamyl alcohol dehydrogenase. cad2.
AAB38774.1	U62394	Pinus radiata	cinnamyl alcohol dehydrogenase. CAD.
AAC31166.1	AF060491	Pinus radiata	cinnamyl alcohol dehydrogenase. CAD.
CAA86073.1	Z37992	Pinus taeda	cinnamyl alcohol dehydrogenase.
CAA86072.1	Z37991	Pinus taeda	cinnamyl alcohol dehydrogenase.
BAA04046.1	D16624	Eucalyptus botryoides	cinnamyl alcohol dehydrogenase. Cad1:Eb:1.
AAD10327.1	U63534	Fragaria x ananassa	catalyzes the reduction of cinnamylaldehydes leading to monolignols. cinnamyl alcohol dehydrogenase. CAD. involved with lignin biosynthesis.

AAK28509.1	AF320110	<i>Fragaria x ananassa</i> cinnamyl alcohol dehydrogenase.
AAB38503.1	U79770	<i>Mesembryanthemum crystallinum</i> cinnamyl-alcohol dehydrogenase Eli3.
AAC35846.1	AF083333	<i>Medicago sativa</i> cinnamyl-alcohol dehydrogenase. MsaCad1.
AAA74882.1	L36823	<i>Stylosanthes humilis</i> cinnamyl-alcohol dehydrogenase. CAD1.
AAF23409.1	AF207552	<i>Brassica napus</i> cinnamyl alcohol dehydrogenase. CADA-1.
AAC15467.1	U24561	<i>Apium graveolens</i> converts mannitol to mannose. mannitol dehydrogenase. Mtd. 1-oxidoreductase; induced with sodium salicylate; similar to the plant defense gene ELI3 in <i>Arabidopsis thaliana</i> , PIR Accession Number S28044; EC number unassigned; MTD.
AAF23411.1	AF207554	<i>Brassica oleracea</i> cinnamyl alcohol dehydrogenase. CADA.
AAF23412.1	AF207555	<i>Brassica rapa</i> cinnamyl alcohol dehydrogenase. CADA.
AAC61854.1	AF067082	<i>Apium graveolens</i> oxidizes mannitol to mannose. mannitol dehydrogenase. Mtd. mannitol 1-oxidoreductase.
AAF23410.1	AF207553	<i>Brassica napus</i> cinnamyl alcohol dehydrogenase. CADA-2.
AAA74883.1	L36456	<i>Stylosanthes humilis</i> cinnamyl-alcohol dehydrogenase. CAD3.
AAD18000.1	AF109157	<i>Eucalyptus globulus</i> cinnamyl alcohol dehydrogenase. CAD.
AAF72100.1	AF146691	<i>Lycopersicon esculentum</i> ELI3. Eli3. similar] to cinnamyl alcohol dehydrogenase.
CAA63410.1	X92754	<i>Hordeum vulgare</i> cinnamyl alcohol dehydrogenase. CAD.
AAF23416.1	AF207559	<i>Brassica rapa</i> cinnamyl alcohol dehydrogenase. CADb.
SEQ ID NO: 351		
AAB71227.1	AF004809	<i>Glycine max</i> Ca ²⁺ -binding EF hand protein. GmPM13. encodes EF-hand motifs.
AAF13743.1	AF109921	<i>Sesamum indicum</i> caleosin. 27 kDa calcium-binding protein.
CAA61981.1	X89891	<i>Oryza sativa</i> EFA27 for EF hand, abscisic acid, 27kD. efa27.
CAB71337.1	AJ250283	<i>Hordeum vulgare</i> putative calcium binding EF-hand protein. bci-4.
CAB42585.1	AJ238627	<i>Chlorella protothecoides</i> putative Ca ⁺⁺ binding protein. dee112.

SEQ ID NO: 353

AAF60316.1 AF236108 Glycine max
putative purple acid phosphatase precursor. PAP. type 5 acid phosphatase.

AAF60315.1 AF236107 Ipomoea batatas
putative purple acid phosphatase precursor. PAP. type 5 acid phosphatase.

AAF60317.1 AF236109 Phaseolus vulgaris
putative purple acid phosphatase precursor. PAP. type 5 acid phosphatase.

SEQ ID NO: 359

CAA55039.1 X78203 Hyoscyamus muticus
glutathione transferase.

AAB65163.1 AF002692 Solanum commersonii
glutathione S-transferase, class-phi. GST1. low temperature induced.

CAA96431.1 Z71749 Nicotiana plumbaginifolia
glutathione S-transferase.

BAA01394.1 D10524 Nicotiana tabacum
glutathione S-transferase. parB.

AAA33930.1 M84968 Silene vulgaris
glutathione-S-transferase.

AAA33931.1 M84969 Silene vulgaris
glutathione-S-transferase.

AAF65767.1 AF242309 Euphorbia esula
glutathione S-transferase. putative auxin-binding GST.

AAF61392.1 AF133894 Persea americana
glutathione S-transferase. GTH.

CAB38119.1 AJ010296 Zea mays
Glutathione transferase III(b). gst3b.

CAB38118.1 AJ010295 Zea mays
Glutathione transferase III(a). gst3a.

BAB39935.1 AP002914 Oryza sativa
putative glutathione S-transferase. P0493G01.17.

AAG34811.1 AF243376 Glycine max
glutathione S-transferase GST 21.

BAB39941.1 AP002914 Oryza sativa
putative glutathione S-transferase. P0493G01.23.

CAA09190.1 AJ010451 Alopecurus myosuroides
glutathione transferase. GST2a.

CAA09192.1 AJ010453 Alopecurus myosuroides
glutathione transferase. GST2c.

CAA09193.1 AJ010454 Alopecurus myosuroides
glutathione transferase. GST2d.

AAG34814.1 AF243379 Glycine max
glutathione S-transferase GST 24.

CAA09191.1	AJ010452	<i>Alopecurus myosuroides</i> glutathione transferase. GST2b.
BAB39939.1	AP002914	<i>Oryza sativa</i> putative glutathione S-transferase. P0493G01.21.
AAG32476.1	AF309383	<i>Oryza sativa</i> subsp. <i>japonica</i> putative glutathione S-transferase OsGSTF4.
AAG34812.1	AF243377	<i>Glycine max</i> glutathione S-transferase GST 22.
BAB39929.1	AP002914	<i>Oryza sativa</i> putative glutathione transferase. P0493G01.7.
CAA39487.1	X56012	<i>Triticum aestivum</i> glutathione transferase. gstA1.
AAD56395.1	AF184059	<i>Triticum aestivum</i> glutathione S-transferase. GST1.
BAB39940.1	AP002914	<i>Oryza sativa</i> putative glutathione S-transferase. P0493G01.22.
CAA68993.1	Y07721	<i>Petunia x hybrida</i> conjugates glutathione to anthocyanin to facilitate transport to the vacuole. glutathione S-transferase. an9 locus.
AAA33469.1	M16902	<i>Zea mays</i> glutathione S-transferase I.
AAG32477.1	AF309384	<i>Oryza sativa</i> subsp. <i>japonica</i> putative glutathione S-transferase OsGSTF3.
AAA33470.1	M16901	<i>Zea mays</i> glutathione S-transferase I.
AAA20585.1	U12679	<i>Zea mays</i> glutathione S-transferase IV. GSTIV.
CAA56047.1	X79515	<i>Zea mays</i> glutathione transferase. GST27.
CAA39480.1	X56004	<i>Triticum aestivum</i> glutathione transferase. gstA2.
AAC64007.1	AF062403	<i>Oryza sativa</i> glutathione S-transferase II.
BAB39927.1	AP002914	<i>Oryza sativa</i> putative glutathione S-transferase. P0493G01.1. contains ESTs AU031696(R0596), C97559(C60386), C28218(C60386), D28287(R0596).
AAG32475.1	AF309382	<i>Oryza sativa</i> subsp. <i>japonica</i> putative glutathione S-transferase OsGSTF5.
AAG34823.1	AF244680	<i>Zea mays</i> glutathione S-transferase GST 15.
AAG34817.1	AF244674	<i>Zea mays</i> glutathione S-transferase GST 9.

CAA05354.1 AJ002380 *Oryza sativa*
glutathione S-transferase. Rgst I.

AAG34820.1 AF244677 *Zea mays*
glutathione S-transferase GST 11.

AAG34821.1 AF244678 *Zea mays*
glutathione S-transferase GST 13.

CAB66333.1 AJ279691 *Betula pendula*
glutathione-S-transferase. gst.

AAG34818.1 AF244675 *Zea mays*
glutathione S-transferase GST 10.

AAG34816.1 AF244673 *Zea mays*
glutathione S-transferase GST 8.

AAG34822.1 AF244679 *Zea mays*
glutathione S-transferase GST 14.

CAA05355.1 AJ002381 *Oryza sativa*
glutathione S-transferase. Rgst II.

SEQ ID NO: 360

AAA33710.1 L16977 *Petunia x hybrida*
glutamate decarboxylase. gad.

AAA33709.1 L16797 *Petunia x hybrida*
glutamate decarboxylase. gad.

AAC24195.1 AF020425 *Nicotiana tabacum*
calmodulin binding protein. glutamate decarboxylase isozyme 1. NtGAD1. calcium-calmodulin-dependent enzyme.

AAB40608.1 U54774 *Nicotiana tabacum*
glutamate decarboxylase. NtGAD1. calmodulin regulated enzyme; calmodulin-binding protein.

AAK18620.1 AF352732 *Nicotiana tabacum*
converts glutamate to gamma-aminobutyric acid. glutamate decarboxylase isozyme 3. GAD; GAD3; NtGAD3; calcium/calmodulin-dependent enzyme.

AAC39483.1 AF020424 *Nicotiana tabacum*
glutamate decarboxylase isozyme 2. NtGAD2. calcium-calmodulin-dependent enzyme.

BAB32870.1 AB056062 *Oryza sativa*
glutamate decarboxylase. GAD.

BAB32868.1 AB056060 *Oryza sativa*
glutamate decarboxylase. GAD.

BAB32869.1 AB056061 *Oryza sativa*
glutamate decarboxylase. GAD.

BAB32871.1 AB056063 *Oryza sativa*
glutamate decarboxylase. GAD.

CAA56812.1 X80840 *Lycopersicon esculentum*
homology to pyrooxal-5'-phosphate-dependant glutamate decarboxylases; putative start codon.

CAA50719.1 X71900 *Lycopersicon esculentum*
histidine decarboxylase. hdc. pyridoxal 5'-phosphate dependant.

SEQ ID NO: 362

AAG13467.1 AC026758 *Oryza sativa*
putative proline oxidase. OSJNBa0015J15.31.

AAD48490.1 AF171226 *Brassica napus*
proline dehydrogenase. pdh.

SEQ ID NO: 363

AAA33967.1 M76981 *Glycine max*
vegetative storage protein. vspA.

AAA34022.1 M76980 *Glycine max*
vegetative storage protein. vspB.

AAA34021.1 M20038 *Glycine max*
vegetative storage protein.

BAA23563.1 D50094 *Phaseolus vulgaris*
pod storage protein.

BAA19152.1 AB000585 *Phaseolus vulgaris*
pod storage protein. PSP.

AAA34020.1 M20037 *Glycine max*
vegetative storage protein.

SEQ ID NO: 364

AAB86939.1 AF030387 *Oryza sativa*
NOI protein.

AAC03022.1 AF045033 *Zea mays*
nitrate-induced NOI protein.

AAB86937.1 AF030385 *Zea mays*
nitrate-induced NOI protein.

SEQ ID NO: 366

AAF75824.1 AF101788 *Pinus taeda*
phytoeyanin homolog.

AAC32448.1 U76296 *Spinacia oleracea*
plantacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Plantacyanins; non-glycosylated.

AAC32421.1 U65511 *Cucumis sativus*
 putative oxygen activation and/or lignin formation. stellacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Stellacyanins; similar to *Rhus vernicifera* stellacyanin: SwissProt Accession Number P00302; similar to umecyanin: SwissProt Accession Number P42849; similar to mavicyanin; SwissProt Accession Number P80728; similar to BCB encoded by GenBank Accession Number Z15058; similar to F18A8.9, encoded by GenBank Accession Number AC003105; similar to F7F1.27 encoded by GenBank Accession Number AC004669; similar to F9D12.16 encoded by GenBank Accession Number AF077407; glycoprotein.

AAF66243.1 AF243181 *Lycopersicon esculentum*
 plantacyanin. naturally occurring cupredoxin with a Val residue in the position of the axial ligand Met; member of the plantacyanin subfamily of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins.

BAA90481.1 AB035146 *Ipomoea nil*
 phytoeyanin-related protein.

SEQ ID NO: 367

AAD11617.1 AF050495 *Lycopersicon esculentum*
 Ca²⁺-ATPase. LCA1A; alternative transcript.

AAA34138.1 M96324 *Lycopersicon esculentum*
 The calcium ATPase is a calcium ion pump. Ca²⁺-ATPase. LCA1.

AAD11618.1 AF050496 *Lycopersicon esculentum*
 Ca²⁺-ATPase. LCA1B; alternative transcript.

CAA63790.1 X93592 *Dunaliella bioculata*
 P-type ATPase. cal. calcium pumping; CA1.

AAF73985.1 AF096871 *Zea mays*
 calcium pump. calcium ATPase. cap1.

AAB58910.1 U82966 *Oryza sativa*
 Ca²⁺-ATPase.

AAG28435.1 AF195028 *Glycine max*
 plasma membrane Ca²⁺-ATPase. SCA1.

AAG28436.1 AF195029 *Glycine max*
 plasma membrane Ca²⁺-ATPase. SCA2.

AAB49042.1 U54690 *Dunaliella acidophila*
 plasma membrane proton ATPase. dha1. DaDHA1; proton pump.

AAB35314.2 S79323 *Vicia faba*
 plasma membrane H(+)-ATPase precursor. plasma membrane H(+)-ATPase. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication.

CAB85495.1 AJ132892 *Medicago truncatula*
 proton pump. H⁺-ATPase. hal.

CAB85494.1 AJ132891 *Medicago truncatula*
 proton pump. H⁺-ATPase. hal.

AAB17186.1 U72148 *Lycopersicon esculentum*
plasma membrane H⁺-ATPase. LHA4. plasma membrane proton pumping ATPase.

CAC29436.1 AJ310524 *Vicia faba*
P-type H⁺-ATPase. ha5. predominantly expressed in guard cells and flowers.

AAB41898.1 U84891 *Mesembryanthemum crystallinum*
plasma membrane proton pump. H⁺-transporting ATPase. PMA.

CAC29435.1 AJ310523 *Vicia faba*
P-type H⁺-ATPase. vha4. predominantly expressed in flowers.

AAF98344.1 AF275745 *Lycopersicon esculentum*
plasma membrane H⁺-ATPase. LHA2. P-type ion pump.

SEQ ID NO: 369

BAB17726.1 AB050900 *Raphanus sativus*
asparagine synthetase. Asn1.

CAA59138.1 X84448 *Brassica oleracea*
asparagine synthase (glutamine-hydrolysing).

AAC16325.1 AF061740 *Elaeagnus umbellata*
asparagine synthetase. AS.

CAA08913.1 AJ009952 *Phaseolus vulgaris*
asparagine synthesis. asparagine synthetase type II. as2.

AAF02775.1 AF190728 *Helianthus annuus*
asparagine synthetase. HAS1.

AAC49613.1 U77678 *Glycine max*
catalyzes the ATP-dependent transfer of the amide group of glutamine to aspartate producing asparagine and glutamate. asparagine synthetase 2. AS2.

AAB81011.1 U89923 *Medicago sativa*
asparagine synthetase.

AAC09952.1 U55874 *Glycine max*
asparagine synthetase.

AAB48058.1 L40327 *Medicago sativa*
asparagine synthetase.

CAA61589.1 X89409 *Lotus japonicus*
asparagine synthase (glutamine-hydrolysing). AS.

CAA67889.1 X99552 *Asparagus officinalis*
asparagine synthetase.

AAF74755.1 AF263432 *Helianthus annuus*
asparagine synthetase. HAS1.1.

AAD05035.1 AF014057 *Triphysaria versicolor*
asparagine synthetase. AS. glutamine-hydrolyzing.

AAD05034.1 AF014056 *Triphysaria versicolor*
asparagine synthetase. AS. glutamine-hydrolyzing.

AAD05033.1 AF014055 *Triphysaria versicolor*
asparagine synthetase. AS. glutamine-hydrolyzing.

CAA96526.1	Z72354	Vicia faba	synthesis of asparagine from aspartate and glutamine. asparagine synthetase. VfAS1.
CAA48141.1	X67958	Asparagus officinalis	asparagine synthase (glutamine-hydrolysing).
CAA61590.1	X89410	Lotus japonicus	asparagine synthase (glutamine-hydrolysing). AS.
CAA36429.1	X52179	Pisum sativum	asparagine synthase (glutamine-hydrolysing).
BAA96252.1	AB035248	Astragalus sinicus	asparagine synthetase. AsAS2.
CAA36430.1	X52180	Pisum sativum	asparagine synthase (glutamine-hydrolysing).
BAA96251.1	AB035247	Astragalus sinicus	asparagine synthetase. AsAS1.
CAB57292.1	AJ133522	Phaseolus vulgaris	asparagine synthetase (type-I). as1.
AAC49614.1	U77679	Glycine max	catalyzes the ATP-dependent transfer of the amide group of glutamine to aspartate producing asparagine and glutamate. asparagine synthetase 1. AS1.
BAA18951.1	D83378	Oryza sativa	asparagine synthetase.
AAB03991.1	U55873	Oryza sativa	asparagine synthetase.
AAF02776.1	AF190729	Helianthus annuus	asparagine synthetase. HAS2.
AAB71532.1	AF005724	Sandersonia aurantiaca	role in flower senescence. asparagine synthetase. SAND1.
CAA58052.1	X82849	Zea mays	asparagine synthetase. AS.
AAB91481.1	AF037363	Helianthus annuus	asparagine synthetase.
CAA73762.1	Y13321	Pisum sativum	asparagine synthetase 1. AS1.
CAA73763.1	Y13322	Pisum sativum	asparagine synthetase 2. AS2.
BAA96452.1	AB021793	Pyrus pyrifolia	asparagine synthetase. PPFRU32.
AAA73943.1	L23833	Glycine max	production of phosphoribosylamine using glutamine and phosphoribosylpyrophosphate as substrates. glutamine phosphoribosylpyrophosphate amidotransferase.

SEQ ID NO: 370

AAG21985.1 AF271636 Zea mays
lysine ketoglutarate reductase/saccharopine dehydrogenase. LKRSDH. bifunctional enzyme;
LKR/SDH; lysine 2-oxoglutarate reductase/saccharopine dehydrogenase.

AAC18622.2 AF003551 Zea mays
lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme.

AAG28387.1 AF191667 Brassica oleracea
lysine-ketoglutarate reductase/saccharopine dehydrogenase.

AAG28386.1 AF191666 Brassica napus
lysine-ketoglutarate reductase/saccharopine dehydrogenase.

AAB97685.1 AF042184 Brassica napus
lysine-ketoglutarate reductase/saccharopine dehydrogenase.

AAG14462.1 AF293461 Brassica napus
lysine-ketoglutarate reductase. LKR.

SEQ ID NO: 371

CAB62537.1 AJ012583 Hevea brasiliensis
pseudo-hevein.

AAA33357.1 M36986 Hevea brasiliensis
hevein (HEV1) precursor.

CAA05978.1 AJ003196 Hevea brasiliensis
N-acetyl-D-glucosamine/N-acetyl-D-neuraminic acid binding lectin. prohevein.

AAF61435.1 AF137352 Pisum sativum
pre-hevein-like protein. PHLP. stress-induced; the coding region is putative in the 5' end.

SEQ ID NO: 372

AAG28503.1 AF196966 Citrus sinensis
hexokinase.

AAF18584.1 AF118132 Spinacia oleracea
chloroplast outer envelope hexokinase 1. Hxk1.

AAF18585.1 AF118133 Nicotiana tabacum
chloroplast outer envelope hexokinase 1. Hxk1.

AAF14186.1 AF106068 Solanum tuberosum
hexokinase 2.

AAG35735.1 AF208543 Lycopersicon esculentum
hexokinase. Hxk2.

CAA63966.1 X94302 Solanum tuberosum
hexokinase. hxk.

BAA99425.1 AP002743 Oryza sativa
putative chloroplast outer envelope hexokinase 1. P0710E05.10.

SEQ ID NO: 374

AAC83688.2 AF083343 Nicotiana tabacum
101 kDa heat shock protein. HSP101.

AAF01280.1 AF174433 Triticum aestivum
heat shock protein 101. HSP101. ClpB family member.

AAD33606.1 AF133840 *Zea mays*
heat shock protein HSP101. HSP101. 101 kDa protein.

AAD25223.1 AF077337 *Zea mays*
heat shock protein 101. HSP101. ClpB/Hsp100 protein homolog; 101 kDa heat shock protein.

AAF91178.1 AF203700 *Phaseolus lunatus*
ClpB. clpB. heat shock protein HSP100.

AAD22629.1 AF097363 *Triticum aestivum*
heat shock protein 101. Hsp101a.

AAC83689.2 AF083344 *Triticum aestivum*
101 kDa heat shock protein. HSP101.

AAD26530.1 AF083327 *Zea mays*
101 kDa heat shock protein. HSP101. similar to HSP100/ClpB; HSP104.

SEQ ID NO: 375

CAA04611.1 AJ001208 *Brassica juncea*
APS reductase. apsr8. putative mitochondrial or plastidic transit peptide.

CAA04610.1 AJ001207 *Brassica juncea*
APS reductase. apsr2. putative mitochondrial or plastidic transit peptide.

AAB05871.2 U63784 *Catharanthus roseus*
reduction of adenylyl sulfate (APS). PAPS-reductase-like protein. par2neu.

CAB65911.1 AJ249831 *Lemna minor*
APR reducing enzyme, sulphur assimilation. adenosine 5'-phosphosulphate reductase. lapr.

AAF18999.1 AF212155 *Allium cepa*
APS-reductase.

AAC26855.1 AF069951 *Enteromorpha intestinalis*
catalyzes the formation of sulfite and 5'-AMP from APS and reduced glutathione. 5'-adenylylsulfate reductase. EAPR1; sulfate assimilation enzyme; similar to Escherichia coli 3'-phosphoadenosine, 5'-phosphosulfate (PAPS) reductase encoded by cysH.

AAD02069.1 AF036939 *Chlamydomonas reinhardtii*
redox-regulator of 5'UTR psbA mRNA binding complex and translation. protein disulfide isomerase. localized to ER and chloroplast.

AAC49896.1 AF027727 *Chlamydomonas reinhardtii*
involved in the redox-regulated binding of chloroplast poly(A)-binding protein to the 5'-UTR of psbA mRNA; regulates chloroplast translational activation. protein disulfide isomerase RB60. PDI.

SEQ ID NO: 376

AAC62017.1 AF077547 *Brassica juncea*
arginine decarboxylase.

AAF26434.1 AF220097 *Brassica juncea*
arginine decarboxylase.

AAF26435.1 AF220098 *Brassica juncea*
arginine decarboxylase.

AAB60880.1 AF002017 *Dianthus caryophyllus*
arginine decarboxylase. gCARADC8.

AAF42972.1	AF127241	Nicotiana tabacum	arginine decarboxylase 2. ADC2.
BAA25685.1	AB012873	Nicotiana sylvestris	arginine decarboxylase. NsADC-1.
CAA85773.1	Z37540	Pisum sativum	arginine decarboxylase.
CAB64599.1	AJ251898	Datura stramonium	polyamine biosynthesis. arginine decarboxylase 1. adcl.
AAD09204.1	U35367	Glycine max	arginine decarboxylase.
BAA84799.1	AP000559	Oryza sativa	ESTs C99670(E21043),C99671(E21043), AU078262(R10938),AU078261(R10938),D15282(C0402) correspond to a region of the predicted gene.; Similar to arginine decarboxylase (U52851).
AAB67887.1	U63832	Dianthus caryophyllus	arginine decarboxylase. ADC.
AAF42971.1	AF127240	Nicotiana tabacum	arginine decarboxylase 1. ADC1.
AAF42970.1	AF127239	Nicotiana tabacum	arginine decarboxylase 1. ADC1.
AAC68511.1	AF045666	Theobroma cacao	arginine decarboxylase. spe2.
CAA65585.1	X96791	Vitis vinifera	arginine decarboxylase. ADC.
AAA61347.1	L16582	Lycopersicon esculentum	decarboxylation of L-arginine. arginine decarboxylase.
AAC68530.1	AF045685	Arabidopsis arenosa	arginine decarboxylase. spe2.
AAC68529.1	AF045684	Capsella bursa-pastoris	arginine decarboxylase. spe2.
AAC68525.1	AF045680	Arabis drummondii	arginine decarboxylase. spe2.
AAC68526.1	AF045681	Barbarea vulgaris	arginine decarboxylase. spe2.
AAC68535.1	AF045690	Nasturtium officinale	arginine decarboxylase. spe2.
AAC68534.1	AF045689	Thellungiella salsuginea	arginine decarboxylase. spe2.
AAC68533.1	AF045688	Thlaspi arvense	arginine decarboxylase. spe2.
AAC68532.1	AF045687	Stanleya pinnata	arginine decarboxylase. spe2.

AAC68531.1	AF045686	Sisymbrium altissimum
arginine decarboxylase. spe2.		
AAC68510.1	AF045665	Aethionema grandiflora
arginine decarboxylase. spe2.		
AAC68528.1	AF045683	Brassica oleracea
arginine decarboxylase. spe2.		
AAC68519.1	AF045674	Arabidopsis arenosa
arginine decarboxylase. spe2.		
AAC68527.1	AF045682	Brassica nigra
arginine decarboxylase. spe2.		
AAC68523.1	AF045678	Thellungiella salsuginea
arginine decarboxylase. spe2.		
AAC68514.1	AF045669	Arabis drummondii
arginine decarboxylase. spe2.		
AAC68524.1	AF045679	Nasturtium officinale
arginine decarboxylase. spe2.		
AAC68522.1	AF045677	Thlaspi arvense
arginine decarboxylase. spe2.		
AAC68513.1	AF045668	Polanisia dodecandra
arginine decarboxylase. spe2.		
AAC68518.1	AF045673	Capsella bursa-pastoris
arginine decarboxylase. spe2.		
AAC68515.1	AF045670	Barbarea vulgaris
arginine decarboxylase. spe2.		
AAC68521.1	AF045676	Stanleya pinnata
arginine decarboxylase. spe2.		
AAC68520.1	AF045675	Sisymbrium altissimum
arginine decarboxylase. spe2.		
AAC68517.1	AF045672	Brassica oleracea
arginine decarboxylase. spe2.		
AAC68516.1	AF045671	Brassica nigra
arginine decarboxylase. spe2.		
AAC68512.1	AF045667	Carica papaya
arginine decarboxylase. spe2.		
CAA40137.1	X56802	Avena sativa
arginine decarboxylase. spe1.		
AAD24801.1	AF132498	Brassica napus
arginine decarboxylase. ADC.		
BAA21617.1	AB005880	Nicotiana tabacum
arginine decarboxylase.		
AAB82607.1	AF026809	Ipomoea nil
arginine decarboxylase. adc.		

SEQ ID NO: 377

- AAG22606.1 AF258809 *Lycopersicon esculentum*
aldehyde oxidase. AO2. molybdenum cofactor-binding enzyme.
- BAA23226.1 D88451 *Zea mays*
aldehyde oxidase. zmAO-1.
- AAG22607.1 AF258810 *Lycopersicon esculentum*
aldehyde oxidase. AO3. molybdenum cofactor-binding enzyme.
- AAG22605.1 AF258808 *Lycopersicon esculentum*
aldehyde oxidase. AO1. molybdenum cofactor-binding enzyme.
- BAA23227.1 D88452 *Zea mays*
aldehyde oxidase-2. zmAO-2. putative.
- AAB41742.1 U82559 *Lycopersicon esculentum*
aldehyde oxidase 1 homolog. TAO1. has sequence properties of the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a multigene family.
- AAG22608.1 AF259793 *Lycopersicon esculentum*
aldehyde oxidase. AO1. molybdenum cofactor-binding enzyme.
- AAB41741.1 U82558 *Lycopersicon esculentum*
aldehyde oxidase 1 homolog. TAO1. has sequence properties of the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a multigene family.

SEQ ID NO: 378

- BAB21211.1 AP002913 *Oryza sativa*
putative DNA binding protein RAV2. P0480E02.17.
- BAB21218.1 AP002913 *Oryza sativa*
putative DNA binding protein RAV2. P0480E02.24.
- BAA90643.1 AP001129 *Oryza sativa*
Similar to *Arabidopsis thaliana* chromosome II BAC F11F19 genomic sequence, putative DNA-binding protein RAV2. (AC007017).
- BAA85426.1 AP000616 *Oryza sativa*
similar to putative DNA-binding protein RAV2 (AC007017).

SEQ ID NO: 380

- CAB65369.1 AJ250832 *Pisum sativum*
germin-like protein. ger1.
- AAF03355.1 AF132671 *Nicotiana plumbaginifolia*
nectarin I precursor. NEC1. germin-like protein.
- AAD38298.1 AC007789 *Oryza sativa*
putative oxalate oxidase (germin protein). OSJNBa0049B20.25.
- BAB18339.1 AP002865 *Oryza sativa*
putative germin protein. P0034C11.30. contains EST C97263(C53484).
- BAA25197.1 AB012138 *Lycopersicon esculentum*
adaptation to Mn-deficiency. germin-like protein. Mdip1.

AAC78470.1	AF067731	Solanum tuberosum	germin-like protein. OXAOXA. similar to oxalate oxidase.
AAC04835.1	AF032974	Oryza sativa	germin-like protein 4. GER4. similar to wheat and barley oxalate oxidase.
BAB39980.1	AP003020	Oryza sativa	probable germin protein 4. P0498A12.8. contains ESTs AU101991(S4037),AU070167(R0031).
BAB39965.1	AP003018	Oryza sativa	probable germin protein 4. OSJNBa0004B13.19. contains ESTs AU101991(S4037),AU070167(R0031).
AAC04833.1	AF032972	Oryza sativa	germin-like protein 2. GER2. similar to wheat and barley oxalate oxidase.
AAG00425.1	AF250933	Hordeum vulgare	germin A. GerA. apoplastic protein; contains prepeptide for targeting into the cell wall.
AAD43972.1	AF141879	Oryza sativa	germin-like protein 2 precursor. RGLP2. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.
AAD43973.1	AF141880	Oryza sativa	germin-like protein 1 precursor. RGLP1. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.
AAD43971.1	AF141878	Oryza sativa	germin-like protein 1 precursor. RGLP1. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.
CAB55559.1	AJ237943	Triticum aestivum	germin-like protein. glp2b.
CAB55558.1	AJ237942	Triticum aestivum	germin-like protein. glp2a.
AAC04837.1	AF032976	Oryza sativa	germin-like protein 6. GER6. similar to wheat and barley oxalate oxidase.
AAC04832.1	AF032971	Oryza sativa	germin-like protein 1. GER1. similar to wheat and barley oxalate oxidase.
CAA63659.1	X93171	Hordeum vulgare	oxalate oxidase-like protein or germin-like protein.
CAB55394.1	AL117264	Oryza sativa	zwh0010.1. similar to Arabidopsis germin-like protein 6 (AF032976); Method: conceptual translation with partial peptide sequencing.
AAB97470.1	AF042489	Oryza sativa	germin-like protein 16. glp16.
AAC25777.1	AF072694	Oryza sativa	germin-like protein 7. GER7. similar to wheat and barley oxalate oxidase.
AAG00427.1	AF250935	Hordeum vulgare	germin F. GerF. apoplastic protein; contains prepeptide for targeting into the cell wall.

AAG00426.1	AF250934	Hordeum vulgare	germin B. GerB. apoplastic protein; contains prepeptide for targeting into the cell wall.
BAA78563.1	AB024338	Atriplex lentiformis	germin-like protein.
AAA20245.1	U01963	Hordeum vulgare	germin subunit.
AAG00428.1	AF250936	Hordeum vulgare	germin D. GerD. apoplastic protein; contains prepeptide for targeting into the cell wall.
AAC99473.1	AF039201	Pinus caribaea	germin-like protein. PcGER1.
AAC04834.1	AF032973	Oryza sativa	germin-like protein 3. GER3. similar to wheat and barley oxalate oxidase.
AAA34271.1	M63224	Triticum aestivum	germin. germin 9f-3.8.
AAC05146.1	AF049065	Pinus radiata	germin-like protein. PRGer1.
AAA34268.1	M21962	Triticum aestivum	germin protein precursor.
AAA34270.1	M63223	Triticum aestivum	germin. germin 9f-2.8.
CAA71052.1	Y09917	Triticum aestivum	germin homolog. pSBGer3.
AAG00429.1	AF250937	Hordeum vulgare	germin E. GerE. apoplastic protein.
BAA86880.1	AB028454	Barbula unguiculata	germin-like protein.
CAB65370.1	AJ250833	Pisum sativum	germin-like protein. ger2a. 1st variant of this clone.
AAA33030.1	M93041	Mesembryanthemum crystallinum	germin-like protein. germin-like protein.
CAB65371.1	AJ250834	Pisum sativum	germin-like protein. ger2b. 2nd variant of the clone PsGER2.
CAA71050.1	Y09915	Triticum aestivum	germin homolog. pSBGer1.
CAA71051.1	Y09916	Triticum aestivum	germin homolog. pSBGer2.
AAA86365.1	U21743	Brassica napus	germin-like protein. similar to product encoded by GenBank Accession Number X84786.
CAC34417.1	AJ311624	Pisum sativum	Germin-like protein. glp3.

SEQ ID NO: 389